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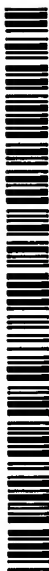


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(54) Title: BREAST, GASTRIC AND PROSTATE CANCER ASSOCIATED ANTIGENS AND USES THEREFOR

(57) Abstract: Cancer associated antigens have been identified by autologous antibody screening of libraries of nucleic acids expressed in breast, gastric and prostate cancer cells using antisera from cancer patients. The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with cancer. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and cytotoxic T lymphocytes which recognize the proteins and peptides. Fragments of the foregoing including functional fragments and variants also are provided. Kits containing the foregoing molecules additionally are provided. The molecules provided by the invention can be used in the diagnosis, monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

**BREAST, GASTRIC AND PROSTATE CANCER ASSOCIATED**  
**ANTIGENS AND USES THEREFOR**

**Field of the Invention**

5       The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with breast, gastric or prostate cancer. The invention also relates to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules, polypeptides coded for by such molecules and peptides derived therefrom, as well as related antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and  
10   therapeutic contexts.

**Background of the Invention**

      The mechanism by which T cells recognize foreign materials has been implicated in cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous  
15   melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been described. In many instances, the antigens recognized by these clones have been characterized.

      The use of autologous CTLs for identifying tumor antigens requires that the target cells which express the antigens can be cultured *in vitro* and that stable lines of autologous  
20   CTL clones which recognize the antigen-expressing cells can be isolated and propagated. While this approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers including breast and colon cancer, have proved refractory to the approach.

      More recently another approach to the problem has been described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous  
25   antisera are used to identify immunogenic protein antigens expressed in cancer cells by screening expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified have been found to elicit a high-titer humoral immune response in the patients from which the antisera were obtained. Such a high-titer IgG response implies helper T cell recognition of the detected antigen. These tumor antigens can then be screened for the  
30   presence of MHC/HLA class I and class II motifs and reactivity with CTLs.

      Since the individual tumor antigens presently known may be expressed only in a fraction of tumors, the availability of additional tumor antigens would significantly enlarge the



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proportion of patients who are potentially eligible for therapeutic interventions. Thus there presently is a need for additional tumor antigens for development of therapeutics and diagnostics applicable to a greater number of cancer patients having various cancers.

The invention is elaborated upon further in the disclosure which follows.

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### **Summary of the Invention**

Autologous antibody screening has now been applied to breast, gastric and prostate cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression  
10 vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis,  
15 monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of several genes, some previously known and some previously unknown, which are expressed in  
20 individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials  
25 and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials and optionally other cancer associated antigen genes and/or gene products can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can  
30 involve 2, 3, 4, 5 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a plurality of such

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materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses, including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention by, for example, quantifying the expression of such gene products. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer. Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 5 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 5 nucleic acids, (g) and agent that binds to a complex of an

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MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (i) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 5 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors. Thus the methods of diagnosis may include use of a plurality of agents, each of which is specific for a different human cancer associated antigen precursor (including at least one of the cancer associated antigen precursors disclosed herein), and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents. Any of the diagnostic methods disclosed herein can be applied sequentially over time to permit determination of the prognosis or progression (or regression) of the disorder.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor, including the breast, gastric and prostate cancer associated antigen precursors disclosed herein.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide. Preferably samples are isolated from tissue or bodily fluids of the subject at

sequential time points, and the samples are assayed as a determination of the regression, progression or onset of the condition from a first sequential time point to a second sequential time point.

According to another embodiment the nucleic acid molecule is one of the following: a  
5 NA Group 3 molecule or a NA Group 5 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different one of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject  
10 enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

15 The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

In another embodiment the agent is selected from the group consisting of (1) an  
20 isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional variants thereof, and an HLA molecule.

25 The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.  
30 The cell can express one or both of the polypeptide and HLA molecule recombinantly. In preferred embodiments the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a

different human cancer associated antigen or functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also  
5 includes an adjuvant.

According to another aspect the invention, a composition is provided which includes an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 2 polypeptide, a PP Group 3 polypeptide, a PP Group 4 polypeptide, and a PP Group 5  
10 polypeptide. In other embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic  
15 agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

The invention in another aspect is a pharmaceutical composition which includes an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one  
20 embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a  
25 promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP  
30 Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

In another embodiment the isolated polypeptide comprises at least two different

polypeptides, each comprising a different cancer associated antigen at least one of which is encoded by a NA group 1 molecule as disclosed herein. In separate embodiments the isolated polypeptides are selected from the following: breast cancer polypeptides or HLA binding fragments thereof and gastric cancer polypeptides or HLA binding fragments thereof.

5 In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule.

10 The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID Nos:1-593, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a  
15 sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of Table 1 and other sequences publicly available as of the filing date of this application, (2) complements of (1), and (3) fragments of (1) and (2). Preferably the unique fragments are fragments of a nucleic acid selected from the group of nucleic acid molecules consisting of  
20 SEQ ID NOs:12, 15, 34-59, 61, 62, 83-95, 186, 190-205, 297, 327-332, and 335-352.

In one embodiment the sequence of contiguous nucleotides is selected from the group consisting of: (1) at least two contiguous nucleotides nonidentical to the sequences in Table 1, (2) at least three contiguous nucleotides nonidentical to the sequences in Table 1, (3) at least four contiguous nucleotides nonidentical to the sequences in Table 1, (4) at least five  
25 contiguous nucleotides nonidentical to the sequences in Table 1, (5) at least six contiguous nucleotides nonidentical to the sequences in Table 1, or (6) at least seven contiguous nucleotides nonidentical to the sequences in Table 1.

In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18  
30 nucleotides, 20 nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides and every integer length therebetween.

In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor (e.g., class I or class II) or a human antibody.

Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

5        According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an MHC, preferably HLA, molecule.

10       In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

      In another aspect the invention is a host cell transformed or transfected with an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and  
15       further comprising a nucleic acid encoding HLA.

      According to another aspect of the invention an isolated polypeptide encoded by the isolated nucleic acid molecules of the invention, described above, is provided. These include PP Group 1-5 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA  
20       or a human antibody.

      The invention includes in another aspect an isolated fragment of a human cancer associated antigen precursor which, or a portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the  
25       fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

      According to another aspect of the invention a kit for detecting the presence of the  
30       expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence

of any of the NA Group 1 molecules and (b) complements of (a), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

5           According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human  
10 cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 5 nucleic acid molecules.

15           In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

20           In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, and PP group 5 polypeptides.

          In yet another embodiment the disorder is cancer.

          According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the  
25 subject. The method includes the steps of (i) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated  
30 antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of



NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

5 The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (i) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid molecule selected from the group  
10 consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid molecule identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to  
15 increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the  
20 host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T  
25 cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

30 Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the

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step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein.

The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (i) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells; (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody, a humanized antibody or a fragment thereof. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The invention includes in another aspect a composition of matter useful in stimulating

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an immune response to a plurality of proteins encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

5 In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin. In still another embodiment, the compositions also includes at least one peptide useful in stimulating an immune response to at least one protein which is not encoded  
10 by nucleic acid molecules that are NA Group 1 molecules, wherein the at least one peptide binds to one or more MHC molecules.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (i) a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to  
15 form the complex, wherein the isolated antibody does not bind to (i) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody, a humanized antibody or a fragment thereof.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular  
20 medicament is for treating cancers including, e.g., one or more of cancers of the breast, cervix, ovary, prostate, testis, lung, colon, pancreas, stomach, liver, skin (e.g., melanoma), bladder, head and neck, thyroid, blood cells, bone and kidney. Diagnostics for specific cancers and groups of cancers also are envisioned.

In certain preferred embodimenst, the nucleic acid molecules are selected from the  
25 group consisting of SEQ ID NOs:1-18, and the polypeptides are encoded by these preferred nucleic acid molecules.

Still other embodiments and aspects of the invention will become apparent in connection with the description of the invention which follows.

### 30 **Detailed Description of the Invention**

In the above summary and in the ensuing description, lists of sequences are provided. The lists are meant to embrace each single sequence separately, two or more sequences

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together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the sequence (less one nucleotide or amino acid so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be  
5 between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the coding region of the isolated DNA and the antigen is a peptide which complexes with MHC,  
10 preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are  
15 preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having breast, gastric or prostate cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing. Of  
20 the foregoing, it can be seen that some of the clones are considered completely novel as no coding regions were found in the databases searched. Other clones are novel but have some nucleotide or amino acid homologies to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not  
25 known that the gene was associated with cancer, or with a particular cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with an antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also  
30 presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides,

genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application  
5 contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

#### Nucleic Acid Sequences

- 10 NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs: 1-593, and which code for a cancer associated antigen precursor,
- (b) deletions, additions and substitutions which code for a respective cancer  
15 associated antigen precursor,
- (c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and
- (d) complements of (a), (b) or (c).
- 20 NA Group 2. Fragments of NA Group 1, which code for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.
- NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the  
25 group consisting of:
- (a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor, e.g., SEQ ID NOs:12, 15, 34-59, 61, 62, 83-95, 186, 190-205, 297, 327-332, and 335-352,
- (b) deletions, additions and substitutions which code for a respective human  
30 cancer associated antigen precursor,
- (c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

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(d) complements of (a), (b) or (c).

NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody  
5 or lymphocyte.

NA Group 5. A subset of NA Group 1, comprising human cancer associated antigens that react with allogeneic cancer antisera.

10 Polypeptide Sequences

- PP Group 1. Polypeptides encoded by NA Group 1.  
PP Group 2. Polypeptides encoded by NA Group 2.  
PP Group 3. Polypeptides encoded by NA Group 3.  
PP Group 4. Polypeptides encoded by NA Group 4.  
15 PP Group 5. Polypeptides encoded by NA Group 5.

Particularly preferred polypeptides are those recognized by allogeneic sera of cancer patients, but not by non-cancer patient control sera. For example, as shown in the Examples below, polypeptides encoded by SEQ ID NOs:1-18 are recognized only by antibodies in  
20 cancer patients antisera.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989,  
25 or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5 mM NaH<sub>2</sub>PO<sub>4</sub>(pH7), 0.5% SDS, 2 mM EDTA). SSC is 0.15 M sodium chloride/0.15 M sodium citrate, pH7; SDS is sodium dodecyl  
30 sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

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There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 80% nucleotide identity and/or at least 90% amino acid identity to the sequences of cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 90% nucleotide identity and/or at least 95% amino acid identity and in still other instances will share at least 95% nucleotide identity and/or at least 99% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the Internet (<ftp://ncbi.nlm.nih.gov/pub/>). Exemplary tools include the BLAST system available at <http://www.ncbi.nlm.nih.gov>, preferably using default settings. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyle-Doolittle hydropathic analysis can be obtained using the MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions can be performed on samples taken from breast, gastric or prostate cancer patients or subjects suspected of having a condition characterized by expression of the cancer associated antigen genes disclosed herein. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast, gastric and prostate cancer associated genes correspond to SEQ ID Nos: 1-593. These sequences represent genes previously known in humans and genes previously

unknown in humans (e.g., SEQ ID NOs: 12, 15, 34-59, 61, 62, 83-95, 186, 190-205, 297, 327-332, and 335-352). Preferred breast, gastric and prostate cancer associated antigens for the methods of diagnosis disclosed herein are those which encode polypeptides that react with allogeneic cancer antisera (i.e. NA Group 5). Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

As used herein with respect to nucleic acids, the term "isolated" means: (i) amplified *in vitro* by, for example, polymerase chain reaction (PCR); (ii) recombinantly produced by cloning; (iii) purified, as by cleavage and gel separation; or (iv) synthesized by, for example, chemical synthesis. An isolated nucleic acid is one which is readily manipulable by recombinant DNA techniques well known in the art. Thus, a nucleotide sequence contained in a vector in which 5' and 3' restriction sites are known or for which polymerase chain reaction (PCR) primer sequences have been disclosed is considered isolated but a nucleic acid sequence existing in its native state in its natural host is not. An isolated nucleic acid may be substantially purified, but need not be. For example, a nucleic acid that is isolated within a cloning or expression vector is not pure in that it may comprise only a tiny percentage of the material in the cell in which it resides. Such a nucleic acid is isolated, however, as the term is used herein because it is readily manipulable by standard techniques known to those of ordinary skill in the art. An isolated nucleic acid as used herein is not a naturally occurring chromosome.

As used herein with respect to polypeptides, "isolated" means separated from its native environment and present in sufficient quantity to permit its identification or use. Isolated, when referring to a protein or polypeptide, means, for example: (i) selectively produced by expression cloning or (ii) purified as by chromatography or electrophoresis. Isolated proteins or polypeptides may be, but need not be, substantially pure. The term "substantially pure" means that the proteins or polypeptides are essentially free of other substances with which they may be found in nature or *in vivo* systems to an extent practical and appropriate for their intended use. Substantially pure polypeptides may be produced by techniques well known in the art. Because an isolated protein may be admixed with a pharmaceutically acceptable carrier in a pharmaceutical preparation, the protein may comprise only a small percentage by weight of the preparation. The protein is nonetheless isolated in that it has been separated from the substances with which it may be associated in living systems, i.e. isolated from other proteins.



The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA, CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus, the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides modified nucleic acid molecules which include additions, substitutions and deletions of one or more nucleotides. In preferred embodiments, these modified nucleic acid molecules and/or the polypeptides they encode retain at least one activity or function of the unmodified nucleic acid molecule and/or the polypeptides, such as antigenicity, enzymatic activity, receptor binding, formation of complexes by binding of peptides by MHC class I and class II molecules, etc. In certain embodiments, the modified nucleic acid molecules encode modified polypeptides, preferably polypeptides having conservative amino acid substitutions as are described elsewhere herein. The modified nucleic acid molecules are structurally related to the unmodified nucleic acid molecules and in preferred embodiments are sufficiently structurally related to the unmodified nucleic acid molecules so that the modified and unmodified nucleic acid molecules hybridize under stringent conditions known to one of skill in the art.

For example, modified nucleic acid molecules which encode polypeptides having single amino acid changes can be prepared. Each of these nucleic acid molecules can have one, two or three nucleotide substitutions exclusive of nucleotide changes corresponding to the degeneracy of the genetic code as described herein. Likewise, modified nucleic acid molecules which encode polypeptides having two amino acid changes can be prepared which have, e.g., 2-6 nucleotide changes. Numerous modified nucleic acid molecules like these will

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be readily envisioned by one of skill in the art, including for example, substitutions of nucleotides in codons encoding amino acids 2 and 3, 2 and 4, 2 and 5, 2 and 6, and so on. In the foregoing example, each combination of two amino acids is included in the set of modified nucleic acid molecules, as well as all nucleotide substitutions which code for the amino acid substitutions. Additional nucleic acid molecules that encode polypeptides having additional substitutions (i.e., 3 or more), additions or deletions (e.g., by introduction of a stop codon or a splice site(s)) also can be prepared and are embraced by the invention as readily envisioned by one of ordinary skill in the art. Any of the foregoing nucleic acids or polypeptides can be tested by routine experimentation for retention of structural relation or activity to the nucleic acids and/or polypeptides disclosed herein.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of the GenBank accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to

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produce fusion proteins for generating antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments  
5 further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic purposes as described in greater detail below. Unique fragments also can be used to create chimeric nucleic acid molecule or polypeptide molecules by, for example, joining all or part of the unique fragment to another nucleic acid or polypeptide molecule (homologous or not). For example, the  
10 unique fragment may be similar or identical in large part to a known molecule but may have a portion which is nonidentical to the known molecule; the known molecule and the unique fragment can be used to construct a molecule containing in large part the known molecule with the portion unique to the unique fragment added. Other chimeric molecules will be known to one of ordinary skill in the art and can be prepared using standard molecular biology  
15 techniques.

As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13,  
20 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long), up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last  
25 nucleotide (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 25 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the  
30 sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed.

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Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g., Thomson et al., Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generate individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-A1, MAGE-A2, MAGE-A3, MAGE-A4, MAGE-A5, MAGE-A6, MAGE-A7, MAGE-A8, MAGE-A9, MAGE-A10, MAGE-A11, MAGE-A12, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, GAGE-7, GAGE-8, GAGE-9, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-B2, MAGE-B3, MAGE-B4, tyrosinase, brain glycogen phosphorylase, Melan-A, MAGE-C1, MAGE-C2, MAGE-C3, MAGE-C4, MAGE-C5, NY-ESO-1, LAGE-1, SSX-1, SSX-2 (HOM-MEL-40), SSX-4, SSX-5, SCP-1 and CT-7. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of

the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al.,  
5 *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990). For example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are  
10 presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient. Polytopes can be prepared which  
15 correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J. Immunol.*  
20 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

In instances in which a human HLA class I molecule presents tumor rejection antigens  
25 derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the vector contains both coding sequences, the single vector can  
30 be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected.

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The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in  
5 any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide,  
10 to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an  
15 oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby, inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules are designed so as to interfere with transcription or  
20 translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with  
25 the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions. Based upon the sequences of nucleic acids encoding breast, gastric or prostate cancer associated antigens, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for  
30 use in accordance with the present invention. For example, a "gene walk" comprising a series of oligonucleotides of 15-30 nucleotides spanning the length of a cancer associated antigen can be prepared, followed by testing for inhibition of cancer associated antigen expression.

Optionally, gaps of 5-10 nucleotides can be left between the oligonucleotides to reduce the number of oligonucleotides synthesized and tested.

In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive  
5 bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA  
10 transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which  
15 proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic  
20 acids encoding cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end of one native nucleotide and the 3' end of another native nucleotide may be  
25 covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

In preferred embodiments, however, the antisense oligonucleotides of the invention  
30 also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters, alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamides, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding breast, gastric or prostate cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term "physiologically acceptable" refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.



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As used herein, a "vector" may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate autonomously or integrated in the genome in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g.,  $\beta$ -galactosidase, luciferase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be "operably" joined when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription

of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

5       The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region  
10       which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

15       Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a cancer associated antigen polypeptide or fragment or variant thereof.  
20       That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

      Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell  
25       lines) and the human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1 $\alpha$ , which stimulates  
30       efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression

vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996).

5 Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously  
10 mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the cancer  
15 associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the cancer associated antigen nucleic acid, in an arrangement which permits amplification of the cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for  
20 amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" and transgenic overexpression in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and  
25 partial proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed recombinantly in a variety of prokaryotic and  
30 eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such

as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of cancer associated antigens will require longer segments to be unique while others will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more amino acids including each integer up to the full length).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point

mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, substitution of L-amino acids with D-amino acids, and the like.

5 Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997,  
10 whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation. Other computational and computer modeling methods for designing polypeptide mimetics which  
15 retain activity of the polypeptides described herein, as well as selection methods such as phage display of peptide libraries are known in the art.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide  
20 linkages. Similarly, certain amino acids can be changed to enhance expression of a cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide  
25 preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random  
30 mutagenesis of a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be

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made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e., the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g., *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs, one can make

conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpennig

- 5 (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amaro and Drijfhout (D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC.
- 10 These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

- Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated
- 15 antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique
- 20 fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing
- 25 the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

- The invention as described herein has a number of uses, some of which are described
- 30 elsewhere herein. First, the invention permits production and/or isolation of the cancer associated antigen protein molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The

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polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause  
5 production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

10 The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any  
15 standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer  
20 associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or  
25 competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of  
30 the target proteins in response to a cellular signal. Similarly, a dominant negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying



promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of breast, gastric and prostate cancer associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York; Roitt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications, Oxford). The pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has

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been enzymatically cleaved, or which has been produced without the pFc' region, designated an F(ab')<sub>2</sub> fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen  
5 binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

10 Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4)  
15 separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies  
20 while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. See, e.g., U.S. patents 4,816,567, 5,225,539, 5,585,089, 5,693,762 and 5,859,205.

Thus, for example, PCT International Publication Number WO 92/04381 teaches the  
25 production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also  
30 provides for F(ab')<sub>2</sub>, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric F(ab')<sub>2</sub> fragment antibodies in which

the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of

cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technetium-99m, iodine-131 and indium-111, and nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminoglutethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon- $\alpha$ , lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods and compositions, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer associated antigens are expressed. An example of such a disorder is cancer, including

breast, gastric and prostate cancer as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

5 In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include CD34<sup>+</sup> hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer  
10 associated antigen, the immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by  
15 a subject's immune system, leading to lysis of antigen presenting cells, such as breast, gastric or prostate cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a  
20 method for T cell differentiation is presented in International Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell. These transfectants present the desired complex at their surface and, when combined with a CTL of interest, stimulate its  
25 proliferation. COS cells are widely available, as are other suitable host cells. Specific production of CTL clones is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

CTL proliferation can be increased by increasing the level of tryptophan in T cell cultures, by inhibiting enzymes which catabolize tryptophan, such as indoleamine 2,3-  
30 dioxygenase (IDO), or by adding tryptophan to the culture. Proliferation of T cells is enhanced by increasing the rate of proliferation and/or extending the number of divisions of the T cells in culture. In addition, increasing tryptophan in T cell cultures also enhances the

lytic activity of the T cells grown in culture.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of  $\beta_2$ -microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio or 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddell et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-1410, 1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex (e.g., dendritic cells) are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA/cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the invention. CTLs can also be provoked *in vivo*, using a number of approaches. One

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approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114, 1991) exemplifies this approach, showing the use of transfected cells expressing HPV-E7 peptides in a therapeutic regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigens, as described elsewhere herein. Nucleic acids encoding one or more cancer associated antigens also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a *Vaccinia* virus, pox virus, herpes simplex virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, shown in the examples below.

The invention involves the use of various materials disclosed herein to "immunize" subjects or as "vaccines". As used herein, "immunization" or "vaccination" means increasing or activating an immune response against an antigen. It does not require elimination or

eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against cancer using a cancer associated antigen nucleic acid. For example, human cancer cells can be introduced into a mouse to create a tumor, and one or  
5 more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization can include the administration of one or more cancer associated antigen  
10 polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the  
15 presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an  
20 immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include  
25 monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant;  
30 complete Freund's adjuvant; montanide; alum; CpG oligonucleotides (see e.g. Kreig et al., *Nature* 374:546-9, 1995); and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with



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a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 µg to about 100 µg. Other adjuvants are known in the art and can be used in the invention (see, e.g. Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (see, e.g., *Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation (Zheng P., et al. *Proc. Natl. Acad. Sci. USA* 95 (11):6284-6289 (1998)).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity (Gajewski et al., *J. Immunol.*, 154:5637-5648 (1995)). Tumor cell transfection with B7 has been discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., (*J. Immunol.*, 154:1-8 (1995)). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization (Kim J., et al. *Nat Biotechnol.*, 15:7:641-646 (1997)) and recombinant viruses

such as adeno and pox (Wendtner et al., *Gene Ther.*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations. The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be considered. Similarly, the inducible co-stimulatory molecule ICOS which induces T cell responses to foreign antigen could be modulated, for example, by use of anti-ICOS antibodies (Hutloff et al., *Nature* 397:263-266, 1999).

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction (Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother.*, 21:2:95-108 (1998)).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction (Fenton et al., *J. Immunother.*, 21:2:95-108 (1998)). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCs (Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998)). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to enhance a response to tumor antigens which are normally encountered outside of a inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes

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have not been defined within known cancer antigen precursors.

A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner which can interact with cancer associated antigen polypeptides is present in the solution, then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and targeted

liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of viruses and virus-like particles which have been used to deliver exogenous nucleic acids include: replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol.* 71:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venezuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur. J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic

viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA.

Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired  
5 proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging  
10 cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene Transfer and Expression, A Laboratory Manual," W.H. Freeman Co., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic  
15 material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention  
20 into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid- $\text{CaPO}_4$  precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a  
25 vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer  
30 associated antigen, alone or as a complex with a MHC molecule. Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis

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may be incorporated into the liposome formulation for targeting and/or to facilitate uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal.

When cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein.

Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in *Remington's Pharmaceutical Sciences*, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as breast, gastric

or prostate cancers, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to diagnostic methods of the invention discussed  
5 herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and weight, the duration of the treatment, the nature of concurrent therapy (if any), the  
10 specific route of administration and like factors within the knowledge and expertise of the health practitioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of  
15 ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable  
20 for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system by measuring downstream effects such as gene expression, or by measuring the physiological effects of the cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of  
25 ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a  
30 response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

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In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100 µg, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen of variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

When administered, the pharmaceutical compositions of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable preparations. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

A cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the



desired pharmaceutical efficacy.

The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

Compositions suitable for oral administration may be presented as discrete units, such as capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

30

### Examples

#### Example 1: SEREX screening of breast, gastric and prostate cancer cells

Breast, gastric and prostate cancer cDNA libraries were established, using standard

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techniques, and the libraries were screened, using the SEREX methodology described by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), each of which is incorporated by reference in its entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M  
5 guanidinium thiocyanate/0.5% sodium N-lauryl sarcosine/25 mM EDTA followed by centrifugation in 5.7 M CsCl/25 mM sodium acetate/10  $\mu$ M EDTA at 32,000 rpm. Total mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed by taking 5  $\mu$ g of mRNA, using standard methodologies to reverse transcribe the material. Breast cancer libraries were prepared from two different  
10 breast cancer patients, referred to as "MT" and "MK". Gastric cancer libraries were prepared from a gastric cancer patient, referred to as "YS".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF *E. coli*, and incubated for eight hours at 37°C. A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane  
15 was then washed, four times, with Tris buffered saline (TBS) which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of human antibodies (1:2000, diluted in TBS with 1% BSA). The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times  
20 with TBS. Those clones which produced antibodies were visualized with 0.06% 3,3'-diaminobenzidine tetrachloride and 0.015% H<sub>2</sub>O<sub>2</sub>, in 50 mM Tris (pH 7.5). Any clones which produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C.  
25 The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02% Na<sub>3</sub>N. The serum had been treated to remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of *E. coli* Y1090 had been attached, followed by passage over a second column which had *E. coli* lysate and lysate of *E. coli* infected with lambda bacteriophage. The screening was  
30 carried out five times. The samples were then diluted to 50 ml, and kept at -80°C, until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed

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twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the peroxidase labeled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, clones were resolved into known and unknown genes. Some clones corresponded to previously identified human proteins and nucleotide sequences, and other clones have not been identified in humans previously, although there were related molecules found in other species. Still other clones represent molecules for which no related sequences were found (most clones contained very short sections (e.g. 25 or fewer nucleotides) that corresponded to portions of unrelated sequences). Some GenBank accession numbers representative of sequences having homology to the cancer associated antigen nucleotide sequences of the invention are presented in Table 1. All of the homologous sequences are accessible in publicly-available databases by reference to the sequences' accession numbers provided in Table 1.

Breast cancer clones:

The nucleotide sequences of clones derived from breast cancer patients "MT" and "MK" are presented as SEQ ID NOs:1-205. Polypeptides encoded by open reading frames of the nucleic acid clones are presented as SEQ ID Nos: 594-829; the correspondence between nucleic acid molecules and encoded polypeptides is shown in Table 2.

20

Gastric cancer clones:

The nucleotide sequences of clones derived from gastric cancer patient "YS" are presented as SEQ ID NOs:206-352 (clones beginning with "YS"). Polypeptides encoded by open reading frames of the YS nucleic acid clones are presented as SEQ ID Nos:830-1083; the correspondence between nucleic acid molecules and encoded polypeptides is shown in Table 2.

25

Prostate cancer clones

The nucleotide sequences of clones derived from prostate cancer patient "ZH" are presented as SEQ ID NOs:353-593(clones beginning with "ZH"). Polypeptides encoded by open reading frames of the ZH nucleic acid clones are presented as SEQ ID Nos:1084-1332; the correspondence between nucleic acid molecules and encoded polypeptides is shown in

30

Table 2.

**Table 1: Sequence homologies (GenBank Accession Numbers)**

5	SEQ ID NO. 1 NGO-Br-38 combined
10	NM_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, Z47807.1, NM_013559.1, L40406.1, AB005282.1, AB005281.1, AB005280.1, AB023420.1, X67643.1, NM_008300.1, D85904.1, AC011661.5, AE003611.1, AL109620.4, AC007049.8, AC005992.15, AC007066.4, AC006080.1, AC009155.3, AF222716.1, AC009223.2, AC004251.1, AC002367.1, AL161553.2, AL161539.2, AL117202.1, AL009183.10, Z97336.1, AB006696.1, AI658961.1, AW571648.1, AW474070.1, AA843693.1, AW608075.1, AW470142.1, AW572452.1, AA543054.1, AW385582.1, AI742981.1, AW612980.1, AW612983.1, AI582881.1, AI751853.1, AI378269.1, AI920808.1, AI654608.1, AI819251.1, AI831339.1, AI753470.1, AI312753.1, AI803588.1, AI563996.1, AA232636.1, AW015796.1, AW117974.1, AI668853.1, AA535277.1, AA993280.1, AA632202.1, AA912023.1, AW627645.1, AW027050.1, AI337175.1, AI123280.1, AA761750.1, AW316651.1, AI223412.1, AW771160.1, AA219263.1, AW068948.1, AA482770.1, AA166716.1, AW236067.1, AA166806.1, AA485151.1, AI369932.1, AI250881.1, AA933881.1, AI262020.1, AI751852.1, AI050716.1, H52653.1, AI651186.1, AA678506.1, AA582157.1, AW628153.1, AI493255.1, AW340810.1, AI223825.1, AW837156.1, AA136424.1, AA953645.1, AI582484.1, AI673134.1, AW820299.1, AA394027.1, T58153.1, T36072.1, AW390368.1, F22410.1, AA417317.1, AW020035.1, AA278231.1, AI361237.1, AI288972.1, AA810686.1, AW103624.1, AW604836.1, AA730742.1, AA082043.1, Z20100.1, D58216.1, AI799265.1, D29622.1, AA435594.1, AA233888.1, AA485036.1, AI612928.1, AI630481.1, F07487.1, AA731716.1, AA417255.1, AA804371.1, AA571359.1, AA465183.1, F08794.1, T34783.1, Z41841.1, F03714.1, AL137142.8, AC012569.3, AP001563.1, AC022671.2, AC020999.4, AC011743.3, AP000635.1, AP000610.2, AC008070.3, AC022797.3, AC005506.6, AL096782.3,
25	SEQ ID NO. 2 NGO-Br-39 MK262/T3 5'
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- 15 SEQ ID NO. 4  
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- SEQ ID NO. 5  
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NGO-Br-61  
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- 55 -

- AI157598.1, AI750915.1, AI596266.1, AI929865.1, AI790736.1, AI649320.1, AI043196.1, AL023060.1, AW630831.1, AI314622.1, AI314243.1, AI098095.1, AI043182.1, AA511211.1, AA434721.1, AA140498.1, AA098508.1, R74754.1, AW532477.1, AI408553.1, AW750607.1, AV218438.1, AI048358.1, AA458054.1, AI763491.1, AV311575.1, AV005809.1, AA091451.1, D58165.1, AI911938.1, AI548180.1, AA086929.1, AI581089.1, AW822437.1, AW208414.1, AW145984.1, AV159067.1, AI607800.1, AW535768.1, AW822436.1, AI182297.1, AA313132.1, AA799539.1, AI971805.1, AV209231.1, AV207950.1, AV154324.1, AV118302.1, AV175071.1, AC016552.5, AC008499.4, AP001803.1, AP000479.2, AC027649.4, AC012429.4, AL353692.3, AC069214.1, AC024096.7, AC008670.3, AC067813.1, AC021601.3, AC023659.2, AC023818.2, AC009009.2, Z97201.7, AP001815.1,
- 10 SEQ ID NO. 7  
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NGO-Br-60

10 MK746/T7 3'

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## SEQ ID NO.16

NGO-Br-68

30 MK442/T3 5'

AF141968.1, AB033077.1, AB029290.1, AF150755.1, U67205.1, U67204.1, U67203.1, NM\_016615.1, U76343.2, NM\_003263.1, U88540.1, AL161557.2, AL009028.1, D13637.1, AL021635.1, AI734450.1, AW865983.1, AW531012.1, AW405405.1, AW148645.1, AI583168.1, AI290663.1, AA451993.1, AA302993.1, AA297912.1, AA288614.1, AA178091.1, R78273.1, AW816433.1, AW816426.1, AW290918.1, AL133903.1, AV221162.1, AI504039.1, AI403713.1, AI238618.1, H23080.1, AL356055.1, AC019071.3, AC061993.2, AC068911.1, AC025594.3, AC009546.3, AC010537.2, AC010687.2, AC010090.3, AC004229.1, AL354956.1, AL162405.2, AP001098.2,

## SEQ ID NO.17

NGO-Br-68

40 MK442/T7 3'

AF141968.1, AB033077.1, AB029290.1, AF150755.1, U67205.1, U67204.1, U67203.1, AC006299.1, AE003771.1, AC005670.1, AJ277889.1, AL121988.10, AC000111.1, AL031599.1, U27560.1, Z99112.1, L08471.1, AC009415.2, AE003507.1, AC006971.2, AL163258.2, AL135879.1, AL121790.2, AL139074.2, Z35640.1, AJ248288.1, U51998.1, AP001713.1, AP000178.1, AP000034.1, AP000266.1, AP000102.1, AC009236.4, NM\_014514.1, AF105235.1, AF104852.1, AE003845.1, AC005137.1, NM\_004857.1, NM\_003672.1, AF165124.1, AF103013.1, AF103011.1, AF103010.1, U73396.1, AF071085.1, AF022044.1, AF001881.1, AF000367.1, AL132773.14, AL132793.24, AL162691.1, AL049588.11, U30274.1, AL035475.6, L76664.1, L76661.1, L41269.1, X97232.1, X97233.1, X94262.1, M90359.1, AB013389.1, AB010073.1, Z99120.1, Z21839.1, AA418046.1, C43219.1, AW565904.1, AW287353.2, AW285203.1, AW283675.1, AI948261.1, AV165647.1, AA393617.1, Z29935.1, AC068280.2, AC009416.2, AC008414.1, AC013858.1, AC007893.6, AC007892.3, AL121993.6, AL122010.2, AP001002.1, AC055822.2, AC068120.2, AC020995.2, AC036118.2, AC068104.1, AC025117.2, AC027113.2, AC067758.1, AC018587.3, AC012693.1, AC007513.13, AC021104.2, AC068921.2, AC068883.1, AC025459.3, AC008684.4, AC026178.2, AC060785.1, AC053491.1, AC041008.1, AC034223.1, AC008706.2, AC027134.1, AC019101.3, AC026193.1, AC026187.1, AC026171.1, AC021696.3, AC015611.3, AC021556.3, AC021287.4, AC018810.2, AC015475.3, AC017113.3, AC019027.2, AC015011.1, AC010073.1, AL139137.2, AL163543.2, AL122035.2, AL158038.2,

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- AI571784.1, AA640190, AA194089, W58500, AI565383.1, AI381941.1, AA053629, AA480214, W58535, AA503086, AI640364.1, D51182, AA253436, AA250750, AA112892, AI025123, T63135, AA969971, AI610993.1, AI207764, AA024425, AA935715, AA385688, AA043276, AA374540, AA083878, T62991, D31140, AI274547, AA775760, AA252726, AA522501, AA987599, AA172101, AI358015, AA092870, AA412321, T11978, H86668, AI247739, R06066, T86931, H86515, H39234, AA064937, AI502660, AI106368, AI444536, C23347, AU056970.1, H32742, C93950, T37393, AI238361, R04882, T38016, C91449, AR009920, I09636, I23493, I09629, I40358, A22940.1, I12873, A40345.1, AR022373, AR022395, I19103, A22942.1, E13132

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## SEQ ID NO. 96

## NGO-Br-37 combined

NM\_006644.1, AB003333.1, AF039695.1, AB003334.1, D86956.1, NM\_013559.1, D67017.1, D67016.1, L40406.1, Z47807.1, AB005275.1, AB005282.1, AB005281.1, AB005278.1, AB005276.1, AB005274.1, NM\_011020.1, U23921.1, D49482.1, AB001926.1, NM\_014278.1, AB023421.1, L12723.1, AB005279.1, X67643.1, AB005280.1, AF077354.1, NM\_008300.1, AB023420.1, D85904.1, AC011661.5, AL109620.4, L08605.1, AC005851.2, AC011294.3, AI658961.1, AW571648.1, AW474070.1, AW572452.1, AW470142.1, AW608075.1, AW385582.1, AW577563.1, AW820299.1, AA232636.1, AI758907.1, AW859988.1, AW859943.1, AW630933.1, AW820234.1, AW604836.1, AW390368.1, AW316651.1, AW771160.1, AA166806.1, AW820232.1, H63595.1, AI002886.1, AL042714.2, AI751852.1, AW631423.1, H91211.1, H54656.1, AA334479.1, AI651186.1, AA777031.1, AW628153.1, AI223825.1, AA136424.1, AA953645.1, AI582484.1, AA394027.1, AA714219.1, AA805016.1, AW103624.1, AA580845.1, F07487.1, AI288972.1, AI337175.1, F08794.1, AI656127.1, AI633338.1, AI203278.1, AI094015.1, AI800379.1, H64073.1, AW389335.1, Z20100.1, AA094644.1, T63090.1, AI799265.1, AA435594.1, AA580712.1, AA105012.1, AI267631.1, AA777564.1, N84915.1, AA485036.1, AA311379.1, AW206874.1, W86141.1, AA571359.1, AA885873.1, N84914.1, AI290252.1, AA624532.1, Z21219.1, AA811573.1, AW609781.1, AI838486.1, AW020035.1, AW210124.1, AI702970.1, T34627.1, Z21220.1, C81194.1, H63551.1, X85639.1, AW238563.1, H64019.1, AW085874.1, AA278231.1, AA580595.1, H91160.1, AA572403.1, H54657.1, AA571473.1, AA843693.1, AW391561.1, Z41841.1, AA417317.1, W45471.1, AW362751.1, AA867489.1, AA749004.1, AL137142.8, AC015501.3, AC021286.3, AC020834.2, AC044841.2, AC023471.2, AC016715.2, AC018818.3, AL138763.2, AC021531.3, AC005506.6, AC018789.2, AC014468.1, AL162502.2, AL034557.7

## SEQ ID NO. 97

## NGO-Br-37

## MK136/T73'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, Z47807.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, AB005282.1, AB005281.1, AC005371.1, AL163279.2, AE003720.1, AE003562.1, AC006548.20, AC006160.9, AF016672.2, AC005951.1, AC004251.1, AL163234.2, Z92838.1, Z83109.1, Z79753.1, Z71259.1, Z83827.1, AL035258.10, AP001689.1, AP000477.2, AW571648.1, AW572452.1, AW474070.1, AI658961.1, AW470142.1, AW385582.1, AW316651.1, AW608075.1, AA232636.1, AW771160.1, AA166806.1, AA136424.1, AI651186.1, AI223825.1, AI751852.1, AA394027.1, AA435594.1, AI337175.1, AI582484.1, AW628153.1, AW103624.1, AA953645.1, AA485036.1, AI288972.1, AW820299.1, AW390368.1, AI799265.1, Z20100.1, AW085874.1, AW604836.1, AA417317.1, AW609781.1, AW020035.1, AI838486.1, C81194.1, AA624532.1, AA571359.1, AA079853.1, T34627.1, Z21220.1, AA843693.1, AA571473.1, AA572403.1, F07487.1, AA278231.1, F08794.1, T63090.1, AW859988.1, AW859943.1, AW820234.1, AW491178.1, AI842560.1, AV275994.1, AA967441.1, AA856248.1, Z41841.1, AW820232.1, AW389335.1, AA777031.1, AA238818.1, AV347805.1, AI970469.1, AV178670.1, AV141053.1, AI365340.1, AI341168.1, AI115351.1, C56104.1, C55163.1, C54236.1, C54007.1, D64277.1, T26732.1, D33807.1, AL137142.8, AC008689.4, AC010785.3, AC016715.2, AC011743.3, AF129408.1, AC025243.3, AC027399.2, AC026927.2, AC012569.3, AC005506.6, AC009039.5, AC007337.2, AC008361.7, AC021326.1, AC014468.1, AF176680.1, AP001895.1, AP001563.1, AC055800.2, AC027502.3, AC044830.2, AC034128.2, AC008155.6, AC016926.4, AC027359.2, AC027002.2, AC027057.2, AC026650.3, AC020991.3, AC009925.3, AC018954.4, AC024681.2, AC016306.3, AC016997.4, AC019032.3, AC021188.2, AC013110.1, AL109916.3, AL162264.4, AL161653.7, AL138705.3, AL161738.4, AL158817.2, AL138694.5, AL137247.3, AP001803.1, Z98863.1,

## SEQ ID NO. 98

## NGO-Br-37

## MK151/T73'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, Z47807.1, AB005282.1, AB005281.1, AB023420.1, X67643.1, AE003589.1, AC005762.1, AC000119.1, AE003522.1, AE003473.1, AC009223.2, AF030511.1, AF067211.2, AC005951.1, U22892.1, U84144.1, AC002312.1, AX002407.1,



X04465.1, AL034582.11, U77302.1, AL078599.19, AL009183.10, Z74617.1, AL035258.10, X16094.1, M36578.1, L08612.1, X01647.1, AB018706.1, G21718.1, G38495.1, G58719.1, AL144420.1, G03936.1, G27119.1, G22600.1, AL149482.1, AL148977.1, AL145762.1, Z94707.1, AL022449.1, G28140.1, G27716.1, G25125.1, G24942.1, L30947.1, G60761.1, G50693.1, G48927.1, G62261.1, G41307.1, AF052368.1, G28922.1, G19992.1, G16172.1, G12990.1, G36232.1, G35802.1, AL158374.1, AL153532.1, AL153227.1, AL151189.1, AL150403.1, AL148989.1, AL147211.1, AL143371.1, G06747.1, G06621.1, G05724.1, AJ229990.1, Z54069.1, Z67861.1, Z66769.1, Z32058.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC027117.2, AC022671.2, AC015904.3, AC025383.2, AC022797.3, AC020725.3, AC021722.4, AC009039.5, AC007337.2, AC023309.1, AC017242.1, AL353894.3, AL162502.2, AC032034.2, AC008902.3, AC008689.4, AC034128.2, AC027057.2, AC025220.2, AC010912.3, AC017150.1, AL137247.3, AL031745.7,

SEQ ID NO. 99

NGO-Br-37

MK212/T3 5'

NM\_006644.1, AB003333.1, AF039695.1, AB003334.1, D86956.1, NM\_013559.1, D67017.1, D67016.1, L40406.1, Z47807.1, AB005275.1, AB005276.1, AB005278.1, AB005274.1, AF077354.1, NM\_008300.1, D85904.1, NM\_011020.1, U23921.1, D49482.1, AB001926.1, AB023420.1, X67643.1, L12723.1, AC005851.2, AC010852.5, AC003099.1, AP001821.1, AC024813.1, AC004668.1, NM\_005742.1, AC004879.1, AC005870.2, AC006518.17, U73002.1, AF004739.1, U41009.1, D49489.1, AJ002201.1, AB023039.1, L16771.1, X67814.1, AW577563.1, AW630933.1, AI758907.1, H63595.1, AI002886.1, AL042714.2, AW631423.1, H91211.1, H54656.1, AA334479.1, AA714219.1, AA805016.1, AA580845.1, AI656127.1, AI633338.1, AI203278.1, AI094015.1, AI800379.1, H64073.1, AA094644.1, AA580712.1, AA105012.1, AI267631.1, AA777564.1, N84915.1, AA311379.1, AW206874.1, W86141.1, AA885873.1, N84914.1, AI290252.1, Z21219.1, AA811573.1, AW210124.1, AI702970.1, X85639.1, AW238563.1, H63551.1, H64019.1, AA580595.1, H91160.1, H54657.1, W45471.1, AA867489.1, AA777031.1, AA749004.1, W86085.1, AA108277.1, AA555929.1, AA555921.1, AW820231.1, AW820224.1, AW391572.1, AW362766.1, AW820299.1, AW859988.1, AW859943.1, AW820234.1, AW820232.1, AW604836.1, AW391561.1, AW362751.1, AW229772.1, AI956648.1, AA870633.1, AA821679.1, AA543642.1, AA518224.1, AA437859.1, AA125191.1, AA103602.1, AW582504.1, AW609867.1, AW817504.1, AW817496.1, AW817440.1, AW817432.1, AW817364.1, AW817315.1, AW817234.1, AW817219.1, AW817153.1, AW609859.1, AW609842.1, AW609816.1, AW609809.1, AW609784.1, AW582499.1, AW391901.1, AW391888.1, AW381775.1, AW372095.1, AW371570.1, AW371556.1, AW371552.1, AW371548.1, AW371546.1, AL135032.1, AI907727.1, AA191559.1, AL137142.8, AC024112.9, AC027009.2, AC009290.2, AC021255.2, AC020834.2, AC044841.2, AC068895.1, AL354918.3, AL138763.2, AL049812.13, AP000886.1, AC058786.7, AC027238.2, AC013545.2, AL159973.2, AP001863.1,

SEQ ID NO. 100

NGO-Br-37

MK212/T7 3'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, Z47807.1, AB005282.1, AB005281.1, AC005215.1, AL163279.2, AF193508.1, AC006080.1, AC009223.2, AF016672.2, U22892.1, AL161539.2, Z98981.2, X04465.1, Z92838.1, Z83109.1, AL035258.10, AB042297.1, Z97336.1, L08612.1, X01647.1, AI658961.1, AW571648.1, AW474070.1, AW572452.1, AW608075.1, AW385582.1, AW470142.1, AW316651.1, AA232636.1, AA166806.1, AI751852.1, AW771160.1, AW628153.1, AW820299.1, AA953645.1, AI337175.1, AI651186.1, AA394027.1, AW390368.1, AA136424.1, AI223825.1, AW604836.1, AA435594.1, AI582484.1, AW103624.1, AA485036.1, AI288972.1, AA624532.1, AA571359.1, F07487.1, AW859988.1, AW859943.1, Z20100.1, F08794.1, AW820234.1, AW085874.1, AI799265.1, T63090.1, AA572403.1, AW609781.1, AI838486.1, AA571473.1, AW820232.1, C81194.1, AA417317.1, AW020035.1, AW389335.1, AA079853.1, T34627.1, AA777031.1, Z21220.1, AW491178.1, AI842560.1, AA843693.1, AV275994.1, AA278231.1, AA967441.1, AA856248.1, Z41841.1, AA238818.1, AI115351.1, AV347805.1, AW147250.1, AV348434.1, AV200611.1, AV181186.1, AV178670.1, AV059415.1, AU055867.1, AI365340.1, AI341168.1, AA882330.1, C78586.1, C56104.1, C55163.1, C54236.1, C54007.1, C34122.1, C31088.1, AA522360.1, C12303.1, D64277.1, R98128.1, T26732.1, D33807.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC027128.3, AC023471.2, AF129408.1, AC021710.4, AC020725.3, AC009039.5, AC007337.2, AC008361.7, AC014468.1, AC026863.3, AC032034.2, AC008902.3, AC027359.2, AC026650.3, AC019267.3, AC024681.2, AC022776.2, AC018519.3, AL109916.3, AL162264.4, AL138705.3, AL158817.2,

SEQ ID NO. 101

NGO-Br-37

MK379/T7 3'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, Z47807.1, AB005281.1, AB005282.1, AC005371.1, AB005280.1, AC009223.2, AC005951.1, Z79754.1, AL009183.10, Z74617.1, AL035258.10, AW571648.1, AI658961.1, AW572452.1, AW474070.1, AW385582.1, AW608075.1, AW470142.1, AW316651.1, AA232636.1, AA166806.1, AI751852.1, AW771160.1, AW628153.1, AA394027.1, AA953645.1, AI651186.1, AA136424.1, AW103624.1, AW820299.1, AI223825.1, AI582484.1, AI337175.1, AW390368.1, AA435594.1, AA485036.1, AI288972.1, AW604836.1, Z20100.1, AI799265.1, AW609781.1, F08794.1, F07487.1, AW859988.1, AW859943.1, AW085874.1, T63090.1, AW820234.1, AA624532.1, AA571359.1, AA417317.1,

AA572403.1, AW020035.1, AI838486.1, AA571473.1, T34627.1, Z21220.1, C81194.1, AW820232.1, AA079853.1, AA278231.1, AA843693.1, AW491178.1, AI842560.1, AA967441.1, AA856248.1, AV275994.1, Z41841.1, AW389335.1, AA238818.1, AA524050.1, AW670042.1, AW467587.1, AW440906.1, AW301952.1, AV347805.1, AW148805.1, AW080765.1, AW073417.1, AW021546.1, AW006027.1, AI870113.1, AI766462.1, AI699756.1, AI680535.1, AI563975.1, AI510837.1, AI378898.1, AI378423.1, AI290741.1, AI288939.1, AI092211.1, AA987850.1, AA877634.1, AA806917.1, AA745943.1, AA725830.1, AA682373.1, AA506124.1, AA465237.1, AA232282.1, AA129977.1, AA035579.1, W58443.1, N91182.1, T63600.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC008689.4, AC027117.2, AC022671.2, AC021710.4, AC020725.3, AC009039.5, AC007337.2, AC023309.1, AF176680.1, AL132989.1, AC034128.2, AC027057.2, AC025225.2, AC024681.2, AC023557.1, AL336059.1, AL139800.1, AP000780.1,

10  
SEQ ID NO. 102  
NGO-Br-37  
MK394/T7 3'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, Z47807.1, AB005281.1, AB005282.1, AB023420.1, X67643.1, NM\_008300.1, AC005371.1, D85904.1, AC005215.1, AC011294.3, AE003589.1, AF241729.1, AC005762.1, AC007161.1, AC005539.1, AC005951.1, Z71259.1, Z99289.1, AL035258.10, Z74739.1, AI658961.1, AW571648.1, AW474070.1, AW608075.1, AW572452.1, AW385582.1, AW470142.1, AI751852.1, AW316651.1, AA166806.1, AW628153.1, AA232636.1, AA953645.1, AW820299.1, AW390368.1, AW604836.1, AW771160.1, AA394027.1, AW103624.1, AI651186.1, AA136424.1, AI223825.1, AI337175.1, AW820234.1, F07487.1, AA485036.1, AW859988.1, AW859943.1, F08794.1, AI582484.1, AA435594.1, T63090.1, AI288972.1, AW820232.1, AW609781.1, AI799265.1, Z20100.1, AA624532.1, AA571359.1, AW085874.1, AW389335.1, AI838486.1, AA572403.1, C81194.1, AA571473.1, AA417317.1, AW020035.1, AA777031.1, T34627.1, AA079853.1, Z21220.1, AA278231.1, AA843693.1, AW491178.1, AI842560.1, Z41841.1, AV275994.1, AA967441.1, AA856248.1, AW861588.1, AW819997.1, AW819755.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AI754819.1, AI567970.1, AA703912.1, AA493400.1, AA173193.1, R54223.1, AW754207.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AA823019.1, AA799083.1, AA445826.1, AA238818.1, AA205597.1, AW604696.1, AW583074.1, AW578928.1, AI626242.1, AA542420.1, AV347805.1, AW619786.1, AW391561.1, AI806597.1, AV059415.1, AI115351.1, R98128.1, AL137142.8, AC008689.4, AC027399.2, AC026927.2, AC022212.3, AC023574.2, AC012569.3, AC020725.3, AC009039.5, AC007337.2, AC017242.1, AF176680.1, AL353894.3, AL353753.1, AL158817.2, AP001895.1, AP001563.1, AC034128.2, AC016926.4, AC024909.8, AC012135.2, AC017024.4, AC025673.2, AC027057.2, AC022537.3, AC025971.2, AC009925.3, AC024681.2, AC021571.3, AC021903.5, AC012434.3, AC009969.4, AC021326.1, AC013759.2, AC013493.1, AL121927.18, AL354749.2, AL136220.2, AL133350.7, AL139800.1, AL031745.7,

35  
SEQ ID NO 103  
NGO-Br-37  
MK401/T3 5'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, Z47807.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, NM\_011020.1, U23921.1, D49482.1, AB001926.1, NM\_014278.1, AB023421.1, L12723.1, AB005279.1, AB005280.1, X67643.1, AF077354.1, NM\_008300.1, AB023420.1, D85904.1, AB005281.1, AL109620.4, L08605.1, AE003589.1, AF161311.1, AF136711.1, AE001434.1, AE001433.1, AC005762.1, AC004045.1, AC006403.3, AE003657.1, AE003645.1, AE003411.1, AC011609.9, AC011662.1, AC006288.1, X94582.1, X94581.1, AB020374.1, AB020372.1, AB020370.1, AB020368.1, AB020366.1, AB020364.1, AB020362.1, AB020360.1, AB020356.1, AB020350.1, AB020347.1, AB020345.1, AB020343.1, AC010722.2, AC011299.3, AF169288.1, AC005161.1, AF198095.1, AF128525.1, Z95559.1, AL109865.36, AL034488.1, AL110490.1, AL117205.2, Z35595.1, AC020876.1, AW820299.1, AW390368.1, AW859988.1, AW859943.1, AW820234.1, AW604836.1, AW608075.1, AI658961.1, AW820232.1, AW628153.1, AI751852.1, AW385582.1, F07487.1, AA777031.1, F08794.1, AA953645.1, AW389335.1, T63090.1, AA166806.1, AW474070.1, AW571648.1, AA394027.1, AW103624.1, AW609781.1, AA485036.1, AW572452.1, AW391561.1, AI838486.1, AA571359.1, AW316651.1, AW362751.1, C81194.1, AW470142.1, AJ397361.1, AA624532.1, AW754210.1, AW583074.1, AI760838.1, AI337175.1, AW819755.1, AW578928.1, AA212025.1, AU080443.1, AW206874.1, AW125594.1, AA919208.1, AA755774.1, AA645750.1, AA615363.1, AA445826.1, AA117945.1, AW819997.1, AI626242.1, AI094015.1, W86085.1, AA885873.1, AA626524.1, W22433.1, H63551.1, T29047.1, AW861588.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AI754819.1, AI567970.1, AU035998.1, AA703912.1, AA493400.1, AA431598.1, AA173193.1, H64019.1, R54223.1, AI758907.1, AW754207.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AI702970.1, AA823019.1, AA799083.1, AA777564.1, AW839103.1, AA555929.1, AA370218.1, AA205597.1, AW604696.1, AA580595.1, AA542420.1, AW861596.1, AI314009.1, C76500.1, AA549968.1, H91160.1, AL137142.8, AC015501.3, AC021286.3, AC008642.3, AC006278.6, AC019327.4, AC017242.1, AL034557.7, AC025358.3, AC011333.4, AC027429.2, AC025673.2, AC027054.2, AC024968.2, AC016459.2, AC021997.2, AC017097.2, AL139034.3, AL157821.1,

60  
SEQ ID NO. 104  
NGO-Br-37  
MK401/T7 3'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM\_013559.1, L40406.1,



- Z47807.1, AB005282.1, AB005281.1, D32136.1, AE003798.1, AE003579.1, AF067211.2, AC005926.1, AC005951.1, U22892.1, AC004429.1, AC002312.1, AL161539.2, X04465.1, AL078599.19, AL009183.10, Z74617.1, AL035258.10, Z97336.1, X16094.1, M36578.1, L08612.1, X01647.1, AW571648.1, AI658961.1, AW572452.1, AW474070.1, AW385582.1, AW470142.1, AW608075.1, AW316651.1, AA232636.1, AW771160.1, AI651186.1, AA166806.1, AA136424.1, AI223825.1, AA435594.1, AI582484.1, AI751852.1, AA394027.1, AI288972.1, AW628153.1, AI337175.1, AA953645.1, AW103624.1, AI799265.1, Z20100.1, AW820299.1, AW390368.1, AW085874.1, AA485036.1, AW604836.1, AA624532.1, AA571359.1, AA572403.1, AA417317.1, F07487.1, AA571473.1, F08794.1, AW609781.1, AW020035.1, AW859988.1, AW859943.1, AW820234.1, T63090.1, T34627.1, AI838486.1, Z21220.1, C81194.1, AA843693.1, AA278231.1, AA079853.1, AW491178.1, AI842560.1, AV275994.1, AW820232.1, AA967441.1, AA856248.1, Z41841.1, AA238818.1, AI115351.1, AV347805.1, AW147250.1, AI937768.1, AV200611.1, AV181186.1, AU055867.1, C34122.1, C31088.1, C12303.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC027117.2, AC022671.2, AC022071.7, AC021710.4, AC022797.3, AC020725.3, AC021722.4, AC009039.5, AC007337.2, AC023309.1, AC018789.2, AC063937.2, AC027648.6, AC008158.3, AC026340.2, AC034128.2, AC027730.2, AC055761.2, AC027057.2, AC022530.4, AC025220.2, AC025973.2, AC025231.2, AC015808.3, AC025225.2, AC009925.3, AC024681.2, AC022461.3, AC023557.1, AC009969.4, AC015976.3, AC020050.1, AC018258.1, AC013493.1, AC007420.3, AC004581.1, AL355294.2, AL356059.1, AL158817.2, AL121750.3, AP001803.1, AL031745.7, AP000780.1,
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- SEQ ID NO. 105  
NGO-Br-37  
MK508/T3 5'
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- NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, Z47807.1, AB005282.1, AB005281.1, AB005280.1, AB023420.1, X67643.1, NM\_008300.1, D85904.1, AF262041.1, AC011661.5, AL163279.2, AL109620.4, AC004684.2, AE003720.1, AE003522.1, AF222716.1, AC009223.2, AC004251.1, AC002367.1, AL163234.2, AL161553.2, AL161539.2, X04465.1, AL139077.2, AL009183.10, AP001689.1, Z97336.1, AI658961.1, AW571648.1, AW474070.1, AW572452.1, AW470142.1, AW608075.1, AW385582.1, AA232636.1, AW316651.1, AW771160.1, AA166806.1, AI751852.1, AI651186.1, AI223825.1, AW628153.1, AA136424.1, AA953645.1, AI582484.1, AA394027.1, AW820299.1, AW390368.1, AW103624.1, AI288972.1, AI337175.1, AW604836.1, Z20100.1, AI799265.1, AA435594.1, AA485036.1, AA571359.1, F07487.1, F08794.1, T63090.1, AA624532.1, AW859988.1, AW859943.1, AW609781.1, AI838486.1, AW020035.1, AW820234.1, T34627.1, Z21220.1, C81194.1, AW085874.1, AA278231.1, AA572403.1, AW820232.1, AA571473.1, AA843693.1, Z41841.1, AA417317.1, AW389335.1, AA079853.1, AW491178.1, AI842560.1, AV275994.1, AW837156.1, AA967441.1, AA856248.1, AA777031.1, AW068948.1, F03714.1, AA238818.1, AV146133.1, AI528497.1, AI115351.1, AA462732.1, AW861588.1, AW819997.1, AW819755.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AV149067.1, AI754819.1, AI567970.1, AA703912.1, AA493400.1, AA173193.1, R54223.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AA823019.1, AA799083.1, AA445826.1, AV160311.1, AI600071.1, AI236601.1, AA205597.1, AW604696.1, AW700938.1, AI790491.1, AA681295.1, AU053616.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC023471.2, AC021531.3, AC005506.6, AC021722.4, AC009039.5, AC007337.2, AC008361.7, AC014468.1, AL162502.2, AC027149.2, AC009634.3, AC019267.3, AC024681.2, AC006281.6, AC022461.3, AL109916.3, AL138705.3, AL161449.2, Z98863.1,
- SEQ ID NO. 106  
NGO-Br-37  
MK612/T3 5'
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- NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, Z47807.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, AB005281.1, NM\_011020.1, U23921.1, D49482.1, AB001926.1, NM\_014278.1, AB023421.1, L12723.1, AB005279.1, X67643.1, AF077354.1, NM\_008300.1, AB023420.1, D85904.1, AB005280.1, L08605.1, AE003589.1, AF161311.1, AF136711.1, AE001434.1, AE001433.1, AC005762.1, AC004045.1, AC006403.3, AC011609.9, AF049895.1, AC006288.1, AC005951.1, AE001393.1, AF068862.1, L04162.1, AB026651.1, L08135.1, L22219.1, AW820299.1, AW608075.1, AW604836.1, AW390368.1, AI658961.1, AW628153.1, AW859988.1, AW859943.1, AI751852.1, AW820234.1, AW385582.1, AW820232.1, AA953645.1, AA166806.1, AW571648.1, AA394027.1, AW474070.1, AA777031.1, AW103624.1, F07487.1, AW572452.1, F08794.1, AW389335.1, AA485036.1, T63090.1, AW316651.1, AW609781.1, AW470142.1, AW391561.1, AI838486.1, AI337175.1, AA571359.1, AW362751.1, C81194.1, AA624532.1, AA079853.1, AA232636.1, AA572403.1, AJ397361.1, AA571473.1, AW771160.1, AW754210.1, AW583074.1, AW206874.1, AI760838.1, AW578928.1, AA212025.1, AI094015.1, AA645750.1, W86085.1, AW819755.1, AA885873.1, AW125594.1, AU080443.1, AA919208.1, AA755774.1, AA615363.1, AA445826.1, AA117945.1, H63551.1, H64019.1, AI758907.1, AI702970.1, AA777564.1, AW819997.1, AA626524.1, AA580595.1, W22433.1, H91160.1, T29047.1, AW861588.1, AW839103.1, AW604699.1, AW366794.1, AW085727.1, AI925201.1, AI754819.1, AI626242.1, AI567970.1, AU035998.1, AA703912.1, AA493400.1, AA370218.1, AA173193.1, H54657.1, R54223.1, AW754207.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1, AW060626.1, AI956869.1, AI314009.1, AA823019.1, AA799083.1, AA555929.1, AA205597.1, AW604696.1, AA542420.1, AL137142.8, AC015501.3, AC021286.3, AC008642.3, AC023574.2, AC006279.6, AC006278.6, AC019327.4, AC009039.5, AC007337.2, AC017242.1, AL353894.3, AL353753.1, AL034557.7, AC055800.2, AC037481.2, AC024891.8, AC026825.2, AC025358.3, AC011333.4, AC008714.2, AC034128.2, AC024909.8, AC015533.4, AC027429.2,

- 83 -

AC016805.3, AC009786.2, AC027057.2, AC027054.2, AC025538.3, AC024968.2, AC024681.2, AC016459.2, AC020712.4, AC021903.5, AC022758.3, AC021997.2, AC017097.2, AC022725.1, AC009728.2, AL353714.2, AL138705.3, AL355483.1, AL355135.1, AL353630.1, AC002421.1, AL157821.1, AL138920.2, AL137247.3,

## 5 SEQ ID NO. 107

NGO-Br-37

MK661/T3 5'

NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, NM\_013559.1, D67017.1, D67016.1, L40406.1, Z47807.1, AB005282.1, AB005281.1, AL163279.2, AF193508.1, AE003720.1, AC009223.2, AC004251.1, AL163234.2, 10 AL161553.2, AL161539.2, AL139077.2, AP001689.1, Z97336.1, AP000477.2, AE003728.1, AE003686.1, AE003627.1, AE003520.1, AF065404.1, AC000104.1, AC005771.1, AF069291.1, U67495.1, AL163285.2, Z68004.1, AW571648.1, AW572452.1, AW474070.1, AW470142.1, AA232636.1, AI658961.1, AW771160.1, AW316651.1, AW608075.1, AW385582.1, AI651186.1, AA136424.1, AI223825.1, AA435594.1, AI582484.1, AI337175.1, AI288972.1, AA166806.1, Z20100.1, AI799265.1, AW085874.1, AA624532.1, AA571473.1, AA571359.1, AA572403.1, AA417317.1, AI751852.1, 15 AA394027.1, AW020035.1, AI838486.1, C81194.1, T34627.1, Z21220.1, AW628153.1, AW103624.1, AW491178.1, AI842560.1, AA843693.1, AV275994.1, AW604836.1, AA278231.1, AW820299.1, AA485036.1, AA953645.1, AA967441.1, AA856248.1, AA079853.1, Z41841.1, AA238818.1, AW390368.1, AI115351.1, AV347805.1, AW147250.1, AV348434.1, AV200611.1, AV181186.1, AV178670.1, AU055867.1, AI365340.1, AI341168.1, AA882330.1, AA834218.1, C56104.1, C55163.1, C54236.1, C54007.1, C34122.1, C31088.1, C12303.1, D64277.1, T26732.1, D33807.1, 20 AW383218.1, AV272251.1, AV269906.1, AW037622.1, AI807000.1, AI804139.1, AA893644.1, AL137142.8, AC012569.3, AP001895.1, AP001563.1, AC027117.2, AC022671.2, AC027128.3, AC023471.2, AC018818.3, AF129408.1, AC021531.3, AC005506.6, AC021722.4, AC008361.7, AC018789.2, AC014468.1, AC044830.2, AC008902.3, AC027359.2, AC009634.3, AC022530.4, AC026650.3, AC025973.2, AC019267.3, AC009925.3, AC018717.5, AC015974.4, AC013110.1, Z98863.1,

25 SEQ ID NO. 108  
NGO-Br-38

MK015/T3 5'

D86956.1, AB003334.1, NM\_006644.1, AB003333.1, AF039695.1, D67017.1, D67016.1, NM\_013559.1, L40406.1, 30 Z47807.1, AB005267.1, AB005269.1, AB005268.1, AB023420.1, L12723.1, X67643.1, AC011013.17, NM\_008300.1, AF077354.1, D85904.1, NM\_014278.1, NM\_011020.1, U23921.1, AB023421.1, D49482.1, AL034403.18, NC\_001145.1, NM\_004455.1, AC007240.2, U67191.1, AL121580.8, AL035448.28, Z49260.1, X67640.1, AC020629.6, AC007018.6, AC004681.2, AE003808.1, AE003644.1, AE003458.1, AE003410.1, AC004740.1, NM\_012980.1, AC004016.1, AC007967.3, AC007447.6, AF132160.1, AC007073.2, AE001517.1, AC005938.1, U46034.1, AC004320.1, AF038606.1, 35 AL034423.18, AL109733.1, AL049548.6, Z98046.1, AW137489.1, AL120219.1, AW665093.1, AI052062.1, AI023309.1, AU077146.1, AL043449.1, AA219339.1, AI052577.1, AA078767.1, AI003212.1, AA081692.1, AW475538.1, AI787816.1, AI746652.1, AA360776.1, AI006526.1, AW209689.1, AW105834.1, AL045611.2, AI931227.1, AW227137.1, AL044212.1, AU066691.1, AA168224.1, AW069322.1, AW318627.1, AI956324.1, AI956249.1, AI316935.1, AA408320.1, AW227160.1, AA407914.1, AA226851.1, AW557363.1, AW416815.1, AW141567.1, AI677492.1, 40 AI087282.1, AA840049.1, AA726333.1, AW223053.1, AV294240.1, AI986092.1, AI904139.1, AV052268.1, AI510184.1, AI108231.1, AA799078.1, AA038974.1, N94129.1, AL137142.8, AL138965.3, AC046137.3, AC020834.2, AC015501.3, AC021286.3, AC019130.3, AL161914.6, AC026223.2, AC023996.2, AL355495.1, AC068988.2, AC053523.2, AC016937.3, AC016496.3, AC019266.3, AC026641.1, AC024429.2, AC019108.4, AC009969.4, AC023395.2, AC060786.2, AC023513.8, AC023599.7, AC068719.1, AC023175.1, AC024943.5, AC027239.2, AC023257.2, 45 AC027676.2, AC027070.2, AC044785.1, AC024673.2, AC009560.3, AC015810.3, AC019276.3, AC021701.3, AC025813.1, AC024370.2, AC008350.3, AC021304.2, AC009972.4, AC012344.3, AC018305.1, AC008232.3, AC014298.1, AC015847.1, AC013236.1, AL109835.12, AL139110.1, AP001998.1, AP001782.1,

## 50 SEQ ID NO. 109

NGO-Br-38

MK015/T7 3'

AF039695.1, D86956.1, NM\_006644.1, AB003334.1, AB003333.1, D67017.1, D67016.1, AB005282.1, NM\_013559.1, L40406.1, Z47807.1, AE003611.1, AL035259.1, AC007677.3, AE003628.1, AE003571.1, AE003567.1, AC007066.4, 55 AL022164.1, AF218257.1, AC016752.2, AC006413.3, AE003477.1, AC005927.2, AC007061.5, U71249.1, AC003078.1, U95740.1, AF104919.1, AC005324.1, AL133419.15, AL034556.3, AL138995.3, AL161492.2, AL035706.10, AL049188.3, AJ010316.1, AB004275.1, AB006696.1, AP000555.1, Z11695.1, AB006689.1, AA843693.1, AA543054.1, AI742981.1, AW612980.1, AW612983.1, AI582881.1, AI751853.1, AI378269.1, AI920808.1, AI654608.1, AI819251.1, AI337175.1, AI753470.1, AI831339.1, AI312753.1, AI803588.1, AI563996.1, AW015796.1, AW117974.1, AI668853.1, AA993280.1, AA912023.1, AA535277.1, AI123280.1, AA632202.1, AW027050.1, AW627645.1, AA761750.1, AI223412.1, 60 AA219263.1, AW068948.1, AA166716.1, AA482770.1, AW236067.1, AA485151.1, AI369932.1, AI250881.1, AA933881.1, AI262020.1, AI050716.1, H52653.1, AA678506.1, AA582157.1, AW340810.1, AI493255.1, AW837156.1, AI673134.1, T58153.1, T36072.1, F22410.1, AA417317.1, AW020035.1, AI361237.1, AA278231.1, AA810686.1, AA730742.1, AA082043.1, D58216.1, D29622.1, AA233888.1, AI630481.1, AI612928.1, D29371.1, AA731716.1, AA417255.1, AA804371.1, AA465183.1, AA780104.1, AA491870.1, T34783.1, Z41841.1, AW771160.1, AI357434.1,

- AI799265.1, AI582484.1, AI288972.1, F03714.1, AW381433.1, AW381418.1, T10428.1, AW163535.1, AW059721.1, AA773435.1, AI651186.1, AW824279.1, AW544862.1, AW061135.1, AL117974.1, AW049097.1, AW011890.1, AI845946.1, AU019569.1, AU019107.1, C78223.1, C78213.1, C77722.1, AA048547.1, AA986561.1, AI154454.1, AW700938.1, AL137142.8, AC011966.3, AC027326.2, AC027323.2, AC010622.3, AC020999.4, AC018938.3, AC018104.1, AC004390.1, AL161779.7, AP001547.1, AP000635.1, AP000610.2, AC022101.3, AC010093.3, AC011799.5, AC023003.2, AC018466.3, AC020183.1, AC014557.1, AC015076.1, AC009849.6, AC011758.5, AC025391.3, AC022516.3, AC044816.2, AC026911.2, AC022462.3, AC015684.3, AC009835.5, AC015714.4, AC011227.3, AC010018.4, AL355575.2, AL133344.21, AL157687.2, AL034359.4
- 10 SEQ ID NO. 110  
NGO-Br-38  
MK249/T7 3'  
AF039695.1, D86956.1, NM\_006644.1, AB003334.1, AB003333.1, Z47807.1, D67017.1, D67016.1, AB005282.1, NM\_013559.1, L40406.1, AC011661.5, AE003611.1, AL035259.1, AC004684.2, AE003571.1, AE003567.1, AC010168.6, AF140273.1, U32370.1, U30930.1, AC002367.1, AE000823.1, AC002292.1, AL158059.2, AJ006409.1, AB026658.1, AF218257.1, AC016752.2, AC009155.3, AC006413.3, U09675.1, AC005927.2, AC007061.5, AF030694.2, AF222716.1, U95740.1, AC009501.3, AC005083.1, AC007590.1, AF104919.1, AF074946.1, AF030693.1, AF030692.1, AC005324.1, AL133419.15, AL034556.3, AL034560.3, AL110502.1, AL049779.4, AL049188.3, U27707.1, U40933.1, U41018.1, AB004275.1, AP000069.1, AB006696.1, Z18921.1, AB006689.1, AA543054.1, AA843693.1, AW612980.1, AI582881.1, AW612983.1, AI78269.1, AI920808.1, AI654608.1, AI742981.1, AI312753.1, AI753470.1, AI831339.1, AI819251.1, AI803588.1, AI751853.1, AI563996.1, AW117974.1, AI668853.1, AA993280.1, AA632202.1, AA219263.1, AW627645.1, AW015796.1, AI337175.1, AI123280.1, AA912023.1, AA761750.1, AW027050.1, AI223412.1, AA535277.1, AA485151.1, AA166716.1, AW236067.1, AI369932.1, AI250881.1, AA482770.1, AA933881.1, AI262020.1, AI050716.1, AI493255.1, AA678506.1, AA582157.1, AW340810.1, AI673134.1, H52653.1, T58153.1, AW068948.1, AI361237.1, AA810686.1, T36072.1, F22410.1, AW837156.1, AA417317.1, AA082043.1, D58216.1, D29622.1, AA278231.1, AW020035.1, AI612928.1, AI630481.1, AA730742.1, D29371.1, AA731716.1, AA417255.1, AA804371.1, AA465183.1, AA233888.1, AA780104.1, AA491870.1, AI357434.1, AW381433.1, AW163535.1, T34783.1, T10428.1, AW381418.1, Z41841.1, AW771160.1, F03714.1, AI799265.1, AI582484.1, AI288972.1, AW059721.1, AA773435.1, AW470142.1, AI651186.1, AI223825.1, AA232636.1, T34627.1, Z20100.1, Z21220.1, AI658961.1, AA136424.1, AW824279.1, AL117974.1, AW049097.1, AI845946.1, C78213.1, AA048547.1, AA986561.1, AW700938.1, AL137142.8, AC011966.3, AC018938.3, AC019338.4, AC018104.1, AP001547.1, AP000635.1, AP000610.2, AC022101.3, AC067877.1, AC018700.3, AC010093.3, AC008107.2, AC022636.3, AC011799.5, AC009919.2, AC014557.1, AC015336.1, AC015076.1, AL354655.3, AL353639.2, AL161449.2, AC025440.3, AC022516.3, AC008395.5, AC027149.2, AC019075.6, AC067945.1, AC026911.2, AC023461.2, AC025246.5, AC055117.1, AC027646.3, AC015714.4, AC026641.1, AC006281.6, AC018934.2, AC009015.2, AC002043.1, AC023302.2, AC006763.1, AC006187.1, AL139318.2, AL132640.1, AL138776.2, AL136303.3, AL049183.5, AL034359.4, AP000840.1,
- SEQ ID NO. 111  
NGO-Br-38  
MK4110/T3 5'  
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- 55 SEQ ID NO. 112  
NGO-Br-38  
MK447/T3 5'  
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- 60

AA757403.1, AA658536.1, AA654568.1, AA618051.1, AA604054.1, AA600804.1, AA588452.1, AA587371.1,  
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AA533130.1, AA531161.1, AA515081.1, AA494515.1, AA486095.1, AA468679.1, AA399366.1, AA373996.1,  
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SEQ ID NO.113

NGO-Br-38

MK447/T7 3'

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AC007049.8, AC005992.15, AC016752.2, AC006586.9, AC004165.2, AL133419.15, AL034556.3, AL117202.1,  
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AI312753.1, AI803588.1, AI563996.1, AW015796.1, AW117974.1, AI668853.1, AA535277.1, AA993280.1, AA632202.1,  
20 AA912023.1, AW627645.1, AW027050.1, AI337175.1, AI123280.1, AA761750.1, AI223412.1, AA219263.1,  
AW068948.1, AA482770.1, AA166716.1, AW236067.1, AA485151.1, AI369932.1, AI250881.1, AA933881.1,  
AI262020.1, AI050716.1, H52653.1, AA678506.1, AA582157.1, AI493255.1, AW340810.1, AW837156.1, AI673134.1,  
T58153.1, T36072.1, F22410.1, AA417317.1, AW020035.1, AI361237.1, AA278231.1, AA810686.1, AA730742.1,  
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25 AA804371.1, AA465183.1, AA780104.1, AA491870.1, T34783.1, Z41841.1, AW771160.1, AI357434.1, AI799265.1,  
AI582484.1, AI288972.1, F03714.1, AW381433.1, AW381418.1, T10428.1, AW163535.1, Z21220.1, AW470142.1,  
AI651186.1, AI223825.1, AA232636.1, Z20100.1, T34627.1, AI658961.1, AA136424.1, AW059721.1, AW571648.1,  
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30 AC068643.5, AC022101.3, AC020183.1, AC009849.6, AC018934.2, AL354895.3, AL353639.2, AL133344.21,  
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SEQ ID NO.114

NGO-Br-38

MK633/T3 5'

15 NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, D67017.1, D67016.1, Z47807.1, NM\_013559.1,  
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AW316651.1, AA166806.1, AI751852.1, AW771160.1, AW628153.1, AI651186.1, AA953645.1, AW820299.1,  
AA394027.1, AI223825.1, AA136424.1, AW390368.1, AI582484.1, AW103624.1, AW604836.1, AI337175.1,  
AI288972.1, AA435594.1, AA485036.1, F07487.1, AA571359.1, Z20100.1, F08794.1, AI799265.1, T63090.1,  
AW859988.1, AW859943.1, AA624532.1, AW820234.1, AI838486.1, AW609781.1, C81194.1, AW085874.1,  
45 AW820232.1, AA572403.1, AW020035.1, AA571473.1, T34627.1, Z21220.1, AA417317.1, AA278231.1, AA843693.1,  
AW389335.1, Z41841.1, AA079853.1, AW491178.1, AI842560.1, AV275994.1, AA777031.1, AA967441.1, AA856248.1,  
AW837156.1, AA238818.1, H52653.1, T34783.1, AI751853.1, F03714.1, AW861588.1, AW819997.1, AW819755.1,  
AW604699.1, AW366794.1, AW085727.1, AW068948.1, AI925201.1, AI754819.1, AI567970.1, AA703912.1,  
AA493400.1, AA173193.1, R54223.1, AI115351.1, AW545353.1, AW545094.1, AW542227.1, AW537735.1,  
50 AW060626.1, AI956869.1, AV146133.1, AI528497.1, AA823019.1, AA799083.1, AA462732.1, AA445826.1,  
AW754207.1, AA205597.1, AW604696.1, AV279553.1, AV149067.1, AI600071.1, AL137142.8, AC012569.3,  
AP001895.1, AP001563.1, AC023471.2, AC018495.3, AC010070.5, AC010069.6, AC015410.1, AF129408.1,  
AC022797.3, AC021531.3, AC005506.6, AC021722.4, AC009039.5, AC007337.2, AC008361.7, AC014468.1,  
AL162502.2, AC034128.2, AC018700.3, AC022530.4, AC019267.3, AC009925.3, AC024681.2, AC022461.3,  
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SEQ ID NO.115

NGO-Br-40 combined

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AF085699.1, AF178650.1, AC007980.1, AC005557.1, AC005669.1, AL109935.39, AL163226.2, AL133283.9,  
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X72016.1, U06117.1, Y10720.1, AP001137.1, AB015429.1, AB020867.1, D10044.1, D11456.1, AW001215.1,

AI830004.1, AW058212.1, AA876142.1, AI983562.1, AI439472.1, AW820994.1, AW468007.1, AI969542.1, AI760378.1, AW078537.1, AW614912.1, AW577433.1, AA075477.1, W37973.1, AI870195.1, AW804484.1, AI906045.1, AI859339.1, AA622193.1, AW341927.1, W37755.1, AI500511.1, AA642656.1, AI492530.1, AI902944.1, AI500507.1, AA837842.1, AI865686.1, AA075671.1, AA131850.1, AA635989.1, AA587444.1, AW297239.1, AI285460.1, AW804456.1, AW821048.1, AI862178.1, AW793466.1, AI922648.1, AA937007.1, AA903286.1, AW373870.1, AI289455.1, AI251115.1, AA533156.1, AI084027.1, AW368079.1, AA627607.1, AW362711.1, AA532369.1, AA579973.1, AW815880.1, AA586545.1, AA917383.1, AW026936.1, AI138455.1, W72748.1, T29528.1, AI962517.1, AI795779.1, AI073859.1, AW797814.1, AW578905.1, AI371522.1, AA044192.1, AW861558.1, AW609821.1, AW797815.1, AI702366.1, AA471169.1, AI683358.1, AI528561.1, AW320458.1, AA424070.1, AA164464.1, AI989871.1, AW474440.1, AI683206.1, AA122936.1, W01896.1, AA880099.1, AA100063.1, AW211765.1, AI905784.1, AI905719.1, AA305909.1, AI811907.1, AW797793.1, AW629741.1, AA354725.1, H05350.1, AW817431.1, AA486849.1, F06345.1, AW239153.1, AA174655.1, AA347633.1, AA315174.1, AA487747.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AC021689.2, AL355818.2, AC060233.1, AC021626.3, AC009729.4, AC026091.3, AC010872.4, AL138889.2, AP000831.1, AC013475.4, AC024551.3, AC024150.5, AC060776.2, AC063963.3, AC008373.6, AC010630.3, AC034166.2, AC021399.3, AC025799.2, AC016190.3, AC025482.2, AC027133.1, AC022015.2, AC024303.2, AC018807.4, AC016720.4, AC016696.4, AC011210.3, AC016474.2, AC019071.2, AC010118.5, AC010743.4, AC017393.1, U82205.1, AL158849.7, AL356126.1, AL158070.2, AP001809.1,

## SEQ ID NO. 116

20 NGO-Br-40

MK121/T3 5'

NM\_004120.2, M55543.1, NM\_002053.1, M55542.1, AK001823.1, NM\_010259.1, M63961.1, M55544.1, M80367.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, U44731.1, NM\_008620.1, M81128.1, X77129.1, Z95388.1, Z78546.1, AE003629.1, AE003472.1, AF085699.1, AC007980.1, AC005557.1, AL133283.9, AL008639.15, X92112.1, AL117265.1, AB015429.1, AF257304.1, AF257303.1, AE003459.1, AC007177.1, U69633.1, AL117319.1, AL031587.3, AW297239.1, AI962517.1, AI795779.1, AW320458.1, AI528561.1, AW368079.1, AA424070.1, AA122936.1, AA880099.1, AA100063.1, AW211765.1, AA305909.1, AW362711.1, AW629741.1, AA354725.1, AW815880.1, AW239153.1, AA347633.1, AA296543.1, AA709608.1, AA337079.1, AA911189.1, AA873192.1, F14838.1, AU076892.1, AA576498.1, AW106727.1, AA878690.1, W77927.1, AW428394.1, AA296485.1, AI906045.1, AA131850.1, AW820809.1, T83604.1, F14828.1, AA487747.1, AW669464.1, AW817439.1, AW609764.1, AA158924.1, AU076806.1, T75545.1, AW817360.1, AI980812.1, AI626652.1, AA848004.1, W13273.1, AI979397.1, AI529783.1, AI194988.1, AA889865.1, C05965.1, R54285.1, R54280.1, F06574.1, T34309.1, T32678.1, AW399587.1, AW398501.1, AA955194.1, C77542.1, AL161639.4, AL160008.1, AL139416.1, AC021689.2, AL138786.3, AL355818.2, AC021626.3, AC010872.4, AC024551.3, AC060776.2, AC063963.3, AC021399.3, AC025482.2, AC022015.2, AC007147.7, AC011210.3, AC016474.2, AC010118.5, AC020189.1, AC017393.1, U82205.1, AL356126.1, AC026877.4, AC064824.2, AC053519.2, AC027322.2, AC008494.7, AC016942.4, AC010289.3, AC019282.2, AC027620.3, AC023888.6, AC037442.1, AC026047.2, AC013693.3, AC021769.3, AC020577.1, AC019338.4, AC013718.3, AC015469.2, AC023823.2, AC013415.3, AC020230.1, AC021758.1, AC016495.1, AC013276.2, AC013485.1, AC012667.1, AC007515.1, AL355532.4, AL356008.1, AL354918.3, AL079302.3, AP002010.1, AP001807.1, AP001642.1, AP001638.1, AP001461.2, AP001324.1, AP001104.1,

## SEQ ID NO. 117

45 NGO-Br-40

MK121/T7 3'

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SEQ ID NO. 118

5 NGO-Br-40

MK221/T3 5'

NM\_004120.2, M55543.1, NM\_002053.1, M55542.1, M80367.1, NM\_010259.1, M63961.1, M55544.1, AK001823.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, U44731.1, NM\_008620.1, M81128.1, X77129.1, Z95388.1, AC004930.1, NC\_001143.1, AF085699.1, AC007980.1, AC005669.1, AL109935.39, AB038490.1, Z28127.1, X72016.1, 10 AB015429.1, AB020867.1, NM\_001567.2, AC005917.2, AE003603.1, NM\_013134.1, NM\_006460.1, AC006312.8, AC004798.1, AC003111.1, AL161516.2, AL133304.2, AL049487.1, L36818.1, Y14385.1, AB021179.1, M29249.1, X93922.1, AI906045.1, AA131850.1, AW368079.1, AW362711.1, AW815880.1, W72748.1, AW297239.1, AW820994.1, AI902944.1, AW578905.1, AW861558.1, AA044192.1, H05350.1, AA486849.1, F06345.1, AW804456.1, W77927.1, AW821048.1, AW804484.1, AI969542.1, AI962517.1, AI683358.1, AA911189.1, AA164464.1, AW468007.1, 15 AI989871.1, AI528561.1, AW474440.1, AI683206.1, AA878690.1, AA487367.1, F07031.1, AW804431.1, AA487747.1, AI905784.1, AI905719.1, AA873192.1, AI922648.1, AW320458.1, AW211765.1, AA122936.1, AW820809.1, AW106727.1, AA174655.1, T83604.1, T75545.1, AW817439.1, AW609764.1, AI811907.1, AW817360.1, AA610352.1, F05698.1, AI859339.1, AW797814.1, AA471169.1, AA880099.1, AW577433.1, AI500511.1, AA044017.1, T87056.1, AI922921.1, AA848004.1, AA506001.1, AV362793.1, AA582749.1, W13273.1, AI651570.1, AI075062.1, AA690573.1, 20 AA665504.1, AA057242.1, AW665096.1, AW454822.1, AL135036.1, AW166154.1, AI811680.1, AI796944.1, AV046437.2, AA955194.1, AI383864.1, AI216433.1, AA928789.1, AA927260.1, AA909971.1, AA890309.1, T43327.1, AA719024.1, C77542.1, AA099506.1, N33318.1, N21081.1, R65420.1, H36685.1, HI6325.1, T41892.1, Z44502.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AL355818.2, AC021689.2, AL137851.3, AP000831.1, AC024150.5, AC034166.2, AC024303.2, AC016696.4, AC011860.3, AL158849.7, AL158070.2, AC036129.2, AC021630.4, 25 AC018354.6, AC012053.2, AC025975.2, AC027743.1, AC024047.2, AC026047.2, AC025865.2, AC013612.3, AC022854.3, AC022679.3, AC020753.2, AC018814.3, AC018497.4, AC023201.2, AC006295.8, AC013759.2, AC017228.1, AF166490.1, AL354770.2, AL356008.1, AL355990.1, AL161658.3, AL160006.2, AP001385.1, AP001157.1, AP000812.1, AP000593.1, AP000485.2,

30 SEQ ID NO.119

NGO-Br-40

MK221/T7 3'

NM\_004120.2, M55543.1, AK001823.1, NM\_002053.1, M55542.1, NM\_010259.1, M63961.1, M55544.1, M80367.1, AC025222.2, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC006642.1, U28927.1, AL163226.2, AL049555.6, 35 AP001681.1, U40937.1, AP001137.1, AE002269.1, AC006241.1, AC004558.1, AF052729.1, AL163235.2, AP001690.1, Y10720.1, AP000476.2, AB005234.1, AB026654.1, M97632.1, AA876142.1, AW001215.1, AI830004.1, AW614912.1, AW058212.1, AI760378.1, AI439472.1, AW078537.1, AI983562.1, AA075477.1, AI870195.1, AW341927.1, AI492530.1, W37755.1, AA622193.1, W37973.1, AA642656.1, AI500507.1, AA837842.1, AI865686.1, AA635989.1, AI862178.1, AA587444.1, AI285460.1, AA937007.1, AA903286.1, AI289455.1, AA533156.1, AA627607.1, AI084027.1, AA532369.1, 40 AA579973.1, AW373870.1, AA917383.1, AA075671.1, AW026936.1, AI138455.1, AI073859.1, AW793466.1, T29528.1, AI702366.1, AW577433.1, AI371522.1, W01896.1, AW609821.1, AI500511.1, AW468007.1, AI969542.1, AI859339.1, AI922648.1, AA586545.1, AI280597.1, AA131800.1, AA487528.1, AA315174.1, AW796865.1, AI081732.1, AI075062.1, AW449506.1, AA937600.1, AI905784.1, AI905719.1, AI251115.1, AA827350.1, AW817431.1, AW799191.1, AI910674.1, AA810201.1, AA650178.1, AA486850.1, AW804484.1, AA424529.1, AA837672.1, AA834863.1, 45 AI861968.1, AW304126.1, AA564905.1, AA056488.1, AW805514.1, AW363341.1, AA424397.1, AW820994.1, AI372935.1, AI246407.1, AI400402.1, AA587703.1, AW799183.1, AW804508.1, W37972.1, AW821048.1, AW799555.1, AW797212.1, AI760921.1, AA947554.1, H05300.1, AI007134.1, AA175795.1, AA139382.1, AL161639.4, AL139416.1, AL160008.1, AC026091.3, AC013475.4, AC027453.2, AC016190.3, AC021149.4, AC027133.1, AC021688.2, AC016774.2, AC006883.2, AC022330.9, AC018461.18, AC022418.3, AC010230.3, AC009051.5, AC009050.4, 50 AC011784.3, AC027168.2, AC009625.3, AC026590.2, AC015972.3, AC016686.4, AC024403.2, AC013404.1, AC012545.1, AL139275.6, AL139274.6, AL354758.3, AL157714.3, AL160058.3, AL157818.2, AL158072.2,

SEQ ID NO.120

NGO-Br-40

55 MK241/T3 5'

NM\_004120.2, M55543.1, NM\_002053.1, M55542.1, AK001823.1, NM\_010259.1, M63961.1, M55544.1, M80367.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, U44731.1, NM\_008620.1, M81128.1, AC006112.2, X77129.1, Z95388.1, Z78546.1, AE003472.1, AC004969.1, AC005053.1, AC005061.2, AF085699.1, AC007980.1, AC005557.1, AL109935.39, AL133283.9, AL008639.15, X92112.1, AL117265.1, AB015429.1, AB020867.1, AF257304.1, AF257303.1, 60 AE003459.1, NM\_013134.1, AC007177.1, AC004798.1, AC003111.1, AF003626.1, U69633.1, AL117319.1, AL034426.4, AL031587.3, U29614.1, M29249.1, AW297239.1, AW368079.1, AI962517.1, AW362711.1, AW815880.1, AI795779.1, AI528561.1, AW320458.1, AA122936.1, AA880099.1, AA424070.1, AW211765.1, AA100063.1, AA305909.1, AA354725.1, AI906045.1, AW629741.1, AA131850.1, AA347633.1, AW239153.1, AA709608.1, AA296543.1, W77927.1, AA911189.1, AA878690.1, AA873192.1, AA337079.1, F14838.1, AW106727.1, AA576498.1, W72748.1, AW428394.1,



- AI905784.1, AI905719.1, AW820809.1, AA487747.1, T83604.1, T75545.1, AW817439.1, AW609764.1, AA296485.1, AW817360.1, F14828.1, AW578905.1, AW861558.1, AW669464.1, AA158924.1, AU076892.1, AI626652.1, AI979397.1, AI922921.1, AI980812.1, AA848004.1, AA506001.1, AA582749.1, W13273.1, AI651570.1, AI529783.1, AI194988.1, AA889865.1, C05965.1, R54285.1, R54280.1, F06574.1, T34309.1, T32678.1, AW399587.1, AW398501.1, AW256377.1, AV046437.2, AA955194.1, C90826.1, C77542.1, AL161639.4, AL160008.1, AL139416.1, AC021689.2, AL138786.3, AL355818.2, AC021626.3, AC007223.1, AC010872.4, AC024551.3, AC060776.2, AC063963.3, AC034166.2, AC021399.3, AC025482.2, AC022015.2, AC024303.2, AC016696.4, AC011210.3, AC016474.2, AC010118.5, AC020825.2, AC019249.3, AC017393.1, U82205.1, AL356126.1,
- 10 SEQ ID NO.121  
NGO-Br-40  
MK241/T7 3'
- 15 NM\_004120.2, M55543.1, AK001823.1, NM\_002053.1, M55542.1, NM\_010259.1, M63961.1, M55544.1, M80367.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC006487.7, AC005028.1, AF235093.1, AC022522.2, U97404.1, AL163226.2, AL163210.2, AP001681.1, AJ010598.1, AL035640.2, AP001137.1, AE002269.1, NM\_007199.1, AF113136.1, AC006241.1, U41556.1, AL163235.2, AL109984.14, Z82288.2, Z81102.1, Z70285.1, AP001690.1, U37429.1, Y10720.1, Z73419.1, AP000476.2, AB005234.1, AW614912.1, AI830004.1, AW001215.1, AA876142.1, AW058212.1, AW078537.1, AI760378.1, AI439472.1, AA075477.1, AI870195.1, AI983562.1, AI492530.1, AW341927.1, AA622193.1, W37755.1, AI500507.1, AA642656.1, AA837842.1, AI865686.1, W37973.1, AA635989.1, AI862178.1, AA587444.1, AI285460.1, AA903286.1, AA937007.1, AI289455.1, AA533156.1, AI084027.1, AA532369.1, AA627607.1, AA579973.1, AA917383.1, AW026936.1, AI138455.1, AW373870.1, AI073859.1, AA075671.1, AI371522.1, AI702366.1, W01896.1, AW793466.1, T29528.1, AW577433.1, AW609821.1, AI922648.1, AA131800.1, AI280597.1, AI500511.1, AA487528.1, AA315174.1, AW468007.1, AI969542.1, AI859339.1, AW449506.1, AI081732.1, AI075062.1, AA937600.1, AA486850.1, AW799191.1, AI910674.1, AA837672.1, AA834863.1, AA827350.1, AA810201.1, AA650178.1, AA424529.1, AW796865.1, AW304126.1, AI861968.1, AA564905.1, AA056488.1, AA586545.1, AW363341.1, AI246407.1, AA587703.1, AI372935.1, AW805514.1, H05300.1, AA424397.1, AW799183.1, AW470713.1, AI905784.1, AI905719.1, AW817431.1, AW797212.1, AI251115.1, AI400402.1, AI760921.1, AW804484.1, AW820994.1, AA947554.1, AI007134.1, AA175795.1, AA139382.1, AW821048.1, AA153021.1, AI386222.1, AA153027.1, W37972.1, AL161639.4, AL139416.1, AL160008.1, AC060233.1, AC026091.3, AC013475.4, AC025799.2, AC016190.3, AC063948.3, AC012264.8, AC024102.5, AC018461.18, AC026737.3, AC026704.3, AC022418.3, AC027630.4, AC027168.2, AC026590.2, AC026549.2, AF235106.1, AC015972.3, AC034223.1, AC012148.2, AC025790.2, AC008248.2, AC009256.7, AC024403.2, AC020798.2, AC022290.2, AC013404.1, AC008031.3, AC012545.1, AL139275.6, AL139274.6, AL136380.2, AL355820.2, AL162421.1,
- 25
- 30
- 35 SEQ ID NO. 122  
NGO-Br-40  
MK255/T7 3'
- 40 NM\_004120.2, M55543.1, AK001823.1, NM\_002053.1, M55542.1, NM\_010259.1, M63961.1, M55544.1, M80367.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC022522.2, AC006487.7, AL135749.2, AC005028.1, AL162873.1, AE003782.1, AL163226.2, AP001681.1, AL035640.2, AP001137.1, AB011093.1, AF227618.1, AE002269.1, AC007347.3, NM\_007199.1, AF113136.1, AC006241.1, AL163235.2, AC002094.1, AL133246.2, AL109984.14, Z49910.1, AP001690.1, X56844.1, Y10720.1, AP000476.2, AB005234.1, AI830004.1, AW001215.1, AA876142.1, AW058212.1, AI760378.1, AW614912.1, AI983562.1, AI439472.1, AW078537.1, AA075477.1, AI870195.1, W37973.1, AA622193.1, AI492530.1, AW341927.1, W37755.1, AA642656.1, AI500507.1, AA837842.1, AI865686.1, AA635989.1, AA587444.1, AI862178.1, AI285460.1, AA903286.1, AA937007.1, AI289455.1, AA533156.1, AW373870.1, AI084027.1, AA075671.1, AA532369.1, AA627607.1, AA579973.1, AA917383.1, AW026936.1, AW793466.1, AI138455.1, AW577433.1, AI073859.1, T29528.1, AI371522.1, AI702366.1, AW609821.1, AI500511.1, AW468007.1, AI969542.1, AI859339.1, W01896.1, AA586545.1, AI922648.1, AI905784.1, AI905719.1, AI251115.1, AW817431.1, AA131800.1, AA487528.1, AA315174.1, AI280597.1, AI081732.1, AI075062.1, AW804484.1, AW449506.1, AA937600.1, AA827350.1, AW799191.1, AI910674.1, AA810201.1, AA650178.1, AA486850.1, AA837672.1, AA834863.1, AA424529.1, AW304126.1, AI861968.1, AA564905.1, AA056488.1, AW820994.1, AW796865.1, AW804456.1, AW797814.1, AI902944.1, AW797815.1, AW797793.1, AW363341.1, AI372935.1, AA587703.1, AW805514.1, AI246407.1, AW821048.1, AA424397.1, H05300.1, AW799183.1, W37972.1, AW470713.1, AA175795.1, AA139382.1, AA153021.1, AI386222.1, AA153027.1, AL161639.4, AL139416.1, AL160008.1, AC060233.1, AC026091.3, AC013475.4, AC008878.6, AC008373.6, AC010630.3, AC025799.2, AC016190.3, AC027133.1, AC011764.5, AC014685.1,
- 45
- 50
- 55
- 60 SEQ ID NO.123  
NGO-Br-40  
MK303/T3 5'
- NM\_004120.2, M55543.1, NM\_002053.1, M55542.1, AK001823.1, NM\_010259.1, M63961.1, M55544.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, M80367.1, AC004930.1, AL135749.2, AP000350.1, NC\_001143.1, NM\_000379.1, AC002288.1, AC005669.1, AF077537.1, AL121654.1, U39487.1, U39646.1, Z28127.1, X72016.1, U06117.1, D10044.1, D11456.1, NM\_001567.2, AC009890.12, AC010489.4, AC007048.4, AC005917.2, AC006832.2,

- AE003603.1, AE003479.1, AC005781.1, AC002526.1, NM\_006460.1, AF202730.1, AC003661.1, AC008125.9, U40939.1, AC007504.3, AC007785.1, L21934.2, AC004596.1, AC000028.1, AC005837.1, U81031.1, AC005215.1, AC003047.1, AC002094.1, AL161516.2, Z81088.1, AL049487.1, L36818.1, X15209.1, X15750.1, Y14385.1, AB021179.1, AW820994.1, AW804484.1, AW468007.1, AI969542.1, AI902944.1, AW804456.1, AI922648.1, AW821048.1, AI859339.1, AI500511.1, AW577433.1, AI251115.1, AW797814.1, AW797815.1, AA471169.1, AA044192.1, AI683358.1, AW861558.1, AW578905.1, AA586545.1, AW001215.1, AW793466.1, AI989871.1, AI683206.1, AW474440.1, AI906045.1, AA164464.1, AA075671.1, AI830004.1, AI811907.1, AW797793.1, AW058212.1, AI983562.1, AA876142.1, H05350.1, AA131850.1, W72748.1, AI439472.1, AA486849.1, F06345.1, AW804431.1, AW373870.1, AA174655.1, AW817431.1, AI905784.1, AI905719.1, F23076.1, AA044017.1, AA610352.1, AA487747.1, AW609821.1, AI760378.1, AW078537.1, AA487367.1, AW614912.1, T87056.1, T29528.1, W37973.1, F07031.1, W37972.1, AA263171.1, AI492530.1, AA424397.1, AI865686.1, AA487528.1, AA294979.1, AW138402.1, AI386222.1, AI180927.1, AI036133.1, AA184762.1, AA153027.1, AA153021.1, AV362793.1, AA315174.1, F05698.1, AW815880.1, AW363341.1, AW362711.1, AA622193.1, AA057242.1, AI796944.1, T41892.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AL355818.2, AC009158.3, AC024026.2, AL138782.5, AL138934.2, AL138889.2, AC024150.5, AC008373.6, AC010630.3, AC021689.2, AC048369.1, AC015803.3, AC019071.2, AC010743.4, AP001809.1,

SEQ ID NO. 124

NGO-Br-40

MK303/T7 3'

- NM\_004120.2, M55543.1, AK001823.1, NM\_002053.1, M55542.1, NM\_010259.1, M63961.1, M55544.1, M80367.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, AC022522.2, AC006487.7, AL135749.2, AC005028.1, AF178650.1, AL163226.2, AP001681.1, AL035640.2, Y10720.1, AP001137.1, AC011282.3, AE002269.1, AC006142.1, NM\_011369.1, NM\_007199.1, AF113136.1, AF017152.1, AC006241.1, AF064699.1, AF069670.1, AF069669.1, AF057284.1, AL163235.2, AC002094.1, AL109984.14, AL139296.2, AL121871.8, AL161581.2, AL136132.15, U86532.1, AP001690.1, AL034567.1, X56844.1, AP000476.2, AB005234.1, L11794.1, L11777.1, X99948.1, AW001215.1, AW058212.1, AI830004.1, AA876142.1, AI760378.1, AW614912.1, AI983562.1, AI439472.1, AW078537.1, AA075477.1, AI870195.1, AA622193.1, W37973.1, AW341927.1, W37755.1, AA642656.1, AI492530.1, AI500507.1, AA837842.1, AI865686.1, AA635989.1, AA587444.1, AI285460.1, AI862178.1, AA937007.1, AA903286.1, AI289455.1, AA075671.1, AW373870.1, AA533156.1, AI084027.1, AA627607.1, AA532369.1, AA579973.1, AW793466.1, AW577433.1, AA917383.1, AW026936.1, AI138455.1, T29528.1, AI500511.1, AI859339.1, AI073859.1, AI969542.1, AW468007.1, AI371522.1, AI702366.1, AW609821.1, W01896.1, AA586545.1, AI251115.1, AI922648.1, AW804484.1, AW820994.1, AI905784.1, AI905719.1, AW817431.1, AA131800.1, AA487528.1, AA315174.1, AI280597.1, AI081732.1, AI075062.1, AW449506.1, AA937600.1, AA827350.1, AW799191.1, AI910674.1, AA810201.1, AA650178.1, AA486850.1, AA424529.1, AA837672.1, AA834863.1, AI861968.1, AW796865.1, AW304126.1, AA564905.1, AA056488.1, AW804456.1, AI902944.1, AW363341.1, AW805514.1, AW821048.1, AI372935.1, AI246407.1, AA587703.1, AW797815.1, AW797814.1, AA424397.1, W37972.1, AW799183.1, H05300.1, AW470713.1, AI007134.1, AA175795.1, AA139382.1, AA153021.1, AI386222.1, AA153027.1, AL161639.4, AL139416.1, AL160008.1, AC060233.1, AC026091.3, AC013475.4, AC068832.1, AC008373.6, AC010630.3, AC025799.2, AC016190.3, AC027133.1, AC018807.4, AC016720.4, AC012444.3, AC036136.2, AC023395.2, AC012264.8, AC022330.9, AC053477.2, AC023347.3, AC018461.18, AC027820.2, AC032036.2, AC026737.3, AC026704.3, AC022418.3, AC010369.5, AC010230.3, AC010396.3, AC008780.4, AC009051.5, AC009050.4, AC027780.2, AC027630.4, AC060807.1, AC027168.2, AC009614.4, AC017106.3, AC026590.2, AC027646.3, AC040964.1, AC015972.3, AC025790.2, AC011080.2, AC022247.2, AC024026.2, AC016686.4, AC024403.2, AC018408.1, AC013404.1, AC010874.2, AC012545.1, AL157771.3, AL139815.3, AL139275.6, AL139274.6, AL136380.2, AL355820.2, AL355886.1, AL354929.1, AL162453.4, AL096870.1, AL157818.2, AP002001.1, AP001985.1, AP001388.1, AP001241.1, AP001230.1,

SEQ ID NO. 125

NGO-Br-40

MK353/T3 5'

- NM\_004120.2, M55543.1, NM\_002053.1, M55542.1, AK001823.1, NM\_010259.1, M63961.1, M55544.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, M80367.1, AC004930.1, NC\_001143.1, NM\_000379.1, AC005669.1, AL121654.1, U39487.1, Z28127.1, X72016.1, U06117.1, D10044.1, D11456.1, NM\_001567.2, AC007048.4, AC005917.2, AC024882.1, AE003603.1, AE003479.1, NM\_006460.1, AF202730.1, AC002565.1, AC008125.9, AC007785.1, AF125463.1, AL163210.2, AL135749.2, AL132880.2, AL161581.2, AL161516.2, AL117204.1, Z81088.1, AL078588.9, AL117193.1, AL034449.1, AL049487.1, AL034567.1, L36818.1, X15209.1, X15750.1, Y14385.1, AB021179.1, AW820994.1, AW804484.1, AI902944.1, AW468007.1, AI969542.1, AW804456.1, AW821048.1, AI922648.1, AI859339.1, AI500511.1, AW577433.1, AI906045.1, AI251115.1, AA131850.1, AW578905.1, AA044192.1, AW861558.1, AW797814.1, AW797815.1, AA471169.1, AI683358.1, AA586545.1, AW001215.1, AW793466.1, AA164464.1, AI989871.1, AW474440.1, AI683206.1, AA075671.1, AI830004.1, AI811907.1, W72748.1, AW797793.1, H05350.1, AW058212.1, AI983562.1, AA876142.1, AA486849.1, F06345.1, AI439472.1, AA174655.1, AW373870.1, AW804431.1, AW817431.1, AA487747.1, F23076.1, AI905784.1, AI905719.1, AA610352.1, AW609821.1, AA044017.1, AI760378.1, AA487367.1, AW078537.1, W37973.1, F07031.1, AW614912.1, T29528.1, T87056.1, W37972.1, AI492530.1, AA263171.1, F05698.1, AI865686.1, AI386222.1, AI180927.1, AI036133.1, AA184762.1, AA153027.1,



- AA153021.1, AW815880.1, AW362711.1, AW400386.1, AV362793.1, AW363341.1, AI075062.1, AA487528.1, AA424397.1, AA315174.1, AA294979.1, AA057242.1, T41892.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AL355818.2, AC021689.2, AL138889.2, AL136985.1, AC024150.5, AC024038.5, AC019071.2, AC010743.4, AP001809.1, AC009770.4, AC023395.2, AC036129.2, AC027820.2, AC035140.2, AC008373.6, AC010630.3, AC008731.4, AC063979.1, AC017106.3, AC040911.1, AC024047.2, AC027362.1, AC012241.4, AC015975.3, AC006295.8, AC013759.2, AC017228.1, AC015394.1, AF166490.1, AC006916.1, AC006719.1, AL121796.4, AL353796.2, AL022594.18, AL035066.20, Z98858.1, Z98855.1, AL021573.1, AP001385.1, AP001157.1, AP000812.1, AP000593.1, AP000485.2,
- 10 SEQ ID NO.126  
NGO-Br-40  
MK451/T3 5'  
NM\_004120.2, M55543.1, M80367.1, NM\_010259.1, M63961.1, M55544.1, NM\_010260.1, AF109168.1, AF077007.1, AJ007970.1, NM\_002053.1, M55542.1, AK001823.1, AC004930.1, AF085699.1, AC007980.1, AL109935.39, X77129.1, Z95388.1, AB015429.1, AB020867.1, AC005103.3, NM\_013134.1, NM\_006460.1, U44731.1, AF047825.1, AC004798.1, AC003111.1, AB021179.1, M29249.1, AI906045.1, AA131850.1, AW368079.1, AW362711.1, AW815880.1, W72748.1, AW297239.1, AW820994.1, W77927.1, AI902944.1, AW861558.1, AW578905.1, AA878690.1, H05350.1, AA044192.1, AA486849.1, F06345.1, AI905784.1, AI905719.1, AI528561.1, AA911189.1, F07031.1, AI962517.1, AA873192.1, AW474440.1, AW820809.1, AA487747.1, AI989871.1, AA487367.1, AA164464.1, AI683358.1, AI683206.1, AW320458.1, T83604.1, T75545.1, AW817439.1, AW609764.1, AW211765.1, AW817360.1, AA122936.1, AW821048.1, AW804484.1, AW804456.1, AW106727.1, AW804431.1, AI811907.1, AI922921.1, AA174655.1, AA848004.1, AA506001.1, AW468007.1, AV362793.1, AA582749.1, W13273.1, AI651570.1, AA880099.1, AW665096.1, AW454822.1, AW166154.1, AI811680.1, AI796944.1, AV046437.2, AA955194.1, AI383864.1, AI216433.1, AA928789.1, AA927260.1, AA909971.1, AA890309.1, AA719024.1, C77542.1, AA514692.1, AA099506.1, N33318.1, N21081.1, H16325.1, Z44502.1, AL161639.4, AL160008.1, AL139416.1, AL138786.3, AC034166.2, AC016696.4, AL158849.7, AC036129.2, AC018354.6, AC012053.2, AC021689.2, AC024047.2, AC026047.2, AC024303.2, AC020883.2, AC006295.8, AF166490.1, AL356008.1, AL161658.3,
- 20 SEQ ID NO.127  
NGO-Br-41  
MK264/T3 5'  
NM\_004602.1, AF061941.1, AF061940.1, AF061939.1, AF061938.1, AJ132258.1, NM\_011490.1, AF061942.1, NM\_007344.1, X83973.1, AC004585.1, NM\_014865.1, NM\_014393.1, AC004002.1, AC007542.2, AF038608.1, AC006064.9, U32712.1, AL121877.13, Y19062.1, AK002152.1, AK001576.1, X67320.1, AB015752.1, M31229.1, L04287.1, L03711.1, X68492.1, D63880.1, AC006142.1, AC010186.6, AC008078.11, AC004131.1, U46596.1, AL121775.2, AL096802.11, AL034345.3, X89870.1, AP000497.1, AW351909.1, AW403841.1, AW836710.1, AW320695.1, AA240112.1, AA218774.1, AA270608.1, AW351905.1, AW141293.1, AA135261.1, U69197.1, H17179.1, T31173.1, T31172.1, AW581619.1, AA153656.1, T74327.1, W28253.1, AL045575.1, AA191685.1, R95466.1, AA209495.1, T06248.1, AA025528.1, AA285302.1, AW366804.1, AW153775.1, AI958903.1, AJ244015.1, AI386266.1, AI326431.1, AA562089.1, AA104976.1, W82776.1, AI353217.1, AA813637.1, AA700898.1, AV182864.1, AA918411.1, AA890493.1, U25927.1, AV398409.1, AV344143.1, AW123407.1, AA388686.1, AA156216.1, AL133174.11, AC063967.1, AC055879.1, AC011492.5, AC051627.3, AC068845.1, AC016960.6, AC015624.2, AC069023.1, AC027538.2, AC025512.2, AC022909.4, AC015944.3, AC009842.7, AC015989.3, AC015809.2, AC022403.3, AC023263.2, AC012595.3, AC012161.7, AC006739.1, AL355854.1, AL160399.2, AL157885.2, AP001397.1,
- 30 SEQ ID NO.128  
NGO-Br-41  
MK264/T7 3'  
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AI799396.1, AA620459.1, AA741223.1, AA090084.1, AW464265.1, AL133174.11, AC011492.5, AL158850.2, AC063967.1, AC068736.1, AC009429.3, AC067887.2, AC024935.8, AC026678.4, AC021057.3, AC021056.3, AC025928.2, AC015929.4, AC013364.7, AC025738.1, AC022049.3, AC017061.3, AC021682.1, AL158840.4, AL133284.12, AC026333.2, AC013625.3, AC009047.4, AC012215.3, AC027402.2, AC007383.3, AC055805.1, AC019088.3, AC026588.2, AC015825.4, AC021186.2, AC022903.3, AC024732.2, AC015834.3, AC021011.2, AC022820.2, AC016930.5, AC010974.4, AC021980.1, AC009642.2, AC005282.1, AL139084.4, AL353709.1, AL354723.1, AP001394.1,

SEQ ID NO. 129

10 NGO-Br-42 combined

AC005069.2, AB011102.1, L23077.1, NM\_013889.1, AF017806.1, AP001253.1, AE001788.1, AL133417.10, AF262044.1, AC008051.3, AF237670.1, AC021043.4, AF022974.1, L14730.1, AL031056.1, Z83313.1, AP001426.1, X01441.1, AB017192.1, AP000606.1, AB025611.1, AB018115.1, AL134426.1, AA972711.1, AW157207.1, AW770787.1, AW468156.1, AW473852.1, AI266259.1, AA599244.1, AI817665.1, AA837101.1, AI377803.1, AW163183.1, AA527031.1, AA721095.1, N33849.1, AA167375.1, AI572106.1, AI251893.1, AI241041.1, H84943.1, AA279430.1, AW609920.1, AA764886.1, AI699744.1, AA725331.1, AI302964.1, AI567039.1, AW379942.1, AI593485.1, D52427.1, D55742.1, AI956843.1, AA210577.1, T10410.1, C01624.1, AA165991.1, AA825378.1, AI642382.1, AA611337.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, N85349.1, AA473146.1, AA167374.1, D55908.1, AA471246.1, AI956621.1, AI606224.1, AA726787.1, R98544.1, AA292113.1, AA279626.1, AW385669.1, W45824.1, AI810043.1, H33984.1, R21996.1, AW416485.1, AV403226.1, AW260960.1, AW222072.1, AV227797.1, AW077780.1, AI820616.1, AV061748.1, AV042292.2, AI632719.1, AI423781.1, AI395491.1, AI014647.1, AA918760.1, AA829983.1, AA395972.1, AA363407.1, AA274077.1, AL139274.6, AL160258.3, AL137180.3, AL138875.3, AL137000.3, AC025451.3, AC023608.1, AC023276.3, AC068334.1, AC027596.2, AC008276.2, AC006451.2, AC019240.4, AC005308.6, AC010109.4, AC014418.1, AL138727.2,

25 SEQ ID NO. 130  
NGO-Br-42  
MK182/T3 5'

AC005069.2, AB011102.1, L23077.1, NM\_013889.1, AF017806.1, AL133417.10, AC004485.1, AC008082.12, AF022974.1, AE003628.1, AE003579.1, AE003420.1, AC012654.2, AC000096.13, AC005137.1, AC003063.7, AC016163.4, AC006317.3, AC004973.1, AC007649.12, AC005454.1, AL132976.2, AL122126.2, AC000392.1, AL121806.2, Z69838.1, AL022722.1, AL049571.1, U64875.1, AJ000521.1, D89336.1, AW163183.1, N33849.1, H84943.1, AA721095.1, AL134426.1, AI642382.1, AA611337.1, AA972711.1, AW609920.1, AW157207.1, AW770787.1, AA726787.1, AI266259.1, AI817665.1, AA837101.1, AA167375.1, N85349.1, AW473852.1, AI699744.1, AI251893.1, AW468156.1, AI572106.1, AA825378.1, AA764886.1, AA599244.1, AA165991.1, AA279626.1, AI956843.1, AI593485.1, AI942680.1, AV403226.1, AW334920.1, AW214633.1, AV227797.1, AW077780.1, AI820616.1, AI014647.1, AL139274.6, AL137180.3, AL160258.3, AC067751.1, AC026297.2, AC022907.3, AC016212.3, AC023608.1, AC069075.1, AC068778.3, AC044835.2, AC023276.3, AC069019.1, AC021870.6, AC068334.1, AC008276.2, AC053489.1, AC021598.4, AC024718.3, AC019240.4, AC024646.2, AC005308.6, AC018580.4, AC024632.1, AC018519.3, AL158166.6, AL158158.4, AL157393.1,

40 SEQ ID NO. 131  
NGO-Br-42  
MK182/T7 3'

AC005069.2, AB011102.1, L23077.1, NM\_013889.1, AF017806.1, AL163231.2, AP001686.1, AP001253.1, AE001788.1, AF262044.1, AF237670.1, AC021043.4, AE003478.1, AF229187.1, AC004658.1, AL163276.2, AL118512.8, L14730.1, Z83313.1, AP001731.1, AP001426.1, X01441.1, AB017192.1, AP000163.1, AB025611.1, AP000021.2, NC\_001136.2, AC009415.2, AE003824.1, AC004460.1, NM\_011261.1, AC008072.3, AC005046.3, AF115517.1, AC005467.1, U24703.1, AE000943.1, AL049834.3, AL049546.3, Z93374.1, AL021939.1, Z74123.1, X51895.1, Z78583.1, D63520.1, AW157207.1, AA972711.1, AW770787.1, AW468156.1, AI266259.1, AA599244.1, AI377803.1, AA527031.1, AI572106.1, AA279430.1, AA725331.1, AI302964.1, AI567039.1, AW379942.1, D52427.1, D55742.1, AI593485.1, AI956843.1, T10410.1, AA210577.1, C01624.1, AA165991.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, AA473146.1, D55908.1, AI606224.1, AW163183.1, R98544.1, AA292113.1, AW385669.1, W45824.1, AI810043.1, H33984.1, R21996.1, AW222072.1, AI632719.1, AI423781.1, AA829983.1, AA395972.1, AA274077.1, AA030373.1, W20048.1, AL139274.6, AL137180.3, AL160258.3, AL138875.3, AL137000.3, AC027490.3, AC025451.3, AC010432.4, AL137249.6, AC069145.1, AC069071.1, AC018473.9, AC006451.2, AC027189.2, AC023844.2, AC021677.3, AC010109.4, AL135932.4, AL137013.3, AC041025.2, AC012211.3, AC027600.1, AC024254.2, AC024026.2, AC023153.2, AC012369.2, AC018873.1, AF188032.1, AL139418.1, AP001813.1,

60 SEQ ID NO. 132  
NGO-Br-42  
MK203/T3 5'

AC005069.2, AB011102.1, L23077.1, NM\_013889.1, AF017806.1, AC016678.4, AE003694.1, AE003528.1, AF063866.1, AP000606.1, AB018115.1, AC016749.4, AC019209.3, AE003706.1, AE003579.1, AE003462.1, AF240628.1,

AC011284.3, AF224669.1, AC006317.3, AC005534.2, AC003037.1, U70823.1, AC004642.1, AL163224.2, AL049588.11, AL161516.2, AL161514.2, AL117386.1, AL078599.19, AL035693.19, Z81089.1, Z69838.1, Z95329.1, AL022722.1, AL035090.10, AP001679.1, AL049571.1, U64875.1, AJ000521.1, AL049482.1, L33820.1, L33819.1, AP001251.1, M76616.1, X61589.1, D89336.1, AP000001.1, AL134426.1, AW473852.1, AA837101.1, AI817665.1, AA721095.1, AA167375.1, AI251893.1, AW609920.1, AI241041.1, AA764886.1, N33849.1, AI699744.1, H84943.1, AW163183.1, AA825378.1, N85349.1, AI642382.1, AA611337.1, AA279626.1, AV424771.1, AW416485.1, AW260960.1, AV061748.1, AV042292.2, AL139274.6, AL160258.3, AL137180.3, AC026297.2, AC025494.2, AL109926.2, AC027596.2, AC020987.4, AC023957.3, AC016187.4, AC062033.1, AC025104.2, AC025526.2, AC022744.2, AC024632.1, AC022691.1, AC009818.4, AC010204.8, AC008250.15, AC020418.1, AC009588.4, AC012259.2, AC014418.1, AC007692.3,

SEQ ID NO. 133

NGO-Br-42

MK2410/T3 5'

AC005069.2, AB011102.1, L23077.1, NM\_013889.1, AF017806.1, AC016678.4, AE003694.1, AF063866.1, AL049874.3, AP000606.1, AB018115.1, NC\_001134.1, AC016749.4, AE003831.1, AE003528.1, AC011284.3, AF224669.1, U91318.1, AC006317.3, AC006004.1, AC005534.2, AC006221.1, U17503.1, U70823.1, AL049588.11, AL133512.10, Z69838.1, Z95329.1, AL035090.10, L33820.1, L33819.1, Z36160.1, X76053.1, AB020865.1, M76616.1, X61589.1, AP000001.1, AL134426.1, AW473852.1, AA837101.1, AI817665.1, AA167375.1, AI241041.1, AI251893.1, AA721095.1, AW609920.1, AA764886.1, AI699744.1, AA825378.1, N85349.1, N33849.1, AA167374.1, AA471246.1, H84943.1, AI956621.1, AW163183.1, AI642382.1, AA611337.1, AV042292.2, AW646457.1, AW642567.1, AW416485.1, AW260960.1, AV061748.1, AI395491.1, AL139274.6, AL160258.3, AL137180.3, AL139223.2, AC016904.2, AC026297.2, AC025494.2, AC016469.4, AC012219.3, AC020987.4, AC023957.3, AC016187.4, AC025104.2, AC009818.4, AC010204.8, AC008250.15, AC020418.1, AC012259.2, AC007692.3, AL157389.3, AC037489.2, AC015846.3, AC037434.2, AF267167.1, AC023156.3, AC010543.4, AC009128.5, AC007716.2, AC009547.3, AC010902.3, AC019171.3, AC008271.3, AC018797.3, AC062007.1, AC026829.2, AC025656.2, AF235099.1, AC026225.2, AC025660.2, AC009562.5, AC021619.3, AC016667.2, AC007413.4, AC007330.5, AC012182.3, AC025348.1, AC010894.3, AC011564.3, AC014418.1, AC013270.2, AC014124.1, AC010826.2, AC007414.4, AL162579.4, AL161647.5, AL157779.4, AL136311.3, AL355312.3, AL354893.3, AL136319.7, AL354711.1, AL157836.3, AL122125.1, AP001448.1, AP001023.1, AP000813.1, AP000675.1, AP000624.1,

SEQ ID NO. 134

NGO-Br-42

MK2410/T7 3'

AC005069.2, AB011102.1, L23077.1, NM\_013889.1, AF017806.1, AL163231.2, AP001686.1, AP001253.1, AF262044.1, AF237670.1, AC021043.4, AE003478.1, AF229187.1, AC008072.3, AC004658.1, AL163276.2, AL118512.8, L14730.1, Z83313.1, AP001731.1, AP001426.1, X01441.1, AB017192.1, AP000163.1, AB025611.1, AP000021.2, NC\_001136.2, AC009415.2, AC004460.1, AC005046.3, AF115517.1, AL049834.3, AL049546.3, Z93374.1, AL021939.1, Z74123.1, D00702.1, X51895.1, Z78583.1, AW157207.1, AA972711.1, AW468156.1, AW770787.1, AI266259.1, AA599244.1, AI377803.1, AA527031.1, AI572106.1, AA279430.1, AA725331.1, AI302964.1, AI567039.1, AW379942.1, D55742.1, TI0410.1, D52427.1, AI593485.1, AI956843.1, C01624.1, AA210577.1, AA165991.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, AA473146.1, D55908.1, AW163183.1, AI606224.1, R98544.1, AA292113.1, AW385669.1, AW061815.1, H33984.1, R21996.1, AW728990.1, AW222072.1, AI810043.1, AI632719.1, AI423781.1, AA829983.1, AA030373.1, AL139274.6, AL137180.3, AL160258.3, AL138875.3, AL137000.3, AC027490.3, AC025451.3, AC010432.4, AL137249.6, AC069145.1, AC019230.3, AC034127.2, AC024687.3, AC006451.2, AC027189.2, AC020695.3, AC009407.3, AC021677.3, AC023095.2, AC010109.4, AC019599.1, AL135932.4, AL137013.3, AC069071.1, AC024223.7, AC018473.9, AC012323.4, AC024272.2, AC044797.2, AC027215.2, AC034298.1, AC016350.3, AC016031.2, AC027600.1, AC024254.2, AC024026.2, AC011272.3, AC023153.2, AC013409.3, AC012369.2, AC011231.3, AC011619.2, AC016407.1, AF188032.1, AL121943.13, AL353786.2, AL161417.5, AL139418.1, AP001813.1,

SEQ ID NO. 135

NGO-Br-42

MK245/T7 3'

AC005069.2, AB011102.1, L23077.1, NM\_013889.1, AF017806.1, AL163231.2, AP001686.1, AP001253.1, AF262044.1, AF237670.1, AC021043.4, AE003478.1, AF229187.1, NM\_011692.1, AC004901.1, U96760.1, AC004658.1, AL163276.2, AL118512.8, L14730.1, Z83313.1, X01441.1, AP001731.1, AP001426.1, AB017192.1, AP000163.1, AB025611.1, AP000021.2, AC005046.3, AC007887.8, AL032637.1, Z78016.1, AL031825.1, AL049546.3, AL031644.1, Z93374.1, AL021939.1, Z74123.1, Z68252.1, X51895.1, Z78583.1, AA972711.1, AW157207.1, AW468156.1, AW770787.1, AI266259.1, AA599244.1, AI377803.1, AA527031.1, AI572106.1, AA279430.1, AA725331.1, AI302964.1, AW379942.1, AI567039.1, AI593485.1, D52427.1, D55742.1, AI956843.1, TI0410.1, AA210577.1, C01624.1, AA165991.1, AW214633.1, AI551647.1, AW489266.1, AI467091.1, AA473146.1, D55908.1, AW163183.1, AI606224.1, R98544.1, AA276787.1, W45824.1, AI942680.1, H33984.1, R21996.1, AI632719.1, AI423781.1, AA829983.1, AA030373.1, AL139274.6, AL137180.3, AL160258.3, AL138875.3, AL137000.3, AC027490.3, AL137249.7, AC069145.1,

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AC018473.10, AC069071.2, AC025451.3, AC010432.4, AC006451.2, AC020695.3, AC021677.3, AC010109.4, AC019599.1, AL135932.4, AL137013.3, AL138725.4, AC012014.5, AC012323.4, AC024272.2, AC044797.2, AC027215.2, AC016350.3, AC027600.1, AC024254.2, AC024026.2, AC016878.3, AC011272.3, AC012369.2, AF188032.1, AL157936.3, AL139418.1, AP001813.1, AP001198.1,

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SEQ ID NO. 136

NGO-Br-43

- AB023420.1, L12723.1, X67643.1, AF077354.1, NM\_008300.1, D85904.1, X67641.1, X67642.1, X67640.1, AC011013.17, U23921.1, NM\_014278.1, AB023421.1, NM\_011020.1, D49482.1, AB001926.1, NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, Z47807.1, NM\_013559.1, L40406.1, D67017.1, D67016.1, AB005279.1, AE003433.1, AC010072.5, AC004674.1, AL078621.19, AL096821.2, Z71263.1, Y13478.1, AC008545.3, AC011751.2, AC009489.3, AE003820.1, AE003518.1, M96150.1, AC007453.1, AC006409.2, AC006502.2, AC002350.1, AC003006.1, AL132793.24, AL121904.13, AL135879.1, AL132994.2, AL121790.2, AL133033.1, AJ251914.1, Z73907.1, AL008713.1, AL034348.5, AL034551.14, AL033522.1, AL008628.1, AP000555.1, AB028948.1, AL135032.1, AW609809.1, AW391888.1, AW609816.1, AW817219.1, AI567970.1, AW578992.1, AI925201.1, AI925201.1, AW363570.1, AW085727.1, AI188118.1, AI560115.1, AI754819.1, AI956648.1, AA493400.1, AW754210.1, AA191559.1, AA173193.1, AW367717.1, AW583074.1, AI907727.1, AI627184.1, AW513086.1, AI952125.1, AW609784.1, AW192860.1, AW489091.1, AW578990.1, AA205597.1, AI274739.1, AI014766.1, AA913650.1, AW363562.1, AI230094.1, AI140781.1, AI375447.1, AI983708.1, W74245.1, AW613658.1, AA913187.1, AA633656.1, AA162193.1, AI678576.1, AW817504.1, AA518224.1, AA210820.1, AW819755.1, AA216635.1, AI866008.1, AA354293.1, AA874242.1, AA761335.1, AA103602.1, AW545353.1, AA227204.1, AW545094.1, AW537735.1, AA991908.1, AW819997.1, AW578928.1, AW262251.1, AI408846.1, AW542227.1, AA125191.1, AA437859.1, AA821679.1, AW754207.1, AA542289.1, AA121736.1, AA591244.1, AW861588.1, AI909282.1, N50726.1, AW582514.1, AI956869.1, AW196018.1, AW609842.1, AW372094.1, AI799801.1, AW817153.1, AW609769.1, AW582510.1, AW817315.1, AW371571.1, AW817164.1, AW817496.1, AW817372.1, AW582499.1, AW391901.1, AW381775.1, AA870633.1, AA498893.1, AA687763.1, AW817440.1, AW371552.1, AW371548.1, R11513.1, AW817445.1, AI314009.1, AI760838.1, AC020834.2, AC015501.3, AC021286.3, AC022550.1, AL137142.8, AC048384.2, AC065723.1, AC063302.1, AC039237.1, AC034727.1, AC034094.1, AC025168.3, AC013883.1, AL135795.3, AL160402.2, AL121814.1, AC034304.2, AC021076.3, AC036128.2, AC068226.1, AC025689.3, AC067810.1, AC027184.2, AC017102.5, AC023692.2, AC018288.1, AL121956.4, AL138965.3,

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SEQ ID NO. 137

NGO-Br-43

MK132/T3 5'

- AB023420.1, L12723.1, X67643.1, AF077354.1, NM\_008300.1, D85904.1, NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1, NM\_014278.1, NM\_011020.1, U23921.1, AB023421.1, D49482.1, AB001926.1, U81260.1, AI132792.1, NM\_013559.1, AE003820.1, AE003518.1, AC007453.1, AC006409.2, U76309.1, AL121775.2, AL133033.1, AL034348.5, AL034551.14, AL008628.1, L40406.1, AP000555.1, AB028948.1, D67017.1, D67016.1, AF245116.1, AC008865.3, AC007171.4, AC006200.2, AC006624.1, NM\_013513.1, AE003750.1, AE003571.1, AC011809.2, AC012380.1, AC011198.2, U78296.2, AF106589.1, Y14213.1, AL078594.36, Z70757.1, Z77657.1, AL049861.18, AL115647.1, AL113847.1, AL111874.1, U04056.1, U04055.1, U03487.1, AB005279.1, AB005275.1, U00035.1, M57719.1, L35933.1, X56682.1, M59962.1, AW578992.1, AW363570.1, AW609809.1, AW391888.1, AW609816.1, AW817219.1, AW367717.1, AW578990.1, AA191559.1, AW363562.1, AW583074.1, AL135032.1, AW609784.1, AI909282.1, AI907727.1, AW754210.1, AW817504.1, AA626524.1, T29047.1, AA370218.1, W26511.1, AA755774.1, AW817215.1, AA125191.1, AW609842.1, AW817153.1, AW609769.1, AW582510.1, AW582514.1, AW817164.1, AW817496.1, AW817440.1, AW817372.1, AW817318.1, AW817315.1, AW817234.1, AW582499.1, AW391901.1, AW381775.1, AW372094.1, AW371556.1, AW371553.1, AW371550.1, AW817445.1, AW817442.1, AW601252.1, AW582504.1, AW371571.1, AW371552.1, AW371548.1, AW817364.1, AW817319.1, AA543642.1, AA437859.1, AW371570.1, AW817432.1, AW372116.1, AW819755.1, AW371546.1, AW609859.1, AW609807.1, AW371549.1, AW609846.1, AW578928.1, AW609867.1, AW609856.1, AA518224.1, AW609844.1, AW384296.1, AI760838.1, AA870633.1, AA117945.1, AI956648.1, AW748834.1, AI827505.1, D29434.1, AA615363.1, AA445826.1, AJ396671.1, AW819997.1, W22433.1, AW839103.1, AA874242.1, AW754207.1, AA103602.1, AW125594.1, AA919208.1, AW366794.1, AW371561.1, AI314009.1, R54223.1, AW371568.1, AI567970.1, AW861588.1, AW229772.1, AA645750.1, AA212025.1, AA821679.1, AV312929.1, AW391883.1, AC020834.2, AL137142.8, AC027421.2, AC025860.2, AC055864.2, AC065723.1, AC063302.1, AC039237.1, AC034727.1, AC034094.1, AC022301.6, AC068812.8, AC012157.9, AC034304.2, AC009781.5, AC009321.5, AC023056.7, AC027672.3, AC025689.3, AC027184.2, AC016065.4, AC009899.5, AC010563.3, AC013243.4, AC018288.1, AC015160.1, AC005450.4, AL356425.1, AL356303.2, AL121589.12, AC002417.1, AL139108.2, AP001180.1,

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SEQ ID NO. 138

NGO-Br-43

MK132/T7 3'

AB023420.1, NM\_008300.1, D85904.1, AF077354.1, X67643.1, L12723.1, NM\_011020.1, U23921.1, D49482.1, AB001926.1, AC010072.5, Z71263.1, AC009489.3, AC024817.1, AE003641.1, AE003408.1, AC012039.10, AC004614.1,

- AF164299.1, NM\_008229.1, AC006355.3, AF071221.1, AC007172.6, AC005856.1, AC005495.1, AC004671.1, U31758.1, AE001016.1, AL031853.1, AL023804.1, X59603.1, L39125.1, D01021.1, AI567970.1, AI925201.1, AW085727.1, AI188118.1, AI560115.1, AI754819.1, AA493400.1, AA173193.1, AI627184.1, AW513086.1, AI952125.1, AW192860.1, AA205597.1, AI274739.1, AI014766.1, AA913650.1, AI140781.1, AI375447.1, AI983708.1, AW613658.1, AA913187.1, AA633656.1, AI678576.1, AA210820.1, AA216635.1, AI866008.1, AA761335.1, AW545353.1, AA227204.1, AW754210.1, AW545094.1, AW537735.1, AA991908.1, AW262251.1, AI408846.1, AW542227.1, AW819755.1, AW819997.1, AW861588.1, N50726.1, AI956869.1, AW196018.1, AI799801.1, AW578928.1, AA687763.1, C76500.1, AW529607.1, R11513.1, AW754207.1, R54223.1, AA061925.1, C81619.1, AW604699.1, AI347806.1, AA558925.1, AI593463.1, AA179753.1, AA542420.1, AW682076.1, AU020108.1, W27793.1, C81004.1, AA180330.1, AA121181.1, Z18817.1, AA823019.1, AI911599.1, AW060626.1, R60452.1, AW583074.1, AI197516.1, AA935133.1, AU015665.1, AA671121.1, AW604696.1, AW366794.1, AI760838.1, N74649.1, AW071627.1, AA408319.1, AA407913.1, AI501198.1, AA799083.1, AA543635.1, AW213908.1, AI576267.1, AV165705.1, AA434598.1, AA703912.1, AW071628.1, AV294079.1, AW754208.1, N79564.1, AW371893.1, AA655993.1, R56469.1, AI569348.1, AA948300.1, AI655547.1, AV301839.1, AC048384.2, AC002518.1, AL160402.2, AC068975.1, AC026382.3, AC020551.2, AC021393.2, AL353725.3, AL354926.1, AC018920.5, AC046135.4, AC064821.2, AC025511.2, AC026745.3, AC010464.4, AC036128.2, AC021573.4, AC068383.1, AC066588.1, AC027012.2, AC018990.4, AC026061.2, AC021717.3, AC024037.2, AC015653.3, AC019002.3, AC022038.2, AC017901.1, AC006911.1, AL121834.8, AL160290.3, AL157819.2,
- 20 SEQ ID NO.139  
NGO-Br-43  
MK261/T3 5'  
AB023420.1, X67643.1, L12723.1, NM\_008300.1, AF077354.1, D85904.1, X67641.1, X67642.1, AC011013.17, U23921.1, NM\_014278.1, AB023421.1, NM\_011020.1, D49482.1, AB001926.1, AL132776.11, AL078621.19, Y13478.1, AC011751.2, AC009489.3, AC006502.2, AC002350.1, AC003006.1, AL135879.1, AL121790.2, AC007244.2, AC019183.3, AC010361.3, AC011292.2, AF248484.1, NM\_013559.1, AC004459.1, AC003984.1, AC002460.1, AC004612.1, AC004822.1, AC006322.2, AC004988.2, AC005050.2, AC008173.2, AC004772.1, AC005406.2, AC006559.6, AC009248.6, AC008071.2, AC007794.1, AF101874.2, AF064254.1, AC003689.1, AC003678.1, AF068862.1, AC004075.1, AC004043.1, U01882.1, AL163207.2, Z72001.1, AL160192.2, AL049555.6, AL078595.12, U50871.1, AL035661.16, AL080316.8, AL050334.12, AL109854.10, AL096802.11, Z68873.1, AL031000.1, AL023806.1, Z97987.1, Z98748.1, Z84477.1, AL021307.1, L40406.1, AP001065.1, D67017.1, D67016.1, W74245.1, AA121736.1, AA542289.1, AA591244.1, AA498893.1, AA354293.1, AA162193.1, AI314009.1, AW489091.1, N85657.1, AI956648.1, AI230094.1, R56974.1, AW861596.1, AV226442.1, AV226379.1, AA063966.1, AA821679.1, AA896038.1, AL135032.1, AA874242.1, AW578931.1, AW578926.1, AA103602.1, AA518224.1, AA499765.1, AA385978.1, AV320109.1, AA121221.1, AV226463.1, H93522.1, AA247166.1, W20649.1, AI956324.1, AW385268.1, AW385266.1, AJ396671.1, AW502280.1, AW501910.1, AW501774.1, AW274501.1, AU037061.1, AI085867.1, AA747312.1, AA102000.1, H23069.1, H10565.1, AC020834.2, AC015501.3, AC021286.3, AL355143.4, AC025168.3, AC016767.3, AL353608.2, AL135795.3, AC036128.2, AC010814.5, AC017022.3, AC022968.2, AC022760.2, AC009875.2, AL353625.2, AL121956.4, AP001587.1, AC021053.7, AC018474.9, AC034305.2, AC068992.3, AC040969.2, AC040965.2, AC040960.2, AC023410.3, AC023538.2, AC026698.3, AC025182.2, AC024569.2, AC022433.3, AC022430.3, AC022135.3, AC008773.6, AC008968.4, AC010234.3, AC011346.3, AC008673.6, AC021595.3, AC062017.2, AC023116.4, AC010133.2, AC058804.1, AC018978.5, AC040961.1, AC026493.3, AC021464.2, AC023858.2, AC021948.3, AC018443.5, AC016763.5, AC021208.3, AC015823.3, AC022039.2, AC023560.2, AC009666.4, AC024010.2, AC010895.3, AC012669.2, AC021319.1, AC012502.2, AC013259.1, AL139375.7, AL355345.2, AL139803.7, AL136087.6, AL158147.4, AL354875.3, AL138702.5, AL353151.2, AL162492.3, AL034378.2, AP001986.1, AP001828.1,
- 50 SEQ ID NO.140  
NGO-Br-43  
MK2912/T3 5'  
AB023420.1, X67643.1, L12723.1, AF077354.1, NM\_008300.1, D85904.1, X67641.1, X67640.1, AC011013.17, X67642.1, U23921.1, NM\_014278.1, AB023421.1, NM\_011020.1, D49482.1, AB001926.1, AL078621.19, AL096821.2, Y13478.1, NM\_006644.1, AC004003.1, AF039695.1, AF117829.1, AF069291.1, AC002350.1, AB003334.1, AB003333.1, D86956.1, L43098.1, L43082.1, AC010352.4, AC007730.2, AC007662.2, AF240629.1, AF123535.1, AC002124.1, AF130247.2, AC005228.1, AC009248.6, AF081491.1, AF081490.1, AF081489.1, AF081488.1, AF081487.1, AF165138.1, AF064254.1, AF112117.1, U96409.1, AC005900.1, AC004636.1, AC004472.1, U69258.1, AL163224.2, AL163206.2, AL161537.2, X15901.1, Y08502.1, Z68873.1, AL022727.1, AL022097.1, AL031073.1, AL035528.2, AP001679.1, AP000957.2, AW489091.1, AI230094.1, AI956324.1, AI956249.1, AA591244.1, AI316935.1, AW069322.1, AA498893.1, AW318627.1, AI506418.1, AA542289.1, AA840049.1, AA205624.1, AI314009.1, AA499765.1, AV320109.1, W74245.1, AA726333.1, AA408320.1, AA247166.1, AW755799.1, AW755396.1, AW568012.1, AW567990.1, AW397511.1, AW234798.1, AA162193.1, AW681906.1, AL045611.2, AI851924.1, AL044212.1, AL043449.1, AA793473.1, AA690112.1, AA675583.1, AA360776.1, AA183406.1, AA120371.1, AV131040.1, AV047607.2, AV047086.2, AI046570.1, AA499782.1, AA498000.1, AA144603.1, AA139245.1, AA138950.1, AA110497.1, AA062258.1, AA060083.1, H23069.1, H10565.1, R59827.1, R28864.1, AC020834.2, AC015501.3, AC021286.3, AC022550.1,

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AC022089.4, AC010428.4, AC011403.2, AC025168.3, AC021755.4, AC016767.3, AL163541.6, AL353608.2, AL135795.3, AL163545.4, AL160031.4, AC026084.2, AC026562.3, AC051613.3, AC008483.4, AC046137.3, AC068226.1, AC016002.5, AC031979.1, AC015578.4, AC019235.2, AC019228.4, AC017102.5, AC008519.2, AC016281.2, AL356272.1, AL139823.2, AL137142.8, AL353625.2, AL121956.4, AL138965.3, AL136456.3,

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SEQ ID NO. 141

NGO-Br-43

MK466/T3 5'

AB023420.1, X67643.1, L12723.1, AF077354.1, NM\_008300.1, D85904.1, X67641.1, X67642.1, X67640.1,  
10 AC011013.17, U23921.1, NM\_014278.1, AB023421.1, NM\_011020.1, D49482.1, AB001926.1, AL078621.19,  
AL096821.2, Y13478.1, AL121904.13, AJ251914.1, AC010352.4, AC007662.2, NM\_013559.1, AE003537.1,  
AC004492.1, AC009248.6, AC007388.3, AF064254.1, U96409.1, AC004636.1, AL121821.5, AL161537.2, Z48006.1,  
Z68873.1, AL022097.1, AL035528.2, L40406.1, M26221.1, D67017.1, D67016.1, AW489091.1, AI230094.1,  
AA591244.1, AA498893.1, W74245.1, AA542289.1, AI314009.1, AI956324.1, AA121736.1, AI956249.1, AI316935.1,  
15 AA162193.1, N85657.1, AW069322.1, AI506418.1, AV226442.1, AI956648.1, AA499765.1, AA354293.1, AV320109.1,  
AW318627.1, AA205624.1, AA063966.1, R56974.1, AV226379.1, AA247166.1, AA840049.1, AW385268.1,  
AW385266.1, AA726333.1, AV340213.1, AI870749.1, AV047607.2, AV047086.2, AI046570.1, AA747312.1, C39670.1,  
AA499782.1, AA498000.1, AA144603.1, AA139245.1, AA138950.1, AA110497.1, AA062258.1, AA060083.1, H23069.1,  
H10565.1, R59827.1, AC020834.2, AC015501.3, AC021286.3, AC025168.3, AC021755.4, AC016767.3, AL163541.6,  
20 AL353608.2, AL135795.3, AL163545.4, AL160031.4, AC026084.2, AC026562.3, AC064862.2, AC016002.5,  
AC019235.2, AC017102.5, AL353625.2, AL121956.4,

SEQ ID NO. 142

NGO-Br-43

25 MK691/T3 5'

AB023420.1, X67643.1, L12723.1, NM\_008300.1, D85904.1, AF077354.1, X67642.1, NM\_014278.1, AB023421.1,  
NM\_011020.1, U23921.1, D49482.1, AB001926.1, NM\_006644.1, AF039695.1, AB003334.1, AB003333.1, D86956.1,  
AE003433.1, AC004674.1, AC008545.3, AC011751.2, AC009489.3, NM\_013559.1, AC006502.2, AC003006.1,  
AL132793.24, AL135879.1, AL121790.2, AL008713.1, L40406.1, Z47807.1, M38250.1, D67017.1, D67016.1,  
30 AC010879.2, AC012082.6, AC020943.5, AC006200.2, AF248484.1, AC009311.2, AC004459.1, AC004745.1,  
AC003984.1, AC002452.1, AC002461.1, AC004612.1, AC004741.1, AC004930.1, AC002519.1, AC008173.2,  
AC005406.2, AC006559.6, AC003666.1, AF101874.2, AC003689.1, AC003678.1, AC005393.1, AC004075.1,  
AC004043.1, U01882.1, U80460.1, AL160192.2, AL049555.6, AL035665.29, AL078595.12, U50871.1, AL050334.12,  
AL096802.11, Z97987.1, Z92844.1, Z98748.1, Z84475.1, AL009176.1, U41995.1, AB005275.1, Y15994.1, AB016880.1,  
35 AB020870.1, AI956648.1, AA354293.1, AL135032.1, AA162193.1, W74245.1, AA821679.1, AA121736.1, AA103602.1,  
AA874242.1, AA518224.1, AI907727.1, AA121221.1, AW861596.1, N85657.1, AA542289.1, AW582514.1, AW372094.1,  
AW817315.1, AW371571.1, R56974.1, AW817219.1, AW817496.1, AW817372.1, AW817364.1, AW817164.1,  
AW817153.1, AW609859.1, AW609846.1, AW609816.1, AW609809.1, AW609769.1, AW582510.1, AW582499.1,  
AW391901.1, AW381775.1, AW371552.1, AW371546.1, AA437859.1, AW609842.1, AW371550.1, AW817440.1,  
40 AW817432.1, AW817319.1, AW609867.1, AW609856.1, AW391888.1, AW384296.1, AW371549.1, AW371548.1,  
AW817445.1, AW817442.1, AW609844.1, AW371570.1, AW817504.1, AW371556.1, AW817234.1, AW371553.1,  
AW817318.1, AA870633.1, AA125191.1, AW609784.1, AW582504.1, AW372095.1, AA191559.1, W20649.1,  
AW601252.1, AA896038.1, AI314009.1, AA543642.1, AW372116.1, AA498893.1, AV226442.1, AW578931.1,  
AV226379.1, AW578926.1, AA063966.1, AA385978.1, AJ396671.1, AW371561.1, AI827505.1, D29434.1, AW748834.1,  
45 AA591244.1, AW371568.1, W26511.1, AW22772.1, H93522.1, AV226463.1, AA549649.1, AW577563.1, AL042714.2,  
AI656127.1, AI633338.1, AI267631.1, AI203278.1, AA714219.1, AA580845.1, AA311379.1, AW210124.1, X85639.1,  
AC020834.2, AC021286.3, AL137142.8, AC013883.1, AL133489.1, AL121814.1, AC069108.1, AC068732.1,  
AC021076.3, AC067810.1, AC010814.5, AC023692.2, AC009875.2, AP001587.1, AP001180.1, AC034305.2,  
AC068992.3, AC040960.2, AC026998.2, AC044809.2, AC023410.3, AC025752.4, AC022433.3, AC022430.3,  
50 AC022135.3, AC008961.4, AC008968.4, AC011346.3, AC008561.3, AC008539.3, AC021595.3, AC017100.3,  
AC010133.2, AC010810.3, AC009657.3, AC026824.2, AC027281.2, AC021548.3, AC011954.5, AC023858.2,  
AC015681.4, AC025411.2, AC021948.3, AC013321.4, AC025218.2, AC013368.4, AC011055.6, AC017082.3,  
AC015943.3, AC021208.3, AC015823.3, AC016421.4, AC013297.4, AC022039.2, AC023560.2, AC023034.2,  
AC025599.1, AC012451.3, AC021350.2, AC021319.1, AC007799.4, AC013759.2, AC011107.2, AC007914.1,  
55 AL355345.2, AL160407.4, AL157785.2, AL139344.4, AL355599.2, AL355332.1, AL353143.2, AL161913.2, AL353624.1,  
AL158819.2, AL133255.9, AL157759.2, AL158140.2, AL034378.2, AP001488.1, AP001336.1,

SEQ ID NO. 143

NGO-Br-44

60 MK062/T3 5'

AF210818.1, AF134894.1, AB014540.1, NM\_009302.1, AF053974.1, AE003678.1, AE003692.1, AC004260.1,  
AC005244.1, AL162633.2, AL138996.2, AL049522.1, AL035603.11, AE003589.1, AE002906.1, AC006926.1,  
AC002080.1, U91322.1, AC006043.1, AC005082.2, AF128252.1, AF128251.1, AF128249.1, AF128247.1, AC005548.1,  
AC005269.1, U32723.1, AL022598.2, AL133391.5, AL121656.2, Z35601.1, AL034561.4, AL033530.1, U35657.1,

- K01711.1, AB027827.1, AB027454.1, M20865.1, J04355.1, Z66517.1, A1181303.1, AW824953.1, AW123265.1, AW504308.1, AW824368.1, AW425515.1, AJ392422.1, AW202793.1, AW029904.1, AW487421.1, AV070180.1, AU013359.1, AC025788.2, AC026250.3, AC011979.3, AC026628.2, AC009800.6, AC023126.2, AC014216.1, AC009539.5, AL160255.5, AL138790.2, AC055752.5, AC055875.2, AC053484.3, AC021515.3, AC024494.1, AC021857.2, AC010097.4, AC016475.1, AC012199.4, AC013013.1, AL031726.16, AL133259.23, AL355073.1, AL353152.2, AL137183.1, AP001852.1, AC024905.7, AC024890.7, AC008713.5, AC011376.2, AC008856.4, AC026958.2, AC024595.2, AC026259.3, AC025966.2, AC025818.2, AC022735.3, AC024387.2, AC022040.2, AC023375.2, AC017402.1, AC009610.1, AL356358.1, AL355293.2, AL008872.1,
- 10 SEQ ID NO.144  
NGO-Br-44  
MK062/T7 3'  
AB014540.1, AF134894.1, AC004834.2, AC006538.1, Z97054.1, AF111168.2, AL109914.16, AL121586.28, AC002094.1, AC006457.3, AL031985.10, AC002400.1, U80017.1, AF030453.1, AL031846.2, Z95152.1, AC005031.1, AL049874.3, Z72006.1, AC007386.3, AC000353.27, AC005207.1, AC003002.1, AL160191.2, AL034429.1, AC004552.1, AC004195.1, AL078639.5, AF168787.1, AC002477.1, AC005796.1, AC005500.2, AP000689.1, AC005081.2, AC002492.1, AC004815.2, AC005049.2, AC006064.9, AC005839.1, AC002350.1, AL163292.2, AP001747.1, AC005412.5, AC003104.1, AL049569.13, AP000505.1, AP000045.1, AC011890.4, AC007225.2, AC005102.1, AL136295.2, Z85994.1, AL050321.8, AC005227.2, AC003663.1, AC008115.3, AC011311.11, AC005793.1, AL024507.7, AL096800.20, AL049795.20, AW467233.1, AA186857.1, AW572140.1, AW473996.1, AW327624.1, AI889579.1, AI049630.1, H68343.1, AW850230.1, AI733856.1, AA135761.1, AA583386.1, AW873261.1, AW833047.1, AI754421.1, AA838091.1, AA468923.1, AA176605.1, AW157005.1, AI452836.1, AI090377.1, AA152253.1, AI474127.1, AI192465.1, AI064786.1, AA721645.1, AI799569.1, AI283938.1, H47736.1, AW798093.1, AI340151.1, AA992126.1, AI762528.1, AI309943.1, AW769687.1, AW089625.1, AW008184.1, AA857812.1, AW167202.1, AA630854.1, AA298365.1, AI310343.1, AW589345.1, AI859906.1, AI249365.1, AA302978.1, AW674631.1, AW516080.1, AW243808.1, AW069227.1, AI634187.1, AI457313.1, AI431513.1, AW242031.1, AW328331.1, AL038936.1, AI446336.1, AA827383.1, AA502991.1, AA487569.1, AA130647.1, AW574899.1, AI815210.1, AI696878.1, AA642809.1, AA176257.1, AI336771.1, AI285493.1, AI797998.1, AI653515.1, AA612727.1, AA218631.1, AI791659.1, AI278972.1, H57439.1, AI065038.1, N38991.1, AA601218.1, AI362442.1, AI066711.1, AA832175.1, AI653776.1, AA604149.1, AI446623.1, AA877992.1, AW082104.1, AI962030.1, F29968.1, AI049845.1, AA287570.1, AA284247.1, AW852684.1, AA633981.1, AA443390.1, AI633294.1, AA594220.1, AA429197.1, AA429020.1, AA290878.1, AA569648.1, AC026250.3, AL356218.1, AC018751.22, AL159970.7, AC027272.2, AC008630.3, AL136222.3, AC008616.3, AC019157.4, AL161671.5, AC012306.3, AC023232.3, AC015795.3, AL135839.3, AC019268.3, AL355001.3, AC011771.3, AC013355.3, AC012652.3, AL158828.4, AC044797.2, AL158039.2, AF235092.1, AC024561.3, AC008379.5, AC009149.4, AL354720.3, AC027472.2, AL137849.2, AC009041.5, AC011423.1, AL355076.1, AC020922.5, AC011895.3, AC026051.3, AL161911.3, AC021016.3, AC025395.2, AC008026.2, AC008745.4, AC015920.4, AL138762.5, AP001462.1, AC011488.5, AC018557.4,
- 40 SEQ ID NO.145  
NGO-Br-45  
MK506/T3 5'  
AC005080.2, AC004883.2, AF015553.1, AF038969.1, AF038968.1, AF038967.1, AF035737.1, AF036613.1, NM\_010365.1, AF017085.1, AC002448.1, AC004637.1, AF133093.1, AC007681.3, AC007138.1, AL161493.2, AL009179.1, AW513878.1, AW440589.1, AW303749.1, AW172719.1, AW150741.1, AI942459.1, AI926534.1, AI890828.1, AI799542.1, AI755197.1, AI669472.1, AI569466.1, AI422057.1, AI366702.1, AI359749.1, AI359734.1, AI342520.1, AI341684.1, AI339415.1, AI334035.1, AI301890.1, AI268293.1, AI189650.1, AI016018.1, AI890844.1, AW503621.1, AW131511.1, AI862016.1, AI832845.1, AI564518.1, AI361033.1, AI356100.1, AW117790.1, AI961455.1, AI708465.1, AI359726.1, AI934639.1, W44732.1, AW157829.1, AA075629.1, AW504960.1, AI829529.1, AA527778.1, AW069097.1, AI653807.1, AW150934.1, AI338067.1, AA412018.1, N26570.1, AI762723.1, AA843358.1, AI633291.1, AA639747.1, AI523792.1, AA758117.1, AA156353.1, N26116.1, AA811496.1, W80780.1, AI613456.1, AI559431.1, AW189020.1, AI305239.1, AI762958.1, N51844.1, N31942.1, AI491778.1, AA113854.1, AI270445.1, AA662713.1, AA732559.1, AI290117.1, AA641906.1, AA632756.1, AI829267.1, AA535035.1, AA612924.1, AI880822.1, N90508.1, AI924215.1, AI689619.1, AA441894.1, AW090502.1, AA581632.1, N58502.1, AI735656.1, AW129208.1, AI750591.1, F21287.1, AA722095.1, AI538729.1, T03439.1, AI040879.1, H68263.1, AI699888.1, AI653613.1, AA720545.1, AW503247.1, AI630929.1, AI582862.1, AC004166.10, AC061712.2, AC006995.2, AC005098.1, AC068263.1, AC027219.1, AC018360.8, AC068475.1, AC013548.2, AC012587.4, AC018360.7, AC046131.3, AC023050.12, AC020741.3, AC026529.2, AC021802.3, AC025847.2, AC026086.2, AC026241.1, AC007400.2, AC009235.2, AL353134.2, AL162251.3, AP001983.1, AP000710.1, AP000643.1,
- 60 SEQ ID NO.146  
NGO-Br-46  
MK283/T3 5'  
NM\_016374.1, AB030181.1, AF245512.1, AF208045.1, AF214114.1, AF227899.1, NM\_002892.1, AL031777.2, S66427.1, AB033596.1, NC\_001136.2, AE003511.1, AC009322.1, AC007229.1, U80436.1, L77119.1, AC004440.1,



- AL121985.13, AB026643.1, J03902.1, AC007188.6, AC002461.1, AP000457.3, AB005240.1, AA485189.1, R20183.1, AW431383.1, F06553.1, AW431576.1, AI153796.1, AV249408.1, AL079586.1, AV295325.1, AV296868.1, AV304343.1, AV335031.1, AV251198.1, AA713956.1, AV323916.1, AV351047.1, R14337.1, AW242991.1, AA296993.1, AV318231.1, AV298138.1, AW820697.1, AV407971.1, AV407307.1, AW611599.1, AW571035.1, AW570959.1, AW570812.1, AW163609.1, AW162962.1, AI506067.1, T86264.1, AW775546.1, AV439780.1, AW696915.1, AW693997.1, AW690655.1, AW589802.1, AW470688.1, AW255547.1, AW243044.1, AW195535.1, AW135177.1, AI912938.1, AI823378.1, AI816820.1, AI809563.1, AI803416.1, AV146241.1, AI770033.1, AI766212.1, AI766190.1, AI632787.1, AI478418.1, AI280988.1, AI246187.1, AI242863.1, AI160538.1, AI143611.1, AI091619.1, AI055903.1, AI034050.1, AI032880.1, AI015057.1, AA988532.1, AA922855.1, AA863243.1, AA811866.1, AA731602.1, AA524142.1, AA375259.1, AA001674.1, W80645.1, W56179.1, W39715.1, W32984.1, W31210.1, R40471.1, AA524073.1, AL353899.3, AL133418.3, AL161423.4, AC010092.3, AL136366.4, AL049185.4, AC021804.3, AC005140.6, AC004153.5, AC022648.1, AC017725.1, AF181450.1, AC006858.1, AL157786.2, AC064811.2, AC027723.2, AF254982.1, AC025820.3, AC027691.1, AC018982.1, AL354653.2, AL049180.3,
- 15 SEQ ID NO. 147  
NGO-Br-46  
MK283/T7 3'  
AF083249.1, AL133010.1, AF227899.1, AF214114.1, AF208045.1, NM\_016374.1, AB030181.1, AF245512.1, AE003519.1, U14635.1, NC\_001147.1, NM\_012269.1, AC002454.1, AC012463.3, AC006029.2, AE001314.1, AF009010.1, AF039906.1, AL163262.2, Z97055.1, AL031429.1, AL096773.6, Z75151.1, AP001717.1, AP000189.1, AP000045.1, AP000300.1, AP000113.1, AI091806.1, AW450239.1, AI632699.1, AI130893.1, AI017851.1, AA279595.1, AA082926.1, AI474175.1, AA169631.1, AI136605.1, AW534954.1, AW047204.1, AA669471.1, AW050083.1, AA249450.1, AI138109.1, AI138113.1, AA248905.1, AW641956.1, AW402551.1, AU079907.1, AI817621.1, AV071325.1, AI472756.1, AA586216.1, AA347968.1, AA273379.1, H84029.1, H57875.1, R90945.1, HI7170.1, AL133418.3, AL353899.3, AC015441.1, AC067880.1, AC007990.2,
- 20
- 25 SEQ ID NO. 148  
NGO-Br-46  
MK482/T3 5'  
NM\_016374.1, AB030181.1, AF227899.1, AF208045.1, AF214114.1, AF245512.1, AF083249.1, AC027657.1, S57162.1, S57160.1, S57153.1, AC006420.3, U23522.2, NM\_002892.1, AC007032.2, AC004440.1, S66427.1, Z48784.1, AC002461.1, AC005207.1, AC004048.1, AL031595.4, AP001819.1, AA485189.1, R20183.1, AL079586.1, AW431383.1, F06553.1, AW431576.1, AW242991.1, AA296993.1, AI153796.1, AV249408.1, AV295325.1, AV296868.1, AV304343.1, AV335031.1, AV251198.1, AV323916.1, AA713956.1, AV351047.1, AV318231.1, AA743290.1, AW496257.1, AV298138.1, AW820697.1, AW611599.1, AW571035.1, AW570959.1, AW570812.1, AW162962.1, H34667.1, T86264.1, AW754057.1, AV439780.1, AW696915.1, AW693997.1, AW690655.1, AW341096.1, AW270194.1, AW207299.1, AV318321.1, AW057255.1, AW043594.1, AV146241.1, AI698675.1, AI698047.1, AI570113.1, AI506941.1, AI393132.1, AI361113.1, AI246187.1, AI22232.1, AA962426.1, AA926638.1, AA837710.1, AA829497.1, C68432.1, C57364.1, AA370189.1, C10349.1, W88641.1, N73528.1, H69420.1, H50563.1, H24328.1, H24314.1, H23256.1, F02811.1, C11969.1, AL133418.3, AL353899.3, AC011267.2, AL136366.4, AC020604.4, AC068607.1, AC008570.3, AC021804.3, AC022944.2, AC022648.1, AC017725.1, AL121987.2, AC064811.2, AC021183.2, AC027723.2, AC026384.2, AF254982.1, AC027412.2, AC009881.3, AC013653.2, AC018982.1, AL034557.7, AL049180.3,
- 30
- 35
- 40
- 45 SEQ ID NO.149  
NGO-Br-46  
MK482/T7 3'  
NM\_016374.1, AB030181.1, AF208045.1, AF227899.1, AF214114.1, AF083249.1, AF245512.1, NC\_001137.2, U18916.2, AC007032.2, L77119.1, AC005687.1, AP001073.1, AP000969.1, AC002038.1, AC007882.3, AC007188.6, AC009230.3, AC007379.2, AE003827.1, AE003758.1, AE003644.1, AE003410.1, AC002041.1, AC004161.1, AC018359.6, AC004827.1, AC004890.2, AC004896.1, AC009322.1, AC006352.3, AC006359.3, AC004671.1, U40947.1, AC005207.1, U00176.1, U67526.1, AL355921.1, AF004387.1, AL080287.1, AL050333.18, AL117353.6, AL034563.1, AL132769.1, U66528.1, Y00354.1, U33010.1, U33008.1, M18061.1, AP000391.1, AP000543.1, J05080.1, AL079586.1, AW242991.1, AA296993.1, AA743290.1, AA485189.1, AW496257.1, R20183.1, AI153796.1, AV318231.1, T61718.1, F06553.1, AV295325.1, AV249408.1, AV304343.1, AV296868.1, AV251198.1, AV335031.1, AV323916.1, AW431383.1, AW875017.1, AW875016.1, AW571035.1, AW570959.1, AW570812.1, T86264.1, AW696915.1, AW693997.1, AW690655.1, AW773470.1, AV439780.1, AW472410.1, AV351047.1, AW056097.1, AW021051.1, AI963428.1, AI741526.1, C93293.1, AA668233.1, C23844.1, W36281.1, T14884.1, AL133418.3, AC010092.3, AC019046.3, AC007990.2, AC023145.4, AC016789.4, AC011267.2, AL136366.4, AC017057.5, AC068607.1, AC008570.3, AC068444.1, AC068256.1, AC067904.1, AC021804.3, AC023200.2, AC016697.2, AP000742.1, AC019071.3, AC064811.2, AC068761.2, AC026273.5, AC021183.2, AC068541.2, AC026740.3, AC008480.3, AC027723.2, AF254982.1, AC010791.2, AC026897.2, AC016108.3, AC025610.2, AC024972.2, AC019110.3, AC024025.3, AC024315.2, AC007908.2, AC023202.2, AC023576.1, AC009209.5, AC010683.3, AC011231.3, AC009981.5, AC021671.1, AC009982.6, AC017924.1, AC014837.1, AL356288.1, AL034557.7, AP001017.2, AP001007.1, AP001109.1,
- 50
- 55
- 60



- 98 -

## SEQ ID NO.150

NGO-Br-46

MK712/T3 5'

- 5 NM\_016374.1, AB030181.1, AF245512.1, AF178849.1, Y17968.1, AC004537.1, AL118523.15, AK000096.1, AL021396.5, AL118494.1, S51239.1, AB032988.1, NM\_008671.1, NM\_008665.1, NM\_001978.1, AF004294.1, U28389.1, U28734.1, X92352.1, L19713.1, AC002039.1, AF222800.1, S79939.1, D86076.1, Z46939.1, D83650.1, D31729.1, NM\_008253.1, NM\_003449.1, AC004186.1, U59897.1, AF022465.1, U09825.1, U17837.1, AC007844.32, NM\_005381.1, AF132047.1, AC006289.1, AE001393.1, AC004659.1, AF030001.1, AL035527.1, X86100.1, U15800.1, AB010266.1, L04162.1, AK001314.1, AK000250.1, AK000221.1, AB015639.1, AB020693.1, AP000344.1, L08135.1, L22219.1, NM\_003204.1, AC007870.3, D37887.1, X84060.1, L14750.1, L24123.1, X77366.1, U08853.1, NM\_010238.1, AF069772.1, AC006925.6, AF045462.1, AF017349.1, AL121754.18, AL132977.1, AL009226.1, U14731.1, D89801.1, AB011480.1, D84418.1, NM\_015866.1, NM\_014977.1, NM\_012749.1, AF124726.1, AF133520.1, AF019611.1, U17838.1, AL163217.2, U89340.1, U19361.1, AP001672.1, U12825.1, D45132.1, AB014570.1, AC018721.1, NM\_008252.1, AC002302.1, AF085279.1, AC006070.1, U46900.1, Z83117.1, Z46757.1, M15825.1, AW431576.1, AA485189.1, AW431383.1, W84569.1, W67770.1, AA262427.1, R20183.1, AW369401.1, F06553.1, AI036486.1, AV340693.1, AV249408.1, AV295325.1, AI153796.1, AV296868.1, AV304343.1, AV335031.1, AA713956.1, AV251198.1, R14337.1, AV323916.1, AV351047.1, AI102488.1, AJ397247.1, AW158536.1, AA960471.1, AL079721.1, AU060883.1, F08518.1, M79841.1, AW281090.1, AI573315.1, AV407435.1, AW561908.1, AW099610.1, AI931397.1, AI505223.1, AI159593.1, AA939911.1, AA838901.1, AA413260.1, D22328.1, AI044390.1, AW366844.1, AI908284.1, H33616.1, R54825.1, AW531362.1, AW162962.1, AI746770.1, AI579779.1, AI579345.1, AI575698.1, AI558058.1, AI408526.1, AI408307.1, AW681502.1, AW398648.1, AU061751.1, AU060420.1, AU053145.1, AU053100.1, AA685125.1, AW682367.1, AW681399.1, AW681336.1, AW619893.1, AW553956.1, AW553928.1, AW550476.1, AW549664.1, AW548257.1, AW547813.1, AW546306.1, AW545571.1, AW545015.1, AW543191.1, AW542602.1, AW541865.1, AW536650.1, AW536323.1, AW320463.1, AW320328.1, AV111141.1, AV071436.1, AI376890.1, AI183692.1, AI182809.1, AU015986.1, C85885.1, C85603.1, AA795177.1, AA636994.1, C80539.1, AA607084.1, AA606813.1, AA590440.1, AA420329.1, T52646.1, AL353899.3, AC040981.1, AC012588.5, AC023288.6, AC018745.2, AC068493.3, AC053536.2, AC025669.2, AC026017.2, AC026462.1, AC006279.6, AC007340.3, AC024173.1, AC020757.2, AC016876.1, AC005136.1, AL163051.1, AC026581.1, AC024111.6, AC002317.1, AL136382.3, AL136998.12, AL355576.1, AL355366.1, AL158172.1, AC026532.2, AC034245.2, AC016569.3, AC068147.1, AC027275.1, AC021768.3, AC016171.4, AL121953.13, AL049796.27, AL133375.3, AP000448.1, AC068909.3, AC012055.6, AC034126.2, AC044806.1, AC019128.3, AC020879.2, AC017104.3, AC021627.2, AC020632.4, AC041041.2, AC021142.4, AC026163.2, AC015535.4, AC016989.4, AC020988.3, AC024625.1, AC015901.3, AL356459.1, AL157895.1, AP001488.1, AP001024.1, AC016142.6, AC020940.4, AC019028.3, AC009717.4, AC023364.3, AC013334.6, AC022565.3, AC020509.1, AC017725.1, AC004123.1, AC005861.2, AL354874.1, AL034557.7, AC009361.17, AC015891.10, AC063968.1, AC027650.2, AC025364.2, AC012296.3, AC022310.2, AC023571.2, AC023284.1, AC009962.3, AC021444.1, AL035477.5,

## SEQ ID NO.151

40 NGO-Br-47

MK265/T3 5'

- 45 NM\_004987.1, U09284.1, AK000906.1, AE003678.1, AF078907.1, AF035583.1, U41021.1, AE003528.1, NM\_000888.1, AL137129.2, AL050403.13, Z69648.1, M35198.1, AC007380.3, AE003454.1, NM\_008407.1, AC004300.1, AE000795.1, Z71186.1, X70393.1, Z99123.1, Z80360.1, X95584.1, AW504514.1, AI327306.1, AA299595.1, AA289280.1, AI862555.1, AI609736.1, AA968535.1, AI608376.1, AA037783.1, AI948956.1, AI956192.1, AA201027.1, AI152133.1, AI195455.1, AI089674.1, AA198689.1, AA732465.1, AA766629.1, AA989985.1, H58225.1, AA970328.1, AW787078.1, AW787072.1, AI450546.1, AA799637.1, AW742584.1, AA510363.1, AA450826.1, AA504265.1, AA110054.1, AI854549.1, AI195654.1, AI986356.1, AI943339.1, AW142146.1, AA102210.1, AI593658.1, Z42656.1, AI722835.1, AI353353.1, H58562.1, AW493431.1, AI237400.1, AA848258.1, AA636357.1, AA220130.1, AW347458.1, AI464258.1, AI408319.1, AW481822.1, AW417049.1, AW312785.1, AW140389.1, AA119018.1, R58438.1, AJ398975.1, AW017114.1, AI386040.1, AA066359.1, AI981121.1, AI262403.1, AA646588.1, AA358612.1, AJ392355.1, AA064613.1, AI986343.1, AA511616.1, AW140647.1, AI929976.1, AV203690.1, AV198544.1, AV194653.1, AV194457.1, AV187669.1, C48705.1, C48492.1, C48145.1, C45906.1, C41445.1, AA471768.1, D76144.1, AW216171.1, AA269965.1, AA069994.1, AA016593.1, T73549.1, AC010095.3, AC011919.3, AC013271.1, AC011922.2, AC010976.4, AC027815.1, AC012487.3, 55 AC014215.1, AC016057.3, AC016797.3, AC022102.3, AC016575.6, AC021017.3, AC020993.3, AC013658.3, AC024522.1, AC010066.5, AC014423.1, AL136985.1, AC026261.3, AC027627.3, AC008864.4, AC008740.3, AC037456.4, AC025781.5, AC025706.3, AC024453.2, AC018914.3, AC021788.2, AC023463.2, AC019902.1, AL022281.20, Z98874.1,

60 SEQ ID NO.152

NGO-Br-48

MK124/T3 5'

AJ251245.1, AC004890.2, NM\_009477.1, D44464.1, AC007371.16, AL034423.18, AL096761.1, AE003806.1, AF022713.2, AF133262.1, AF133263.1, U69607.1, AC004287.1, U65480.1, AF007190.1, AL035420.15, AW630547.1,

- AI769091.1, T58810.1, AA403044.1, AW436458.1, AI713670.1, AI712879.1, AI060054.1, AI412971.1, AI010977.1, AW318411.1, AW012719.1, AA817712.1, AA943539.1, AA404342.1, AW121356.1, AI837465.1, AI823387.1, AI877170.1, AI118479.1, AI325217.1, AA023318.1, AA020155.1, W34889.1, AI099015.1, W08125.1, R51103.1, AW820705.1, AA475225.1, AA411125.1, AA171085.1, AI160054.4, AC021561.3, AP001490.1, AC027461.1, AC027462.2, AC023571.2, AL355353.3, AC018714.3, AC016883.3, AC022244.2, AC027559.1, AC018671.5, AC016402.1, AL353782.3, AL161937.5, AL022335.6, AP001000.1, AC021874.12, AC021023.4, AC018352.8, AC018656.5, AC012674.7, AC022504.9, AC055882.3, AC018752.3, AC010396.3, AC008596.3, AC013747.5, AC068557.1, AC034137.2, AC024948.2, AC007944.2, AC022830.2, AC024504.2, AC011635.3, AC012378.5, AC021874.11, AC016346.2, AC021250.2, AC018352.7, AC020957.1, AC017056.3, AC020077.1, AC016510.1, AC012123.1, AL356217.2, AL122125.1, AL031301.1, AP001888.1, AP001123.1, AP000850.1,
- SEQ ID NO.153  
NGO-Br-48  
MK124/T7 3'
- AJ251245.1, NM\_006703.1, AF062530.1, AF062529.1, AI117352.12, AJ249395.1, Z98036.1, AC010305.3, AC006474.3, AC002098.1, AC000396.1, AL078603.4, Z66560.2, M20162.1, AE003687.1, AE003539.1, AE003452.1, AC005005.1, AC004466.1, AC005268.1, AF015725.1, AL163300.2, AL163268.2, Z73972.1, Z99714.2, Z83001.1, Z97200.1, AJ011930.1, AP001068.1, AB012242.1, AB008267.1, AJ229042.1, Z48305.1, X14710.1, AI270576.1, AA349855.1, H60027.1, AA639612.1, R25924.1, AW392280.1, AW450452.1, AI014725.1, AA092495.1, W58640.1, AW022648.1, AI179962.1, AW431718.1, N55875.1, AI178673.1, AW427283.1, R14767.1, AI179961.1, AW868962.1, D21042.1, AW062717.1, AW062693.1, AI654799.1, AI652271.1, AI493530.1, AI435022.1, AI289025.1, AI126256.1, AI086076.1, AI032793.1, AA838460.1, AA781029.1, AA643067.1, AA629918.1, AA594551.1, AA573873.1, AA505932.1, AA479474.1, AA447455.1, AA446652.1, AA256802.1, AA150300.1, AA148791.1, AA086458.1, AA030012.1, W05069.1, N51389.1, R34884.1, AI158210.1, AW785190.1, AV305650.1, AU080152.1, AI987624.1, AI810108.1, AI764741.1, AI607860.1, AI546326.1, AI388669.1, AU033961.1, AI144326.1, AI13962.1, AI020516.1, AA951467.1, AA736165.1, AA701889.1, AA700625.1, AA504833.1, AA404221.1, AA404687.1, AA159318.1, H84256.1, H34335.1, H05385.1, AC021561.3, AP001490.1, AC025405.2, AC011945.3, AL354740.4, AL137801.1, AC068548.2, AC027395.2, AC018358.6, AC068739.2, AC026022.2, AC021088.2, AC068386.1, AC020552.3, AC018966.3, AC007721.15, AC016427.3, AC015622.3, AC009703.2, AC005910.4, AC002320.1, AL161452.3, AP001257.1, AL022276.1, AC009522.3, AC063940.4, AC025005.2, AC016572.4, AC008513.6, AC027074.2, AC012184.3, AC016883.3, AC011794.4, AC009871.5, AC010966.2, AC015676.3, AC024237.3, AC018232.1, AC018272.1, AF165146.1, AC006171.1, AC004847.1, AL356461.1, AL159154.3, AL162399.3, AL133410.10, AL162589.1, AL136001.1, AP001078.1, AP000899.2, AP001029.2, AP001113.1, AL008875.1,
- SEQ ID NO.154  
NGO-Br-49  
MK4111/T3 5'
- NM\_004349.1, S78158.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, NM\_009822.1, X79989.1, D32007.1, S78159.1, D14823.1, AF018276.1, AF018275.1, AF018283.1, D14822.1, AF018274.1, NM\_009824.1, AF038029.1, AB010420.1, AF010419.1, AF018277.1, AB013280.1, AF052215.1, S74096.1, NM\_005187.2, AF069747.1, NM\_005093.1, AF068266.1, AF052210.1, AF013970.1, AF039200.1, AF212198.1, AF076455.1, AL034421.4, AC007842.1, AF022978.1, AB037757.1, AC023838.1, AC004011.1, AC006208.3, AE001039.1, AC002297.1, AC001229.1, AL133445.2, AL049766.14, AL096843.11, AL008634.1, Z84466.1, AL022721.1, AJ005682.1, U01337.1, AJ005077.1, L24038.1, AP000385.1, X77694.1, H18342.1, AW659083.1, AL134801.1, H18378.1, R91340.1, AW409814.1, AA597034.1, AI880924.1, AW047315.1, AW526016.1, AW319793.1, AW319604.1, AW125686.1, AW060692.1, AV127503.1, AI606504.1, AA996736.1, AI407074.1, AI176767.1, AI171652.1, AI152215.1, AI046358.1, AA914494.1, AA822901.1, AA674424.1, AA529559.1, AA261311.1, AA222118.1, AA222011.1, AA963424.1, W39519.1, N75171.1, R70443.1, AV170567.1, AA924939.1, AI169429.1, W89980.1, AA015563.1, AC015952.3, AC013551.1, AF181450.1, AC068674.1, AC011671.3, AC009149.4, AC021125.2, AL121906.12, AC031998.2, AC013552.4, AL158160.1, AC012485.4, AC009989.6, AC006431.8, AC021193.3, AC022029.3, AC009438.2, AC027023.2, AC019055.3, AC007779.2, AC015667.3, AC027146.1, AC021291.3, AC023300.3, AC023545.2, AC015598.3, AC023438.2, AC020713.2, AC016279.2, AC007936.1, AL109823.21, AL160211.1, AL135961.1, AP001892.1, AP001637.1, AP000798.1, AP000662.1,
- SEQ ID NO.155  
NGO-Br-49  
MK4111/T7 3'
- NM\_004349.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, S78158.1, NM\_009822.1, D32007.1, X79989.1, AF018282.1, AC007161.1, AC003006.1, AE000663.1, AC011494.2, AC012147.7, AC004846.2, AC005058.1, AC007630.3, AF109907.1, M13209.1, AL034365.1, Z70782.1, AL031176.7, S55844.1, X67119.1, X16144.1, X01978.1, K03329.1, J02070.1, K01729.1, M17293.1, AJ224792.1, AJ224790.1, D49508.1, AI420591.1, AI033811.1, H94855.1, AW411005.1, AI167424.1, AW409570.1, AI264845.1, AA904353.1, F02579.1, N75054.1, AU041415.1, AW192965.1, AA992855.1, R38996.1, AV162276.1, N86959.1, AA247686.1, AV240937.1, AI078840.1, AV245662.1, F01701.1, AI080687.1, AV347330.1, N88058.1, AA463390.1, AA095305.1, AI825475.1, H46432.1, AW450741.1, AW063104.1,

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AI723657.1, AI604144.1, AI574526.1, AA257797.1, AW859690.1, AW177930.1, AW849569.1, AW849241.1, AW575067.1, AW257554.1, AV332137.1, AV153186.1, AI476165.1, AI445297.1, AI445224.1, AI181996.1, AI116642.1, AA469797.1, AA469776.1, AA194741.1, AA125063.1, AC015952.3, AF181450.1, AC068674.1, AC010295.4, AC017222.1, AC008197.2, AL136968.4, AL096708.33,

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SEQ ID NO.156

NGO-Br-49

MK571/T3 5'

- 10 NM\_004349.1, S78158.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, NM\_009822.1, X79989.1, D32007.1, S78159.1, D14823.1, AF018276.1, AF018283.1, AF018275.1, S74096.1, D14822.1, AF018274.1, NM\_009824.1, AF038029.1, AF018277.1, AB010420.1, AB010419.1, AB013280.1, AF052215.1, NM\_005187.2, AF018278.1, AF069747.1, NM\_005093.1, AF068266.1, AF052210.1, AF013970.1, AF039200.1, AF212198.1, AF076455.1, AL034421.4, AC010285.4, AC007842.1, AF022978.1, AB037757.1, AC023838.1, AC004011.1, U91322.1, AC006208.3, AE001039.1, AC001229.1, AL133445.2, AL049766.14, AL096843.11, AL031682.1, AL008634.1, Z84466.1, AL022721.1, AJ005682.1, U01337.1, AJ005077.1, L24038.1, AP000385.1, X77694.1, H18342.1, AW659083.1, AL134801.1, H18378.1, R91340.1, AW409814.1, AA597034.1, AW411004.1, AI880924.1, AW047315.1, AW526016.1, AW319793.1, AW319604.1, AW125686.1, AW060692.1, AV127503.1, AI606504.1, AA996736.1, AI407074.1, AI176767.1, AI171652.1, AI152215.1, AI046358.1, AA914494.1, AA822901.1, AA674424.1, AA529559.1, AA261311.1, AA222118.1, AA222011.1, AA963424.1, W39519.1, N75171.1, R70443.1, AW433933.1, AV170567.1, AI555661.1, AA924939.1, 20 AI169429.1, AA196015.1, AA120052.1, W89980.1, AA015563.1, AC015952.3, AC013551.1, AF181450.1, AC068674.1, AC011671.3, AC009149.4, AC021125.2, AL121906.12, AC031998.2, AC013552.4, AL158160.1, AC025418.5, AC010313.4, AC016533.5, AC023924.2, AC011094.2, AC027737.2, AC050049.1, AC038905.1, AC013648.3, AC012485.4, AC009989.6, AC012154.9, AC006431.8, AC021193.3, AC012626.4, AC009078.4, AC022029.3, AC009438.2, AC027023.2, AC019055.3, AC007779.2, AC026911.2, AC026958.2, AC015667.3, AC027146.1, 25 AC021291.3, AC023300.3, AC023545.2, AC015598.3, AC006404.20, AC023438.2, AC020713.2, AC016279.2, AC009878.3, AC007936.1, AL160211.1, AL135961.1, AP001892.1, AP000798.1, AP000662.1,

SEQ ID NO. 157

NGO-Br-49

30 MK571/T7 3'

- NM\_004349.1, D14821.1, D43638.1, D14289.1, D13979.1, X79990.1, S78158.1, NM\_009822.1, D32007.1, X79989.1, AF018282.1, AE003739.1, AC007161.1, AC003006.1, AE000663.1, AC012147.7, AC004846.2, AC005058.1, AC007630.3, AL031176.7, S55844.1, X67119.1, X01978.1, AI420591.1, AI033811.1, H94855.1, AW411005.1, AI167424.1, AW409570.1, AI264845.1, AA904353.1, F02579.1, N75054.1, AU041415.1, AW192965.1, AA992855.1, 35 R38996.1, AV162276.1, N86959.1, AA247686.1, AV240937.1, AI078840.1, AV245662.1, F01701.1, AI080687.1, AV347330.1, AA463390.1, N88058.1, AI825475.1, AA095305.1, H46432.1, AW450741.1, AW063104.1, AI885714.1, AI723657.1, AI604144.1, AI574526.1, AA257797.1, AW859690.1, AW575067.1, AW257554.1, AV332137.1, AV153186.1, AI476165.1, AI445297.1, AI445224.1, AI181996.1, AI116642.1, AA469797.1, AA469776.1, AA194741.1, AA125063.1, AC015952.3, AF181450.1, AC068674.1, AC017222.1, AC008197.2, AL096708.33, AC011005.4, 40 AC024483.2, AC012431.5,

SEQ ID NO.158

NGO-Br-50

MK253/T3 5'

- 45 NM\_013235.1, AF116910.1, AK001121.1, AE003484.1, AL135784.4, L33180.1, L22858.1, Z83744.1, L35905.1, X71415.1, AF178030.1, Z95126.1, Z98266.1, AB025632.1, X78287.1, AC008969.5, AC027659.1, AC024799.1, AC013453.1, AC007038.3, AC007591.2, AC005284.1, Y14344.1, AA543176.1, AW237908.1, AA153374.1, AA144562.1, AA114761.1, AA460045.1, AW834734.1, H34369.1, AA549506.1, AA623764.1, AA797275.1, AW246359.1, AW702080.1, AA083888.1, AA199399.1, AA461807.1, AW860954.1, AI681138.1, C72137.1, AW836479.1, 50 AW416148.1, AV141668.1, AI678836.1, AI035692.1, C84814.1, AA768917.1, AA722287.1, R66162.1, R59232.1, AC008768.4, AC008159.1, AC026712.3, AC008419.4, AC010348.3, AC008550.3, AC018857.3, AC013905.1, AC008035.8, AC046148.2, AC010243.3, AC016555.4, AC026300.2, AC012586.6, AC015725.3, AC009591.3, AC010897.3, AC016998.1, AC012338.2, AL136987.2, AC021874.12, AC021023.4, AC018916.6, AC012041.8, AC011312.5, AC055789.2, AC067752.2, AC026780.2, AC010457.5, AF260012.1, AC026167.2, AC011050.4, 55 AC011148.4, AC016099.3, AC026205.3, AC023780.2, AC023571.2, AC024598.2, AC020755.2, AC021874.11, AC020856.1, AC024159.1, AC006595.1, AC006788.1, AL355353.3, AL139143.4, AL138885.4, AL355482.1, AL354864.1, AL161639.4, AL160008.1, AP001280.1, AP001085.2, AP000577.1,

SEQ ID NO.159

60 NGO-Br-50

MK253/T7 3'

NM\_013235.1, AF116910.1, AK001121.1, AC006349.3, AL023807.6, AC008082.12, AC008160.11, AF060568.1, AF016679.1, U51999.1, X52871.1, M15387.1, AE003826.1, AC007056.4, AF088189.1, AC006216.1, AF099810.1, AC002397.1, AE000092.1, AL163221.2, U96131.1, AL117672.3, AL049758.11, AL035427.17, AL022578.1, AP001676.1,

-101-

D87952.1, AP000403.1, AW246572.1, AA827562.1, AA514488.1, A1190270.1, AL135673.1, A1539185.1, AA778031.1, AA083889.1, AW874309.1, AA255533.1, AW662264.1, A1539830.1, AA532881.1, F19104.2, AA459956.1, AW701839.1, AA749416.1, A1972095.1, A1874853.1, AW656237.1, AW793352.1, AW793354.1, AA247961.1, AW246359.1, AW793373.1, AU042596.1, N66268.1, AA271691.1, A1630888.1, AW522844.1, AA255505.1, A1502808.1, AA384265.1, 5 AW438881.1, AA729375.1, AA364111.1, AW363733.1, AW638275.1, AA538198.1, AV084911.1, AA702934.1, A1940043.1, AW428205.1, AV008608.1, AW702080.1, AL134250.1, A1159057.1, AA711797.1, AA120508.1, T06791.1, AV319126.1, AA739069.1, AV319605.1, AV038838.1, U94841.1, AA461807.1, AW803473.1, A1937621.1, A1673094.1, A1105163.1, AA638281.1, AA559086.1, AA473595.1, AA331632.1, H87048.1, AC026712.3, AC008768.4, AC008159.1, AC068577.1, AC020880.2, AC021229.2, AC012557.7, AC021482.4, AC022782.2, AC024656.2, AC020742.2, 10 AC019262.3, AL354712.2, AL354656.1, AP000908.1, AC024898.7, AC009716.3, AC068132.2, AC020930.4, AC010393.4, AC010266.7, AC010500.4, AC034195.2, AC023478.2, AC024928.4, AC049149.1, AC021380.3, AC023761.2, AC016498.4, AC026219.1, AC026198.1, AC026188.1, AC025978.1, AC005653.8, AC017064.4, AC011981.3, AC022668.3, AC022335.6, AC022002.2, AC022989.2, AC021141.2, AC016397.4, AC009673.2, AC013573.2, AC017933.1, AC008031.3, AC010167.1, AF165425.1, AC007715.1, AL096868.7, AL353585.3, 15 AL160403.3, AL160281.3, Z82199.1, AL132638.1, AP001445.1, AP001194.1, AP001130.1,

SEQ ID NO.160

NGO-Br-50

MK496/T3 5'

20 NM\_013235.1, AF116910.1, AK001121.1, AE003484.1, L33180.1, L22858.1, Z83744.1, L35905.1, X71415.1, Z98266.1, AC008969.5, AE003629.1, AC000370.1, AC013453.1, AC007591.2, AE001718.1, AC004673.1, AC005751.1, AC002995.1, AL031670.6, Z81133.1, AL035467.23, AA460045.1, AA153374.1, AA144562.1, AW246359.1, AA549506.1, AW834734.1, AA623764.1, AA083888.1, AA114761.1, AL134250.1, AA543176.1, AW702080.1, AA797275.1, AA199399.1, AW428205.1, AA461807.1, AA711797.1, AW237908.1, AA538198.1, AA120508.1, 25 A1987530.1, A1681138.1, C72137.1, AW836479.1, AW559878.1, AW416148.1, AU039592.1, R66162.1, R59232.1, AC026712.3, AC008768.4, AC008159.1, AC046148.2, AC013905.1, AC010190.7, AC063946.3, AC025265.5, AC010243.3, AC016555.4, AC026300.2, AC015725.3, AC010897.3, AL136987.2, AC021874.12, AC021023.4, AC011312.5, AC012114.2, AC067752.2, AC010457.5, AC010381.4, AC025546.3, AC009135.6, AC068121.1, AC067828.1, AC025700.3, AC018508.4, AC025039.3, AC022526.4, AC016099.3, AC021736.3, AC010785.3, 30 AC021242.3, AC023860.2, AC024598.2, AC021874.11, AC020856.1, AF230637.1, AC016906.3, AC015747.1, AC020115.1, AC007300.5, AC004387.1, AL353194.6, AL138885.4, AL355482.1, AL354933.1, AP001869.1,

SEQ ID NO.161

NGO-Br-51

MK071/T3 5'

35 NM\_003137.1, U09564.1, NM\_016795.1, AB012290.1, AJ224115.1, Z99128.1, NM\_009274.1, U92456.1, AB006036.1, NM\_003138.1, U88666.1, AF043288.1, AC005070.1, AE003811.1, AF133093.1, AF043289.1, AB017067.1, AC023279.2, AC005220.1, AL160231.2, AL023634.1, AB023037.1, D13447.1, AE003484.1, AF002725.1, AE000541.1, AE001458.1, AF052290.1, AL021127.2, AL021180.1, AL022311.5, AB035133.1, AB006605.1, AW611721.1, AA060080.1, 40 AA492926.1, AL048784.3, AW006865.1, AU051027.1, AL046120.2, AA382461.1, AW500688.1, AW637436.1, AW701629.1, AJ396085.1, AA864027.1, AA211241.1, A1605657.1, AW635365.1, AW422773.1, AW421817.1, AW128008.1, A1722256.1, AW629710.1, AW381192.1, AW153931.1, A1626169.1, N28924.1, A1595541.1, A1038250.1, A1854277.1, A1787785.1, A1599584.1, W92175.1, AA428487.1, N23469.1, AW701402.1, AW462697.1, A1848239.1, A1414590.1, A1184192.1, AA553654.1, AW149364.1, AW016345.1, A1869878.1, A1830963.1, A1808855.1, A1808450.1, 45 A1555245.1, A1248681.1, A1247996.1, A1200995.1, A1199780.1, A1127471.1, A1075315.1, A1032748.1, A1018413.1, A1018139.1, A1000892.1, AA573426.1, AA479899.1, W92176.1, N35218.1, H98745.1, AA537749.1, A1296396.1, W12836.1, AW668908.1, AW392218.1, A1810017.1, AA968079.1, AA062255.1, AW736509.1, AW705048.1, AW704786.1, AW277878.1, AW277356.1, AW277342.1, AV375020.1, AV293419.1, AV287373.1, AV284759.1, AV234361.1, AW099987.1, AW036092.1, A1960739.1, AV174923.1, A1794688.1, AV118805.1, A1703778.1, A1507200.1, 50 AA972378.1, AA891069.1, AA863700.1, AA086829.1, AL133507.3, AC022452.2, AC017471.1, AC022525.3, AC023305.2, AC022106.2, AC011540.2, AC010787.3, AC021963.3, AC023913.4, AC016956.6, AC060815.2, AC068798.4, AC024102.5, AC023158.4, AC020570.3, AC023052.13, AC025765.3, AC025178.3, AC022444.3, AC022423.3, AC008411.3, AC008803.3, AC023779.2, AC024479.3, AC037484.1, AC016985.4, AC019298.3, AC027165.1, AC009072.2, AC016956.5, AC013441.2, AC013907.1, AC008108.1, AL160162.4, AL133356.3, 55 AL157696.2, AL009027.1,

SEQ ID NO.162

NGO-Br-51

MK071/T7 3'

60 Z99128.1, NM\_003137.1, U09564.1, NM\_016795.1, AB012290.1, AJ224115.1, AJ005937.1, AE003588.1, AC004116.1, AL031534.1, AL137450.1, AL023534.1, AW594310.1, AW082913.1, A1672149.1, A1126291.1, AW338805.1, AA490202.1, AA629288.1, AW848261.1, AA921804.1, R78142.1, A1076709.1, AW510886.1, AW275479.1, AW376532.1, T77446.1, AA284106.1, R29335.1, AA323127.1, R78141.1, W25929.1, AW123035.1, A1648020.1, AA899108.1, AU024203.1, AU020306.1, N76402.1, N77083.1, AA383402.1, AW674276.1, AW275654.1, AW103361.1,

- AW091907.1, AW039956.1, AW008221.1, A1799557.1, A1598063.1, A1458262.1, AA915976.1, AA373583.1, AA059466.1, W73010.1, N36259.1, N24536.1, H26379.1, AW727130.1, AW702067.1, AW489711.1, AW421443.1, AW144384.1, AV167622.1, AV060461.1, A1697622.1, A1630968.1, A1325483.1, A1235699.1, A1210173.1, A1152339.1, A1034064.1, A1006140.1, AA798365.1, AA764641.1, AA450512.1, AA408261.1, AA122933.1, AA097370.1, AA024303.1, W36820.1, W11581.1, W08677.1, D19317.1, D24037.1, AL157823.3, AP001449.1, AL139347.2, AC026566.1, AC018197.1, AC024107.9, AC021650.9, AC008810.4, AC026466.3, AC026959.2, AC023271.3, AC024193.2, AC009792.4, AC020730.2, AC021155.2, AF178220.1, AP000794.1,
- 5
- SEQ ID NO.163  
NGO-Br-52  
MK111/T3 5'
- 10
- NM\_003373.2, NM\_014000.1, M33308.1, NM\_009502.1, L18880.1, J04126.1, Y00312.1, L13300.1, S52276.1, S52271.1, AF067624.1, AL163852.1, AL138646.2, AC007138.1, AF047564.1, U82828.1, AL161552.2, AL161493.2, AL161492.2, U55724.1, Z98946.15, AL080253.2, X52256.1, AC007347.3, AC002485.1, AF107675.1, AC005026.1, AC008170.2, AC007560.3, AF147259.1, AC004063.1, AL163290.2, AL132793.24, AL161506.2, AL049871.3, AP001745.1, AP001619.1, AP001800.1, X91233.1, AB033053.1, AL048129.1, AA853564.1, AA375439.1, AV441119.1, AA585825.1, AW202184.1, AW577790.1, AW498327.1, AV404553.1, AV402299.1, AU004063.1, AU004045.1, AU003308.1, A1042965.1, AJ003662.1, AC025425.4, AC021191.3, AC006874.1, AC025212.2, AC011797.4, AC025104.2, AC015687.3, AL354652.3, AP001925.1, AP001808.1, AP000838.1, AC024933.7, AC023598.10, AC022072.8, AC051642.2, AC015891.10, AC068973.1, AC055869.2, AC068886.1, AC025477.3, AC018753.3, AC008859.4, AC026557.2, AC068246.1, AC022993.3, AC012211.3, AC046149.2, AC012068.3, AC026824.2, AC026087.3, AC034111.1, AC025061.2, AC020672.3, AC012252.4, AC026566.1, AC018911.4, AC015938.3, AC018973.3, AC022041.2, AC023916.2, AC011298.2, AC021950.1, AF216674.1, AC013695.1, AF191252.1, AL118506.16, AL161442.7, AL139157.4, AL138744.7, AL136980.3, AL354744.1, AL354696.1, AL137022.7, AP001954.1,
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- 25
- SEQ ID NO.164  
NGO-Br-52  
MK111/T7 3'
- 30
- NM\_003373.2, NM\_014000.1, M33308.1, AL121751.12, AC007237.3, AC005405.1, Z50070.2, AC006332.3, NM\_005509.1, AE003635.1, AC006979.2, AF204929.1, AF185647.1, U80443.2, AC000104.1, AL138478.2, AL078605.30, AJ005821.1, D90900.1, AB017062.1, AL043388.1, AL048130.1, AW613219.1, AL042874.1, AL047646.1, A1564569.1, AW338462.1, A1871828.1, AW341948.1, A1744828.1, A1754173.1, A1889651.1, C06476.1, A1564600.1, AW189900.1, A1583605.1, AW316646.1, AA776250.1, AW268882.1, AW268623.1, A1833189.1, AA564112.1, AA486728.1, AA458903.1, AW067932.1, AW026609.1, AA284505.1, A1808349.1, A1041865.1, AA744683.1, AA744677.1, N35013.1, A1367320.1, AW070464.1, AA723251.1, AA478033.1, A161355.1, AA521095.1, A1956152.1, A1753120.1, AA653613.1, A1890467.1, AA173528.1, AA160880.1, AA653144.1, W72421.1, AA031689.1, A1095313.1, A1243169.1, AA744691.1, N27658.1, AA909152.1, A1381956.1, AA548423.1, A1240491.1, AA705238.1, AA150688.1, W76280.1, H24935.1, A1290052.1, A1953995.1, AA099284.1, A1003089.1, A1041158.1, AA299485.1, H47593.1, R87481.1, H06272.1, AA670014.1, A1750559.1, AW081510.1, H62215.1, T92938.1, F32136.1, W15223.1, H28559.1, AA045285.1, H57205.1, AW438657.1, AA490932.1, R78919.1, AA165451.1, A1206471.1, AA370855.1, A1952389.1, AA853565.1, AW118302.1, AW193451.1, T92716.1, H51597.1, AA831147.1, H38452.1, AA776247.1, T23463.1, T93331.1, A1694888.1, H97605.1, T92712.1, AA904909.1, R62767.1, AC025425.4, AL110115.28, AL138753.3, AL139114.3, AC015970.4, AC010278.5, AC008883.3, AC008446.3, AC012583.3, AC021516.4, AC011944.3, AC024317.2, AL139042.3, AL162411.1, AL023673.1, Z81488.1, AC041006.2, AC036146.2, AC068429.1, AC068020.1, AC026458.3, AC024492.2, AC015873.2, AC022770.4, AC010579.8, AC025134.1, AC023828.1, AC011066.4, AC011750.3, AC019782.1, AC013663.1, AC010213.2, AC009339.1, AL096888.26, AL161671.5, AL161653.7, AL160172.4, AL109824.23, AL135901.4, AL162759.1, AL136301.4, AL136985.1, AL137785.2, AP000863.1, AP000784.1,
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- SEQ ID NO.165  
NGO-Br-53  
MK282/T3 5'
- 55
- X98494.1, AL133363.1, AE002611.1, Z83848.1, AF036707.1, AF118145.1, AC002060.3, AF022981.2, AF125969.1, D87023.1, AC008757.5, AE003498.1, U76408.1, AC009303.2, AF197947.1, AF242181.1, AE003844.1, AE003477.1, NM\_011241.1, AF098623.1, AF098622.1, AF098621.1, AF098620.1, AF098619.1, AF098618.1, AF098617.1, U48809.1, AF046092.1, AF046084.1, U53154.1, AF057293.1, AE000661.1, U20857.1, Y14591.1, AJ242625.1, Y18000.1, Y14592.1, D87010.1, AC010252.3, AC008174.2, AF216973.1, AF220200.1, AF030052.1, Z73905.1, U10577.1, U67889.1, AL031652.1, AK001686.1, AP000501.1, AB011164.1, AA848124.1, AW365568.1, T24602.1, AW365559.1, AA603307.1, A1844833.1, W33952.1, W75630.1, W64795.1, AV113531.1, AV113797.1, AV114982.1, A1709759.1, AW365540.1, A1137651.1, A1070777.1, AW376006.1, A1546038.1, C94041.1, AV294399.1, A1959638.1, A1793667.1, A1406906.1, L37652.1, AV427570.1, AV409781.1, AW638224.1, AW560695.1, AW517166.1, AJ398790.1, AW345759.1, AW187449.2, AV314465.1, AV312363.1, AW128487.1, A1994267.1, AV024242.1, AV020965.1, A1641607.1, AA388279.1, R90246.1, T75711.1, AV420624.1, AW703701.1, AW604496.1, AW579832.1, AW443988.1, AW373650.1, AW361293.1, AW361221.1, AL038706.1, C99888.1, A1384793.1, AA147878.1, W26394.1, T92366.1, T90227.1,
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-103-

AC007881.3, AC007345.2, AC007342.2, AC009673.2, AC016033.2, AC025138.2, AC018348.1, AC023310.1, AC027794.1, AC026150.1, AC036148.2, AC022113.4, AC020980.3, AC016621.4, AC027472.2, AC018409.3, AC018491.7, AC014030.1, AC011402.5, AC026275.3, AC009792.4, AF178220.1, AC006844.1, AC027245.1, AC013451.7, AC012931.1, AC009682.3, AC023659.2, AC025303.1, AL355178.2, AC034214.3, AC027621.3, AC064793.1, AC025856.2, AC015454.3, AC022783.2, AC018510.3, AC015672.3, AC014497.1, AL353612.5, AL163151.1,

SEQ ID NO.166

NGO-Br-53

10 MK282/T7 3'

X98494.1, AF135002.1, AI760199.1, AI742680.1, AW384883.1, AI284853.1, AI222419.1, AA992199.1, AW044708.1, AI862023.1, AI681988.1, AI867639.1, AI955575.1, AA992130.1, AI087795.1, AI263606.1, AA025657.1, AA083314.1, AI094541.1, AA847842.1, AA731098.1, AA047545.1, AI420376.1, W80758.1, AA770202.1, AI357730.1, AW592097.1, AA909134.1, AW369791.1, AI271912.1, AA810790.1, N68965.1, AI806559.1, T97061.1, AI056034.1, AW591044.1, AA668325.1, AA504113.1, AA347116.1, AW606827.1, AW608731.1, AI244315.1, AA837327.1, Z25156.1, AI809694.1, AA888598.1, H88801.1, F00393.1, AW130117.1, AI884600.1, AI679865.1, AI679289.1, AI386428.1, AI000365.1, AA162148.1, AW556570.1, AA213194.1, H89025.1, AI177638.1, T96950.1, AA881872.1, AV146345.1, AA916136.1, AW539498.1, AV077858.1, AI647220.1, AI326008.1, AA590060.1, C02251.1, AI406906.1, AW632569.1, AW532104.1, AA817668.1, AV218492.1, AA619205.1, AC007881.3, AC021225.3, AC027794.1,

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SEQ ID NO.167

NGO-Br-54

MK123/T3 5'

AK001917.1, AF035606.1, NM\_013232.1, U58773.1, NM\_011051.1, U49112.1, AC008925.3, AC007790.1, AC004485.1, AC004025.1, AC004923.2, AC008078.1, AC002288.1, AE001146.1, AC000385.1, U73627.1, AC000389.1, AL078590.27, AL049839.3, Z73424.1, Z95397.2, U40412.1, X14938.1, U03396.1, AB020682.1, AB020863.1, D89223.1, AC010083.5, AF203377.1, AE003750.1, AE003637.1, AE003550.1, AC007514.5, AC010198.8, AC012039.10, AC004893.1, AC004128.1, AF090189.1, AC006207.5, AC005007.1, AC005891.1, AC002366.1, AL031664.1, AL161587.2, AL161577.2, AL133453.2, U22376.1, Z46267.1, Z97055.1, AL049649.4, AL049713.19, AL035246.13, AL031177.1, AL023805.1, AL021879.3, AL031599.1, AL022198.1, AL109787.1, AL022604.1, U49956.1, AB012766.1, AB022220.1, L20858.1, AW439592.1, AW058001.1, AI982775.1, AI912340.1, AA825538.1, AW513884.1, AW074361.1, AI872206.1, AI798286.1, AI522238.1, AI758821.1, AW474823.1, AI572080.1, AA831357.1, AW337178.1, AI690445.1, AI360561.1, AA775261.1, AI140796.1, AA835492.1, AI361820.1, AW004890.1, AA100279.1, AI277190.1, AW517943.1, AI917776.1, AI469550.1, AI015234.1, AA581345.1, AI689240.1, AI744762.1, AW769512.1, D20022.1, AA122332.1, AI811224.1, AI355770.1, AW265061.1, AA485257.1, AA092467.1, AI471817.1, AI702026.1, T34498.1, AI597962.1, AW545016.1, AW544484.1, AI852320.1, AI839826.1, AV173766.1, AI646046.1, AI415428.1, AA959713.1, AA855573.1, AA116476.1, C85464.1, AW545749.1, AV269112.1, AV262681.1, AI884872.1, AV169832.1, AV064737.1, AV012020.1, AU019447.1, AV299656.1, AV154525.1, AV335637.1, AV301925.1, AI835781.1, AV160371.1, AV139152.1, AV138338.1, AV065117.1, AV051902.1, AV245530.1, AV338545.1, AV273829.1, AV214086.1, AV251164.1, AV249977.1, AV234666.1, AV163377.1, AV167956.1, AV136391.1, AV064067.1, AV062993.1, AV061701.1, AV057279.1, AV028650.1, AV232758.1, AV064377.1, AV063220.1, AV062771.1, AV059304.1, AV244517.1, AV215643.1, AV301794.1, AI706252.1, AW254397.1, AA956495.1, AI180308.1, AW465410.1, AC061974.2, AC060789.2, AC019267.3, AC026124.3, AC021067.5, AC025543.2, AC018428.3, AC024418.2, AC021067.4, AL163533.5, AL355887.1, AC068587.1, AC032016.2, AC009664.4, AC027523.2, AC026135.2, AC025830.2, AC013389.3, AC015474.3, AC023518.3, AC011774.4, AC012552.2, AF231129.1, AC016460.1, AC013750.4, AC015980.1, AL161658.3, AL050340.7, AL136373.2, AP001848.1, Z99293.1,

SEQ ID NO.168

NGO-Br-54

50 MK123/T7 3'

AK001917.1, AF035606.1, NM\_013232.1, U58773.1, NM\_011051.1, U49112.1, AC008925.3, AC007790.1, AC004485.1, AC004923.2, AC008078.1, AE001146.1, AC000385.1, U73627.1, AC000389.1, AL049839.3, Z95397.2, U03396.1, D89223.1, AW439592.1, AW058001.1, AI982775.1, AI912340.1, AA825538.1, AW513884.1, AW074361.1, AI872206.1, AI798286.1, AI522238.1, AI758821.1, AW474823.1, AW337178.1, AI690445.1, AI572080.1, AA831357.1, AI360561.1, AA775261.1, AI140796.1, AW517943.1, AW004890.1, AI361820.1, AA835492.1, AI917776.1, AA100279.1, AI277190.1, AI469550.1, AI015234.1, AI689240.1, AW769512.1, AA581345.1, AI744762.1, D20022.1, AA122332.1, AI811224.1, AI355770.1, AI471817.1, AI702026.1, AW265061.1, AA485257.1, AI597962.1, AA092467.1, T34498.1, AI624976.1, AI811439.1, AV262681.1, AV249977.1, AW545749.1, AW545016.1, AW544484.1, AV335637.1, AV303323.1, AV299656.1, AV324700.1, AV273829.1, AV269112.1, AV251768.1, AV235453.1, AV232758.1, AV214086.1, AI852320.1, AI839826.1, AI835781.1, AV173766.1, AV138338.1, AV070618.1, AV065117.1, AV064737.1, AV063220.1, AV062993.1, AV062771.1, AV061701.1, AV057279.1, AV051902.1, AV028650.1, AV012020.1, AI646046.1, AA959713.1, C85464.1, AA116476.1, AV303717.1, AV338545.1, AV301925.1, AV296289.1, AV259612.1, AV245530.1, AV244517.1, AV234666.1, AV215643.1, AV210921.1, AV167956.1, AV154525.1, AV153177.1, AV152413.1, AV136391.1, AV132769.1, AV064791.1, AV064377.1, AV064067.1, AV059304.1, AC061974.2, AC060789.2,

AC019267.3, AC027145.1, AL163533.5, AC011699.5, AC025164.7, AC026102.5, AC055810.2, AC068587.1, AC034259.2, AC032016.2, AC025615.2, AC027523.2, AC026135.2, AC025965.2, AC025543.2, AC013389.3, AC023518.3, AC018428.3, AC011774.4, AC011699.4, AF231129.1, AF228730.1, AC013750.4, AC007310.1, AL096888.26, AL353663.2, AL050340.7, AP001848.1,

SEQ ID NO. 169

NGO-Br-56

MK271/T3 5'

U13369.1, X03205.1, M10098.1, K03432.1, X00686.1, X82564.1, M11188.1, X01117.1, V01270.1, X06778.1, K01593.1, X00640.1, AF173638.1, AF173637.1, AF173636.1, AF173635.1, AF173634.1, AF173633.1, AF173632.1, AF173631.1, AF173629.1, AF173628.1, AF173627.1, AF173625.1, AF173624.1, AF173623.1, AF173622.1, AF173621.1, AF173620.1, AF173619.1, AF173618.1, AF173617.1, AF173616.1, AF173615.1, D84514.1, AF173630.1, AF173626.1, AF173613.1, X04025.1, X59734.1, AF173612.1, AF173610.1, AF173609.1, AF173608.1, AF173607.1, AF173606.1, M97576.1, X59733.1, M91180.1, AF173611.1, AF115860.1, X02995.1, J00999.1, K01373.1, AF173614.1, AF173605.1, AF169014.1, X98843.1, M91182.1, M91179.1, M91183.1, M91181.1, X98841.1, X98846.1, L11288.1, X98844.1, AF102857.1, AJ270031.1, AJ279506.1, U87963.1, X98840.1, X98837.1, NM\_007841.1, D50494.1, X98842.1, X98838.1, X98836.1, AJ277531.1, X98839.1, X98845.1, AF030250.1, M33066.1, AJ270032.1, L24123.1, M59402.1, M97575.1, M59384.1, M97573.1, AF157625.1, M59401.1, M59393.1, M59392.1, AF021880.1, M59386.1, M59385.1, AF236803.1, AF236802.1, AJ007613.1, M59396.1, M59390.1, AW794857.1, AW579814.1, AW580540.1, AW601150.1, AW601147.1, AW601146.1, AW803842.1, AW773277.1, AW773263.1, AW579819.1, AW864483.1, AW801020.1, AW579820.1, AW802332.1, AW795520.1, AA409121.1, AW869663.1, AW820465.1, AW860385.1, AW601994.1, AJ241168.1, AU080818.1, AW866280.1, AW841972.1, AW802330.1, AW601111.1, AW866367.1, AW866279.1, AW804859.1, AW604972.1, AW602533.1, AW866444.1, AW803373.1, AW206333.1, AA900286.1, AW866441.1, AW804923.1, AW801069.1, AW607233.1, AW804888.1, AI058227.1, AW793732.1, AW750335.1, AW867019.1, AW868469.1, AW864482.1, AW804283.1, AW868207.1, AW864334.1, AW804702.1, AW581420.1, AW803872.1, AW527555.1, AW864530.1, AW864525.1, AW804289.1, AW773310.1, AW864624.1, AW864534.1, AW868455.1, AL353644.2, AL158197.6, AC011630.2, AC023572.3, AC027604.2, AC068192.1, AC026915.1, AC064866.2, AL355134.1, AC069087.1, AC025654.2, AC064825.3, AC025630.1, AC010970.2, AC010554.1, AC018688.4, AC025968.1, AC064844.1, AC027174.1, AC068900.1, AC016828.4, AC006763.1, AL049183.5, AC019020.4, AC025330.2, AP000639.1, AC012647.15, AC008031.3, AC005806.2, AC012386.9, AC060712.1, AC064263.1, AC067527.1, AC067410.1, AC065739.1, AC065644.1, AC065474.1, AC064126.1, AC064016.1, AC063445.1, AC062950.1, AC062797.1, AC062782.1, AC060627.1, AC060379.1, AC060840.1, AC059708.1, AC059318.1, AC059021.1, AC058845.1, AC058431.1, AC057969.1, AC057826.1, AC056563.1, AC057287.1, AC057204.1, AC057180.1, AC056774.1, AC051336.1, AC051335.1, AC050735.1, AC050283.1, AC050278.1, AC050261.1, AC048611.1, AC048549.1, AC043304.1, AC043037.1, AC045314.1, AC044975.1, AC042630.1, AC042522.1, AC041360.1, AC041109.1, AC039370.1, AC039308.1, AC039109.1, AC038920.1, AC038318.1, AC037587.1, AC036362.1, AC036088.1, AC035291.1, AC034717.1, AC034385.1, AC034335.1, AC030306.1, AC030238.1, AC029865.1, AC029864.1, AC029705.1, AC035311.1, AC034638.1, AC033832.1, AC029523.1, AC027847.1, AC056957.1, AL157407.2, AC025184.3, AC011135.2,

SEQ ID NO.170

NGO-Br-57

MK3710/T3 5'

AF025438.1, AL050353.1, AE003680.1, AC005539.1, AL024458.1, AC004680.2, AC004455.1, AC005966.1, U63928.1, Y18930.1, Z48544.1, X79080.1, AW161135.1, W58718.1, N32746.1, AA313566.1, AA024784.1, AA236836.1, AA007319.1, R72404.1, AA236656.1, AI090162.1, AI630438.1, AA701988.1, AA852227.1, AA137279.1, AA541923.1, AA000683.1, AI337332.1, AW161742.1, AW427494.1, AI828070.1, AI935340.1, AI760923.1, AI765742.1, W10638.1, AI630424.1, H30501.1, R17187.1, AI964006.1, AI304319.1, W43974.1, AI765022.1, AA236789.1, AW051324.1, H25699.1, AW592648.1, N56244.1, AW485468.1, AA865602.1, AI631687.1, AA000401.1, AI765999.1, N66532.1, AI888263.1, AW557853.1, H35482.1, AA003291.1, AI076924.1, AI461713.1, AW466965.1, AA637410.1, AW805299.1, AI808237.1, AW536613.1, AA687041.1, AA452088.1, AA916723.1, AI585560.1, AA024685.1, AW152251.1, AI430072.1, AA007455.1, AA759800.1, AA546383.1, AW614505.1, AW772254.1, AA916358.1, AW272790.1, AI336121.1, AA607321.1, AI599140.1, AA521369.1, AI167263.1, AI283104.1, AI140745.1, AA345744.1, AW645427.1, AA995467.1, AA451907.1, N23163.1, AI753758.1, AI841918.1, R77800.1, AA505618.1, AA110039.1, AI685071.1, AU024430.1, AA959647.1, AA913049.1, AW636012.1, AI538205.1, AA385531.1, AI073755.1, AW823008.1, AU024429.1, AI352390.1, R72405.1, R41738.1, AU022981.1, AI119291.1, AI171338.1, AI136131.7, AL355349.1, AL138706.1, AC032027.2, AP000831.1, AP000713.1, AC013237.1, AL160276.2, AC069160.1, AC011168.4, AC046152.2, AC017106.3, AC023448.2, AC012335.2, AC006279.6, AC013779.3, AC007345.2, AC007342.2, AC015860.2, AC012273.1, AL353640.6, AL354937.2, AL159996.4, AL138815.4, AL157366.3, AL161780.3,



AL163973.1, AL136298.1,

SEQ ID NO. 171

NGO-Br-57

5 MK3710/T7 3'

AL050353.1, AF025438.1, AL121924.12, U42838.1, AL031055.1, AL121931.10, AL139076.2, AL024458.1, AC004680.2, AC010889.2, NM\_007050.2, AF043644.4, AE003844.1, AE003787.1, AE003676.1, AE003533.1, AE003519.1, AE003480.1, AE003422.1, AE003217.1, AE002799.1, AC004455.1, AC009320.7, AC007478.1, AC007123.1, AC005548.1, AL163232.2, AC000389.1, AL035633.18, AL032654.1, Z68335.1, AL024473.1, Z92844.1, AL110503.1, AP001687.1, AP001297.1, AP000459.3, AB005234.1, D17799.1, D17798.1, D17797.1, AB009052.1, AB006621.1, AI964006.1, AI337332.1, AI765742.1, AA236789.1, AI304319.1, AA701988.1, AW592648.1, AI765022.1, AA865602.1, AI828070.1, AI765999.1, AI760923.1, N66532.1, AI631687.1, AI935340.1, AA916723.1, AW161742.1, AA024685.1, AW152251.1, AW772254.1, AA916358.1, AI336121.1, AW614505.1, AW051324.1, AI888263.1, N23163.1, AA007455.1, AW272790.1, AI167263.1, AI283104.1, AA451907.1, AA995467.1, AI753758.1, AA505618.1, AI073755.1, AA913049.1, AI538205.1, AA670386.1, AI352390.1, AA680352.1, AW151295.1, AA720562.1, AA723980.1, AI808237.1, AW466965.1, AI081040.1, AA992256.1, AI267913.1, AA532854.1, R41738.1, AA928158.1, AW117185.1, AA016221.1, AA345744.1, R72405.1, AI140745.1, AI084344.1, AI079153.1, AA852226.1, H89982.1, AI539552.1, AA385531.1, AA236836.1, N50079.1, AI090162.1, AW557853.1, AA858049.1, AW536613.1, AI461713.1, AI599140.1, AI678339.1, AW172462.1, AA637410.1, AI678340.1, R77800.1, AI198148.1, AA546383.1, AW433804.1, AI841918.1, AI585560.1, AW823008.1, AA541923.1, AU024430.1, AA959647.1, AA924460.1, AU022981.1, H30501.1, AA024784.1, T26930.1, AI630424.1, AA137279.1, AI630438.1, AW161135.1, W58718.1, AA607321.1, AU024429.1, AA963706.1, AA765777.1, AI505865.1, AI963259.1, AL136131.7, AL355349.1, AL138706.1, AL050335.24, AC016073.2, AC023651.2, AL354992.1, AC026285.4, AC055116.2, AC012133.3, AC006756.1, AC012031.7, AC007953.7, AC027502.3, AC008926.5, AC009679.3, AP000841.1, AP000783.1, AC012151.5, AC022226.7, AC018728.2, AC068509.1, AC026961.2, AC011036.3, AL136231.5, AL157824.2,

SEQ ID NO. 172

NGO-Br-58

30 MK436/T3 5'

AF118652.1, NM\_006541.1, AJ010841.1, AF118649.1, AF118650.1, AF118651.1, AC021044.4, W73086.1, AA307154.1, W58564.1, AA363862.1, AW327841.1, AI902183.1, T06444.1, AW014738.1, AI822071.1, AI813451.1, AA452335.1, W15560.1, H78479.1, H59799.1, F11379.1, R63123.1, T83390.1, N24488.1, T83556.1, F07471.1, N76641.1, T36308.1, H17884.1, AW743314.1, AL024195.1, AI892878.1, AI541284.1, AI121283.1, AA423088.1, AA124189.1, AA119742.1, AA086801.1, W14808.1, AA222785.1, AA293188.1, AA985756.1, AA711181.1, AA218282.1, W33933.1, AI685717.1, T10785.1, AA815685.1, AA273544.1, AA238334.1, AA157103.1, AI595622.1, AI316625.1, AI119458.1, AA879644.1, AA879757.1, AA390040.1, AA220693.1, AA217769.1, AA106608.1, W90901.1, W85535.1, AA050409.1, AA000754.1, W57189.1, W36243.1, AA120515.1, AI929984.1, AA623076.1, AA939357.1, AA914937.1, AA674174.1, W16243.1, AA009010.1, AA536703.1, W01696.1, AL117714.1, AW652677.1, AA929573.1, AA667299.1, AA561056.1, AA177257.1, AA172553.1, AA117786.1, AA066010.1, W16154.1, AA048263.1, W76881.1, C83514.1, C82658.1, R84921.1, AA198255.1, H96310.1, W23637.1, AA833367.1, AA822615.1, AA140412.1, AI561434.1, AA545088.1, AA049167.1, AW672942.1, AA222090.1, AA212687.1, AA866363.1, AA867450.1, AL161648.5, AL139123.2, AL138831.2, AC050138.1, AL158828.4, AL353613.2,

SEQ ID NO. 173

45 NGO-Br-58

MK436/T7 3'

NM\_006541.1, AJ010841.1, AC020610.6, AC005666.1, AC004381.1, AC005972.1, AC004099.1, AC005519.2, AC005899.1, AL034343.17, AL008582.11, AC005516.1, AC004601.1, AL110120.11, AC018511.4, AC005726.1, AL035420.15, Z99128.1, AL022159.1, U91323.1, AC005520.2, AJ011930.1, AC002036.1, AC007676.19, AF205588.1, AC004525.1, AC004961.2, AL117337.25, U07000.1, AL034427.1, AL020997.1, AC009946.2, AC004584.1, AC003043.1, AC002070.1, AC004552.1, AC005232.1, AC002425.1, AC006312.8, AC004968.1, AC005480.3, AC004821.2, U72787.1, AL355916.1, AL117375.12, Z83840.7, Z94801.1, AL008718.23, AC007240.2, AC004463.2, AC004771.1, AL160231.2, AL121825.19, AL022322.1, AL022238.1, AL021391.2, AL031296.1, AL031681.13, AC005015.2, AC007435.12, AL163262.2, AL121658.2, AL121655.1, Z84486.1, AP001717.1, AC010285.4, AC000003.1, AC004883.2, AC005288.1, AL163265.2, AL133396.1, Z83819.1, AP001720.1, AC009516.19, Z82243.1, AC009145.4, AC002544.1, AC005562.1, U52111.1, AC011449.6, AC022149.3, AC005907.1, AL133243.1, AL035699.4, AC006509.15, AC007055.3, AL049779.4, AL035658.7, Z82245.1, AP000557.2, AL049759.10, AC006581.16, AL049712.12, AC005778.1, AC002558.1, Z85996.1, AL024474.1, AL008716.1, AC005755.1, AC003002.1, AI074462.1, H99205.1, AI038375.1, AL119361.1, AA299728.1, AA732982.1, AA602488.1, AI963281.1, AI345497.1, AI371278.1, AA570441.1, AA487512.1, AW149972.1, AI829381.1, AL079763.1, AA614595.1, AA491864.1, AW768439.1, AL135639.1, AI963725.1, AI858632.1, F25696.1, AI610602.1, AI370302.1, AI285709.1, AA618392.1, AA618346.1, AA602468.1, AA306530.1, H70245.1, H66503.1, AA708669.1, AA620386.1, AA362670.1, M77904.1, AW877774.1, AW467676.1, AI469586.1, AI375374.1, AI052628.1, AA700279.1, AA613177.1, AA528405.1, AA515254.1, AA504694.1, AA382130.1, AA347199.1, AA338281.1, AA174071.1, AA167567.1, R86266.1, AL134669.1, AI745457.1, AI734060.1, AI734052.1, AI732085.1, AI370199.1, AI288162.1,



- AA876148.1, AA846808.1, AA678733.1, AA631915.1, AA489797.1, AA226144.1, AA226095.1, AA225949.1, AW500075.1, AW177901.1, AW177895.1, AW177822.1, AW177816.1, H41308.1, AI073735.1, AA601218.1, AA482054.1, AI174701.1, AW074405.1, N38996.1, AI500315.1, H62161.1, AW847624.1, AI597931.1, AW084237.1, AI791265.1, AI468269.1, AI382183.1, AA194502.1, C05882.1, AA001398.1, AA828783.1, AA688148.1, AA455088.1, AA194944.1, AA487225.1, AI005219.1, H73907.1, AA280681.1, N55212.1, AI082472.1, AA578774.1, AL161648.5, AL139123.2, AL109615.18, AC020603.3, AC068727.1, AC011355.3, AL109843.17, AP001885.1, AC068847.1, AC068583.1, AC021991.3, AC011022.4, AC010481.4, AC009038.5, AL050329.11, AC046162.2, AL136458.2, AL162733.2, AC008474.6, AL139815.3, AC005047.2, AC026495.1, AL353596.2, AP001809.1, AL135787.8, AL157789.1, AC024096.7, AC026603.2, AC007217.2, AL109823.21, AL355837.1, AL353641.1, AP001447.1, AC036206.2, AC008403.5, AC004873.1, AP001787.1, AC063950.3, AC018462.3, AL139384.3, AL139327.12, AC068785.4, AC063962.3, AP000717.1, AC010277.3, AC008484.3, AC064860.2, AC025692.3, AC020781.4, AC023183.2, Z93015.7, AL355392.2, AL354932.4, AL139324.5, AC025265.5, AC026115.10, AC008622.4, AC025778.2, AC025277.2, AC011486.5, AC022307.7, AC012659.3, AC010260.3, AC008671.3, AC025142.2, AL133458.12, AL161789.3, AC009027.4, AC023089.2, AL356009.2, AP001855.1, AC068077.1, AC022795.3, AC020754.2, AL353794.1, AP001279.1, AC008121.13, AC023831.3, AC019255.2, AP000846.1, AL353691.2, AL158153.2, AC022156.4, AC016701.2, AC016525.3, AL161756.1, AL139396.1, AC008158.3, AC068786.4, AC009021.3, AC010503.5, AC008614.4, AC009120.5, AC027394.2, AL353622.3, AC064835.3, AC011445.4, AP001187.1, AL354760.1, AC012635.1,
- 20 SEQ ID NO. 174  
NGO-Br-59  
MK337/T3 5'  
X56687.1, M61725.1, NM\_014233.1, X53461.1, X53390.1, L42571.1, M61726.1, NM\_011551.1, X60831.1, L42570.1, M61724.1, AC004596.1, U65487.1, AF241726.1, X59863.1, X57201.1, X57561.1, X65698.1, X65697.1, AF164119.1, AF102773.1, AL078477.5, AC010083.5, AC018765.4, AF157625.1, AC006254.10, U78553.1, AC002986.1, AE000747.1, AE000803.1, AL353815.2, AL163290.2, U49246.1, AL049659.2, AL163812.1, AL117200.2, Z83125.1, Y09788.2, L20418.1, U41548.1, AP001745.1, AP001618.1, X73942.1, AB014538.1, AA683270.1, AI990923.1, AI652105.1, W56216.1, AI424653.1, AI361257.1, AW373605.1, AI263742.1, W28568.1, AA134165.1, AW867502.1, AI407688.1, AV098625.1, AW607456.1, AI121071.1, AA322474.1, AA494480.1, AA254648.1, AW362484.1, AA306865.1, AI947817.1, AV207877.1, AV140171.1, AV122483.1, AI594085.1, AI551499.1, AI463712.1, C85526.1, AA606502.1, AV083972.1, AI267702.1, AV392783.1, AV392203.1, AV392190.1, AV392165.1, AV387615.1, F15738.2, AI047080.1, C65313.1, AA437706.1, AC011606.6, AC060757.2, AC021999.2, AC020754.2, AC011606.5, AC024234.4, AC024899.4, AL158052.2, AC068918.2, AC026801.2, AC008795.5, AC008855.4, AC011145.3, AC023857.2, AC007555.1, AL137780.2, AL138811.1, AC016955.9, AC012522.7, AC011318.8, AC024891.8, AC061979.2, AC025638.3, AC037426.2, AC034103.4, AC062039.1, AC009237.2, AC021015.3, AC023582.2, AC040893.1, AC019008.4, AC019250.3, AC015801.3, AC013713.4, AC024253.2, AC022302.3, AC025598.1, AC022609.2, AC019251.2, AC024119.1, AC016490.2, AC012499.3, AC018665.2, AC012340.2, AC009408.2, AL049715.21, AL157875.4, AL355535.1, AL355506.1, AL162582.2, AL162372.3, AL161615.2, AL136447.4, AP001769.1, AP000941.2, AP000869.1, AP000846.1, AP000827.1,
- 40 SEQ ID NO.175  
NGO-Br-59  
MK337/T7 3'  
NM\_014233.1, X53461.1, X53390.1, X56687.1, NM\_011551.1, X60831.1, AC004596.1, U65487.1, L42571.1, L42570.1, M61725.1, M61726.1, X56688.1, AF241726.1, AF170811.1, AC007372.4, AC004912.1, AC007011.1, AC005295.1, AL132896.1, AL049837.4, AJ009934.1, AC004983.2, NM\_014771.1, AC005782.1, AL121934.15, AB040880.1, AK000425.1, AK000265.1, AP000696.1, AB014561.1, AW373933.1, AW373896.1, AA626575.1, AA374794.1, AI915777.1, AI798277.1, AI521078.1, AI087037.1, AW249403.1, W31280.1, AA651656.1, R36455.1, AA919770.1, AA664208.1, AA329246.1, R36454.1, AA134166.1, AA961221.1, AA914265.1, AA911482.1, D56068.1, D56028.1, AI907998.1, AA623692.1, AA413864.1, AA308880.1, AI740529.1, AA637361.1, AW793731.1, AA889124.1, AA377594.1, AI907995.1, AA377898.1, AA438075.1, AA211953.1, W83843.1, AI762169.1, AA611296.1, AW519549.1, AW390831.1, AI893975.1, AA500491.1, AA492907.1, W80099.1, W77364.1, W33457.1, AI105117.1, AA518740.1, AW814069.1, AW814073.1, AI154308.1, AW438655.1, AW298403.1, AW243881.1, AW166393.1, AW001988.1, AI989406.1, AI971828.1, AI831668.1, AI208785.1, AI077671.1, AI027548.1, AA890545.1, AA768775.1, AA577311.1, AA056073.1, AA022622.1, AA021002.1, AA020748.1, AA019643.1, AA013126.1, H84980.1, H85537.1, AW819846.1, AW556048.1, AW433907.1, AI968114.1, AI678953.1, AI651215.1, AI202697.1, AI220802.1, AW196586.1, AW175973.1, AI513981.1, AI348282.1, AI297541.1, AI257079.1, AI187754.1, AA973975.1, AA942224.1, AA816918.1, AA478079.1, AA126812.1, H39217.1, AA183999.1, W79356.1, AC011606.6, AC060757.2, AC021999.2, AC020754.2, AC011606.5, AC009237.2, AC017099.3, AP001769.1, AP000827.1, AL162372.3, AC024234.4, AC021987.2, AP000668.1, AC026803.2, AC008749.4, AC026930.2, AC026285.4, AC018761.4, AC023154.4, AC012482.3, AC011200.2, AL353609.2, AL139423.4, AL161662.1, AC010189.4, AC007834.20, AC053546.3, AC007339.3, AC022197.3, AC015867.2, AC022783.2, AC000005.1, AC020968.1, AL355293.2,
- 60 SEQ ID NO.176

-107-

NGO-Br-62

MK804/T3 5'

- 5 NM\_005134.1, AF111106.1, AC007736.3, AC008168.3, NM\_013658.1, AC005324.1, X85991.1, AC004539.1,  
NM\_009134.1, AC006287.1, AF075627.1, AL122020.3, U58743.1, Y09108.1, AC009486.3, AE003769.1, AC004888.1,  
AC005013.1, AC007463.3, AC008067.3, AF189157.1, AE001980.1, AC009888.1, AC005549.1, AL008733.10, Z68760.2,  
L46672.1, X94768.1, AP001278.1, AP000816.1, M24411.1, Z99105.1, AB006424.1, AW673704.1, AW371829.1,  
AW382321.1, AW371827.1, AJ081867.1, AW382320.1, AW371825.1, AI687366.1, AL120881.1, N41948.1, AW239384.1,  
AI286014.1, N40656.1, AW382480.1, AA161066.1, AW367894.1, AA332078.1, AW382482.1, AW659290.1,  
10 AW500241.1, AA611470.1, AW392387.1, AA906014.1, AW535590.1, AW534364.1, AW533907.1, AW534600.1,  
AW535963.1, AI552086.1, AW535977.1, AW535929.1, AW535612.1, AW535599.1, AW535574.1, AW535542.1,  
AW535538.1, AW535507.1, AW535217.1, AW534451.1, AW534434.1, AW534374.1, AW534356.1, AW534229.1,  
AW534224.1, AW534199.1, AW534112.1, AW534076.1, AW534005.1, AW533992.1, AW533915.1, AW532274.1,  
AW532226.1, AW532183.1, AW532169.1, AW531827.1, AW531069.1, AW530797.1, AW530120.1, AW530107.1,  
AW529979.1, AW529973.1, AW254242.1, AW254201.1, AW251947.1, AW251307.1, AW251102.1, AI709485.1,  
15 AI578408.1, AI555305.1, AI549564.1, AI549513.1, AI549263.1, AI549090.1, AI548886.1, AI548373.1, AI548339.1,  
AI547780.1, AI547618.1, AI547615.1, AI535377.1, AI535100.1, AI535055.1, AI535053.1, AI511474.1, AI501242.1,  
AA900666.1, AI137299.1, AI072600.1, AI072263.1, AI072230.1, AI071899.1, AI071691.1, AI071396.1, AI071193.1,  
AI071165.1, AI070019.1, AI058437.1, AI045860.1, AI045612.1, AI044996.1, AC021927.3, AP001381.1, AC015956.3,  
AC007140.1, AC026964.2, AC018989.3, AC024046.2, AC012596.3, AC009574.3, AC021114.3, AC018940.4,  
20 AC022971.2, AC011172.4, AC016068.2,

SEQ ID NO.177

NGO-Br-62

MK804/T3 3'

- 25 AF100744.1, U79267.1, NM\_005134.1, AF111106.1, AE003449.1, AL163301.2, NM\_000236.1, AC016041.5, M29193.1,  
AL035653.12, AL023807.6, Z84475.1, J03895.1, M35432.1, J03540.1, X07228.1, D83548.1, AC010102.3, AC006283.5,  
AE003514.1, AE003440.1, AC005690.8, AC006465.2, AC008075.2, AF101438.1, AL163302.2, AL163254.2,  
AL163233.2, AL136018.2, AL133097.1, AL109627.18, Z76735.1, AP001709.1, AP001688.1, U23442.1, AP000950.2,  
AP000204.1, AP000244.1, AP000126.1, AI076775.1, AI215696.1, AI601253.1, AA581865.1, AI371049.1, H97837.1,  
30 AI131196.1, AI184641.1, AI754673.1, AI139064.1, AI142447.1, AI374783.1, AI204302.1, AA772102.1, AA435767.1,  
AI659941.1, AA860292.1, AI569647.1, AA706309.1, AA732402.1, AA706694.1, AA192742.1, N56938.1, AA766582.1,  
AA171536.1, N59159.1, AI336886.1, N49858.1, AA994358.1, AI191899.1, N47550.1, AA074753.1, N30433.1,  
AA536150.1, AI348314.1, AI342660.1, N29328.1, AA401497.1, AA854769.1, AI220586.1, AI025515.1, AA936114.1,  
AA825278.1, AA492553.1, N77882.1, AA804953.1, AW068965.1, AA860331.1, N89882.1, AA769019.1, N47895.1,  
35 N63879.1, Z39560.1, AA805421.1, W73239.1, N66463.1, T62952.1, AI093651.1, AW839754.1, R68907.1, W57588.1,  
AI970730.1, W92205.1, AA602432.1, F10765.1, AA074836.1, R22227.1, AA255616.1, AA987948.1, F03184.1,  
AA852934.1, H04250.1, R42968.1, AW503224.1, R67269.1, AI621152.1, AI536774.1, AW503670.1, H83900.1,  
AI743459.1, AW439253.1, AI571914.1, T92192.1, AW264100.1, AW172934.1, F04772.1, AI588862.1, H56904.1,  
R40975.1, AI915335.1, AW467646.1, AI678364.1, R43639.1, AI625453.1, AA643894.1, AI560721.1, R00485.1,  
40 W73294.1, AW270022.1, AA397947.1, AC015956.3, AC021927.3, AP001381.1, AL121900.7, AL121780.3, AC026570.2,  
AL354706.2, AC046148.2, AC027566.1, AC008658.2, AC015405.1, AL133499.1, AC016956.6, AC024153.10,  
AC008019.37, AC027489.2, AC016994.3, AC025130.2, AC016956.5, AL356377.1, AL121759.19, AL162381.3,  
AL139094.5, AC068908.2, AC069028.4, AC023057.6, AC012117.3, AC046161.2, AC010631.4, AC009118.6,  
AC021471.2, AC009639.3, AC026967.2, AC027067.2, AC027059.2, AC026505.3, AC022050.2, AC019334.3,  
45 AC016910.2, AC012585.4, AC009384.5, AC012071.3, AC017069.3, AC012855.1, AC015230.1, AL356140.3,  
AL353578.2, AL158146.2, AL160057.4, AL162759.1, AL136975.1, AP001392.1,

SEQ ID NO.178

NGO-Br-63

MK467/T3 5'

- 50 NM\_014731.1, AB011124.1, AF123659.1, AF123658.1, AF123657.1, AF123656.1, AF123655.1, AF123653.1,  
AL133215.16, AE003506.1, NM\_003980.1, AJ242502.1, AJ242501.1, AL023284.1, X73882.1, AF130782.1, AF190465.1,  
AC006544.19, AC005033.1, AC003065.1, AC006985.2, U84269.1, U84268.1, AC003047.1, AL031295.1, AE001862.1,  
U51197.1, AC004231.1, AP000279.1, AB004043.1, AB004042.1, AB002339.1, AW416906.1, D56085.1, AW263065.1,  
55 AJ281091.1, AI911142.1, AI501468.1, W45377.1, AW530214.1, AW140903.1, AA819761.1, AI293560.1, AI230840.1,  
AA799815.1, C25135.1, AA086491.1, AW727488.1, AW657062.1, AW648093.1, AW581571.1, AW576745.1,  
AV306266.1, AW138828.1, AW045957.1, AJ892415.1, AV014939.1, AI325725.1, AI069094.1, AA727234.1,  
AA400580.1, AL121891.18, AC025853.2, AC012162.9, AC012693.1, AC009216.8, AC011498.4, AC017241.1,  
AC027118.2, AC026497.1, AC009850.9, AC014014.1, AC017674.1, AC012600.4, AC012515.11, AC010189.4,  
60 AC008129.10, AC007834.20, AC023501.7, AC012293.9, AC044820.2, AC068126.2, AC068588.1, AC068557.1,  
AC027764.2, AC062037.2, AC024948.2, AC055811.1, AC024474.2, AC021467.2, AC027267.1, AC026244.1,  
AC010121.6, AC015867.2, AC016439.4, AC016753.4, AC011575.3, AC012600.3, AC013934.1, AC013499.2,  
AC011135.2, AL138753.3, AL136990.14, AL136439.2, AL138757.4, AL137025.2, AL138955.1, AL136104.3,  
AL022335.6, AP001979.1,

## SEQ ID NO.179

NGO-Br-63

MK467/T7 3'

- 5 NM\_014731.1, AB011124.1, AC019209.3, AC005829.1, AF045453.1, AL135999.2, AL132719.2, Z98946.15, AL021326.1, AC010385.3, AC007115.1, AC002477.1, NM\_012654.1, AF179633.1, AL121809.4, AL035460.15, M85300.1, D14905.1, D14904.1, AW134487.1, AW005916.1, AI918105.1, AI369140.1, AI362807.1, AI536952.1, AA233070.1, AI800560.1, AI570845.1, AI084111.1, AI805727.1, AI566887.1, AI885796.1, AW205146.1, AA631005.1, AW088686.1, Z38359.1, AI570882.1, AI889744.1, F03249.1, T23438.1, AI093242.1, AI151303.1, H64737.1, T91286.1, AA682753.1, AW057576.1, AW752274.1, AA577015.1, AA319634.1, H65227.1, AW246038.1, AA862950.1, AI573262.1, 10 AA639497.1, AI148651.1, AI129016.1, R44479.1, AW874175.1, AI849112.1, AA118865.1, W53946.1, AW611372.1, AW359586.1, W96834.1, AA339527.1, AA320970.1, AA317924.1, AW523114.1, AI229250.1, AI229142.1, AA943809.1, AW658594.1, AW655764.1, AW426231.1, AW359271.1, AI863241.1, AI007273.1, AA832546.1, AA619805.1, AA571164.1, AA422555.1, AA260212.1, AA259669.1, AA240477.1, W16289.1, H51681.1, AL121891.18, AC008133.2, 15 AC021420.3, AC025898.2, AC009608.2, AC024225.8, AC024224.6, AC025194.2, AC016018.7, AL355482.1, AC024105.7, AC023504.4, AC064837.2, AC025772.3, AC012636.3, AC034138.2, AC021355.3, AC027688.2, AC023819.3, AC015478.3, AC016868.4, AC009962.3, AC012505.3, AL354652.3, AL355884.2, AC009453.7, AC046135.4, AC068633.3, AC026084.2, AC026285.4, AC026792.2, AC011356.3, AC024230.3, AC024537.2, AC027216.2, AC027526.2, AC026423.3, AC027685.2, AC015928.4, AC011033.3, AC011957.2, AC016180.5, 20 AC011213.4, AC023920.2, AC016483.6, AC023291.2, AC005052.1, AL356154.2, AL355590.2, AL354726.2, AL355476.1, AL353589.1, AL157375.1, AP001855.1, AP000752.1, AP000721.1,

## SEQ ID NO.180

NGO-Br-64

MK731/T3 5'

- 25 NM\_014963.1, AB023180.1, AC005390.1, AF060974.1, AC007246.3, AL049754.1, AE001274.1, AJ242840.1, AJ242839.1, Y15791.1, AE003835.1, AE003596.1, AC005290.3, AF117761.1, AF117760.1, NM\_000506.2, AC007655.1, U73167.1, U90094.1, M24461.1, AL133224.2, AL121756.14, U50596.1, U00012.1, AL022374.1, X82071.1, AB001030.1, V00595.1, J00307.1, M33031.1, D17389.1, X54794.1, M60789.1, Y10403.1, AW410223.1, AW468990.1, AI827893.1, 30 AW081199.1, AA977476.1, AL045506.1, AL079747.1, AW206971.1, AW073064.1, AI559848.1, AI760801.1, AI430503.1, AA245512.1, AA245370.1, W62920.1, AW729115.1, AW668796.1, AW431830.1, AW348976.1, AW649811.1, AW623969.1, AW056157.1, AI987383.1, AI941796.1, AI896465.1, AI691275.1, AI670672.1, AI465663.1, AI456906.1, AI397644.1, AI054620.1, AA855993.1, C32683.1, AA354150.1, AA334812.1, AA286992.1, H69659.1, H59101.1, AC011474.2, AC020781.4, AC020582.3, AC068633.3, AC032027.2, AC048370.2, AC012334.2, AC008713.5, 35 AC016573.4, AC025868.2, AC023826.2, AC018445.3, AC019356.3, AC027817.1, AC012286.2, AC007524.2, AC026086.2, AC023356.4, AC011951.3, AC015930.3, AC012568.3, AC012374.9, AC024610.1, AC010011.3, AC012454.3, AC013279.3, AC013750.4, AC020372.1, AC013563.2, AC017853.1, AC007471.3, AC007597.2, AC007503.1, AL356138.3, AL138720.5, AL137162.5, AL137225.11, AL162499.3, AP001337.1,

## 40 SEQ ID NO.181

NGO-Br-64

MK731/T7 3')

- AC005390.1, NM\_014963.1, AB023180.1, AC002351.1, Z82215.1, AE003544.1, NM\_004474.1, NM\_000758.1, AC005950.1, U37501.1, AF042832.1, AC004511.1, AC003675.1, AL163299.2, AC001228.1, AL050318.12, Z85994.1, 45 AJ006345.1, M13207.1, AP001754.1, AP001062.1, X03021.1, M11220.1, M10663.1, M28860.1, M28859.1, AC068783.2, AE002501.1, AC007537.3, AC005261.1, AL162756.2, AL122127.3, X97051.1, X17215.1, X57133.1, X16489.1, U18978.1, AB019441.1, X13972.1, M37277.1, AI200815.1, AI417909.1, AI459189.1, AI560887.1, AW270083.1, AI564758.1, AI745070.1, AI355293.1, AI815176.1, AL047897.1, AL047898.1, AW474741.1, AI469279.1, AI359252.1, AA722975.1, AA444008.1, AI220310.1, AI624704.1, AI289062.1, AI623674.1, AL045507.2, AA456471.1, Z25344.1, 50 AA444037.1, AA427461.1, R96945.1, AW472864.1, AA654248.1, AA456804.1, AA427462.1, AA954685.1, AI932512.1, AA485597.1, AI433817.1, AA485433.1, AA454577.1, AA457134.1, T30158.1, AA476273.1, AW138346.1, AA464482.1, T95376.1, T95296.1, AA299621.1, AA293227.1, AI866076.1, AI801586.1, AA884991.1, AA435961.1, AW013846.1, AW410224.1, AI391545.1, AA971658.1, AA932895.1, AW431713.1, AW547208.1, AW345308.1, AI085206.1, AI022933.1, AI912784.1, AI677936.1, AI655452.1, AA096946.1, T29160.1, AW749596.1, AW213795.1, AW207707.1, 55 AW005369.1, AV131761.1, AV062291.1, AI695173.1, AI524311.1, AI508690.1, AI462638.1, AI417791.1, AI232789.1, AI072326.1, AA288479.1, AA135536.1, W73276.1, W03892.1, D51085.1, T33074.1, AL162423.2, AC016525.3, AC018930.3, AC010033.7, AC034216.3, AC026699.2, AC009175.3, AC010590.4, AC011361.3, AC021424.3, AC013791.3, AC011182.3, AC018891.2, AC009899.5, AC023171.1, AC022754.1, AC013287.6, AC016743.3, AC021389.1, AC014953.1, AC003656.1, AP001356.1, AC016968.11, AC015545.10, AC024097.8, AC022296.8, 60 AC037471.2, AC025468.3, AC025460.3, AC024075.3, AC010378.3, AC008681.5, AC024293.2, AC023484.2, AC021328.3, AC019345.3, AC022051.3, AC018427.3, AC021200.4, AC011281.3, AC027171.1, AC024951.9, AC021585.3, AC017096.2, AC011140.3, AC009575.4, AC016968.10, AC015545.9, AC016757.3, AC010136.3, AC013567.2, AC009647.2, AC010782.1, AL035662.50, AL136079.3, AL157939.3, AL158817.2, AL158143.1,

## SEQ ID NO.182

NGO-Br-65

MK385/T3 5'

- 5 AF086824.1, U39904.1, AF039218.1, AF070066.1, AC004811.2, AC002563.1, NM\_015239.1, AK001544.1, AC007023.3, AC007078.3, AC000039.3, AC006480.3, AC005488.2, AC005088.2, AF030453.1, AL121823.12, AL161571.2, AL022326.1, AL078579.1, L09233.1, AE003628.1, AC005537.2, AC005036.1, AC007038.3, AC007451.1, AC006254.10, AF063424.1, AF092090.1, AC005359.1, AC000378.1, AL161513.2, AL035703.20, Z75543.1, AL035681.13, Z93020.1, X59046.1, X65624.1, AB037724.1, M22462.1, AW449442.1, AW444459.1, AI826767.1, AI674481.1, AA570498.1, H62116.1, AW760341.1, AW733957.1, AW598733.1, AW459885.1, AU082470.1, AV403875.1, AW325533.1, 10 AW325530.1, AW162177.1, AW149411.1, AW076876.1, AW076660.1, AI924223.1, AI510359.1, AA968035.1, AA508904.1, AA508038.1, AA236748.1, AA177241.1, AA140828.1, AA116487.1, AA107365.1, W62286.1, H16776.1, T18197.1, AC026363.3, AC026765.5, AL157828.5, AC012032.11, AC023923.2, AL159156.4, AL157362.2, AC019315.2, AL139429.4, AC019071.3, AC025232.3, AC023593.3, AC018720.3, AC012406.3, AC023811.7, AC005236.3, AC004980.2, AC007674.2, AC026507.1, AC016294.2, AC022253.2, AL139182.14, AL137118.8, AL162387.3, 15 AL161642.3, AL049770.1, AP001809.1, AC009774.4, AC021064.7, AC024505.3, AC023493.6, AC026418.2, AC024991.2, AC068482.1, AC027104.2, AC023170.3, AC019063.3, AC019043.3, AC027184.2, AC058808.1, AC026043.3, AC018513.3, AC026002.2, AC019356.3, AC016875.3, AC011952.4, AC009933.5, AC020796.2, AC018887.4, AC022245.3, AC016513.2, AC011009.4, AC022182.3, AC012306.3, AC016245.3, AC020201.1, AC016521.1, AF162757.1, AL133268.6, AL121955.9, AL136114.2, AL136159.4, AL353762.3, AL354720.3, AL355526.2, 20 AL161908.3, AL160400.3, AL138896.2, AL137838.2, AL133167.1, AL138689.1,

## SEQ ID NO.183

NGO-Br-65

MK385/T7 3'

- 25 AC002563.1, AB023166.1, U75698.1, U93872.1, AP000542.1, AE003597.1, AC004506.1, AC004695.1, AL049781.4, AL034404.1, X58358.1, AP001819.1, AI861788.1, H10788.1, AW386741.1, AW581596.1, AW386738.1, AA308642.1, N57796.1, AI933041.1, AI984971.1, T91324.1, W42440.1, AI933217.1, N57810.1, AI933106.1, R50756.1, R44891.1, H79564.1, H63135.1, AA353105.1, AA224531.1, AI861826.1, AI245941.1, AW054833.1, AA778789.1, AI806134.1, AW483290.1, AW416772.1, AI936328.1, AA379967.1, AA677294.1, AW047976.1, AW047308.1, AW046893.1, 30 AA617920.1, AA546601.1, AW046868.1, AA822334.1, W78614.1, AI183534.1, AW525869.1, AW665288.1, AA957183.1, AI807388.1, AI228556.1, AI698168.1, AI102448.1, AA955912.1, AI017868.1, AI767064.1, AW797442.1, AW859870.1, AW248416.1, AW117872.1, AC026363.3, AC023264.2, AC069045.1, AC027398.2, AC009268.2, AC024485.2, AC022188.3, AC024111.6, AC011138.2, AC024217.6, AC022132.4, AC024927.2, AC023641.2, AC034147.4, AC013447.3, AC025690.3, AC019311.4, AC023974.2, AC023205.2, AC022460.2, AC018349.2, 35 AC017535.1, AC010689.2, AC004064.1, AL118502.34, AL139241.4, AL138693.6, AL161939.2, AL157716.2, AC001235.1, AP000452.2, AP001833.1,

## SEQ ID NO.184

NGO-Br-66

MK805/T3 5'

- 40 U73200.1, AB000214.1, AC003080.1, AC002395.1, AC005244.1, Z68279.1, AC007327.1, AC005817.7, AC007665.24, AC008266.3, AE003615.1, AE003580.1, NM\_010559.1, AC004615.1, AF140707.1, NM\_003688.1, AF130357.1, AC004893.1, AC005839.1, AF111102.1, AC005807.1, AC005855.1, U58494.1, AC005356.1, AC003052.1, AC005211.1, AC004598.1, M17551.1, AF035582.1, AF032119.1, AJ403418.1, AF027865.1, X97915.1, AC002094.1, AJ290445.1, 45 AL021127.2, AL080241.14, Z83844.5, AL031347.1, U70381.1, U70380.1, U26425.1, X51976.1, X98188.1, X01709.1, X91192.1, AB029009.1, M27972.1, M18252.1, M36323.1, L35243.1, AB011297.1, AB011096.1, U08129.1, AL048447.2, AA378192.1, AA312335.1, AW501959.1, AA675911.1, AA015476.1, AA220385.1, AA681477.1, AW321789.1, AW701965.1, AW171289.1, AW140423.1, AI618679.1, AI617588.1, AI545690.1, AI416377.1, AW727131.1, AI878211.1, AA867310.1, AW822989.1, AW822908.1, AW140419.1, AW107372.1, AI876330.1, AI876315.1, AI787888.1, 50 AI673281.1, AI661565.1, AI647986.1, AI596598.1, AI593550.1, AI563647.1, AI448821.1, AI429489.1, AI416269.1, AI316550.1, AI286579.1, AI272572.1, AI272468.1, AI272432.1, AI265094.1, AI265081.1, AI265039.1, AI265016.1, AI227615.1, AI098293.1, AI097946.1, AU017425.1, AU016228.1, AU014817.1, AA983005.1, AA981167.1, AA930951.1, AA920957.1, AA920358.1, AA920053.1, AA919936.1, AA896813.1, AA896091.1, AA896033.1, AA896016.1, AA867305.1, AA797842.1, AA791920.1, AA734060.1, AA672803.1, AA656916.1, AA647396.1, AA561026.1, 55 AA432827.1, AA415676.1, AA239702.1, AA197111.1, AA118415.1, AA104979.1, AA104928.1, AA045964.1, AA014354.1, W38611.1, H93255.1, H89667.1, R15163.1, AC069071.2, AC018473.10, AC007775.2, AC025911.2, AC026386.4, AC024042.3, AC005805.1, AC002405.1, AC055890.2, AC021494.3, AC022701.1, AL355994.1, AL121750.3, AP000780.1,

60 SEQ ID NO.185

NGO-Br-66

MK805/T7 3'

AB020671.1, D23673.1, D26154.1, U73200.1, AD001527.1, AC003003.1, AF048729.1, AL353012.1, AL096799.4, AJ011517.1, U66909.1, AE003569.1, AC007243.3, AC005071.2, NC\_001224.1, AC007284.4, AC007514.5, AC002401.1,

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- AF055066.1, AL163218.2, AJ011856.1, Z82195.1, AL031985.10, V00695.1, L36887.1, AP000521.1, AB023058.1, AC007040.2, AC005060.2, AC005353.1, Z98551.1, AL035475.6, AL031390.4, AC009233.3, AC020717.3, AF185568.1, U82670.2, AE003491.1, AC004553.1, AC002540.1, AF030694.2, AF214529.1, AC004992.1, AC004998.2, AC004999.1, AC007077.2, AC007402.3, AF006055.1, AC005081.2, AF052006.1, AC004814.2, AC006275.1, AE001368.1, AC000084.1, AC005031.1, U80017.1, AF045555.1, AC003968.1, AL033528.19, AL033385.1, AL034548.25, AL121601.13, AL031117.1, Z84486.1, Z93018.1, AL008734.10, Z84718.2, Z83841.1, Z92542.2, AL009181.1, U46165.1, AL008983.1, L36890.1, AP000211.1, AP000150.1, AP000138.1, AP000563.1, AP000224.1, AP000133.1, AP000086.1, AP000009.2, AB020863.1, A1742600.1, AW409781.1, AA487042.1, A1570591.1, A1052677.1, AW189149.1, AA732243.1, A1342608.1, AA813983.1, A1864433.1, AL121497.1, A1313170.1, AA535345.1, A1819339.1, A1140858.1, AA463855.1, AA622061.1, AW071972.1, A1039825.1, A1739551.1, A1681889.1, N63033.1, A1916806.1, A1189978.1, AA812039.1, AW009437.1, A1926737.1, AA551298.1, AA128822.1, A1222960.1, A1656010.1, A1147461.1, A1367859.1, AA732922.1, A1335920.1, AA405100.1, AL039337.2, AA602783.1, A1138662.1, A1128055.1, A1288513.1, A1192368.1, AA514278.1, AW009113.1, A1222961.1, A1929221.1, AA128823.1, W95443.1, A1804032.1, R53599.1, AA625309.1, A1308061.1, A1308050.1, AA604594.1, AW393654.1, N68947.1, A1570799.1, AW021963.1, AW419279.1, N34337.1, A1681778.1, T70294.1, AA628356.1, AA040382.1, H66939.1, AA497027.1, AW816672.1, A1332322.1, AA758762.1, R83381.1, AA026077.1, AA349890.1, A1301205.1, A1825535.1, R92218.1, AA829906.1, AA626936.1, W95788.1, AA861469.1, A1085101.1, AA576806.1, N51568.1, AA761610.1, AA040476.1, T77759.1, AA923625.1, A1090324.1, AA410392.1, R86315.1, A1125301.1, AA911222.1, H44545.1, T47795.1, AW630895.1, A1039856.1, A1344296.1, A1978577.1, H42397.1, T77760.1, AA928570.1, AC007775.2, AC015847.1, AC069071.2, AC015849.2, AC018473.10, AC024725.2, AC024710.2, AC055811.1, AC011374.4, AC016098.3, AC005308.6, AC006286.13, AL354739.3, AL122018.22, AL162491.3, AC016928.10, AC025511.2, AC011461.2, AC005073.2, AC012198.3, AC019092.2, AC007926.6, AC007862.4, AC010999.2, AC015652.6, AC021574.3, AC025994.2, AC021786.2, AC025025.2, AC005140.6, AC004153.5, AC023441.2, AC020966.1, AC013409.3, AC005139.3, AL162417.1, AC036200.2, AC010397.5, AC008742.6, AC008813.4, AC027733.2, AC009977.3, AC026379.3, AC026549.2, AC024986.2, AC005505.6, AC015623.3, AC016071.2, AC005504.3, AC004710.3, AL122035.2, AP001392.1, AP001104.1, AC069126.1, AC005842.6, AC069111.1, AC013553.10, AC062030.2, AC027632.4, AC068850.1, AC022150.4, AC016586.4, AC022147.4, AC009143.4, AC027548.2, AC067898.1, AC016385.3, AC025481.2, AC025928.2, AC027272.2, AC027586.1, AC010787.3, AC024969.2, AC012428.4, AC017030.4, AC021305.3, AC025337.1, AC022928.1, AC018879.3, AC011694.2, AL355385.4, AL109825.17, AL161911.3, AL157831.2, AL121747.21, AL109815.2, AL096782.3,

SEQ ID NO. 186

NGO-Br-67

MK495/T3 5'

- U13369.1, X13993.1, AA161421.1, AA214215.1, AA166833.1, AA166827.1, AA085249.1, AC025630.1, AC010554.1, AC011630.2, AL355134.1, AL158197.6, AC026915.1, AC068881.1, AC023572.3, AC018688.4, AC064866.2, AC064825.3, AC010970.2,

SEQ ID NO. 187

NGO-Br-67

MK495/T7 3'

- U20938.1, NM\_000110.2, U09178.1, AB003063.1, U20981.1, U09179.1, D85035.1, U39742.1, U56248.1, AF220294.1, AE003647.1, AE003413.1, AE002206.1, AC007501.2, AC004535.1, AC004945.1, AC006977.3, AE001615.1, AC004962.1, AC002981.1, AC002546.1, AC002436.1, AL050342.42, AL139074.2, U88171.1, U39654.1, AP000003.1, A1752078.1, A1786904.1, A1746780.1, W49558.1, A1119026.1, W03174.1, AW630700.1, A1931647.1, AU076411.1, AW175385.1, AW174937.1, D36086.1, AW829780.1, AW829729.1, AW829453.1, AW828679.1, AW828317.1, AW421789.1, A1765768.1, AW859693.1, AW531377.1, AV008918.1, A1599543.1, AA926321.1, AA818512.1, AA891593.1, AA851914.1, AA886930.1, R04419.1, AL354881.3, AL162575.4, AC006448.10, AC008603.4, AL137159.1, AC008961.4, AC008561.3, AC021003.4, AL356266.2, AL133548.6, AP002006.1, AC068969.1, AC055784.2, AC036131.2, AC011333.4, AC034128.2, AC009579.3, AC027374.2, AC060828.3, AC025091.3, AC067805.1, AC046147.2, AC027618.2, AC015953.3, AC024606.2, AC025821.2, AC016310.5, AC011155.4, AC023814.2, AC023246.2, AC022206.2, AC025338.1, AC015567.3, AC019239.3, AC007490.3, AC019133.3, AC020173.1, AC006846.1, AL355493.2, AL355498.2, AL158210.6, AL356101.1, AL353759.3, AL161740.4, AL139243.3, AL139244.2, AL138920.2, AL139000.2, AP001934.1, AP001484.1,

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SEQ ID NO.188

NGO-Br-69

MK319/T3 5'

- NM\_007186.1, AF049105.1, AL121586.28, AF022655.1, NM\_008383.1, U33198.1, AE003526.1, AC006933.3, AC006486.1, U34932.1, AC004877.1, AF072845.1, AC005602.1, AD000864.1, AD000833.1, L08845.1, AE003795.1, U94409.1, A1124555.1, AW060335.1, AA647911.1, W83246.1, AW732245.1, AW590218.1, AW340426.1, A1989500.1, A1983119.1, A1808699.1, A1654406.1, A1653050.1, A1650974.1, A1638614.1, A1637922.1, AA977540.1, AW626159.1, AW622831.1, AW622685.1, A1397298.1, AW504867.1, AW399321.1, AW405716.1, AW096606.1, AW094388.1, AW094030.1, A1912988.1, A1886821.1, A1823876.1, A1782590.1, A1780656.1, A1775035.1, A1771616.1, A1695784.1,

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-111-

- AI539054.1, AI488077.1, AI486997.1, AI435874.1, AI391305.1, AI382942.1, AI288287.1, AI277512.1, D89319.1, AA824970.1, AA824942.1, C23550.1, AA243659.1, AA131248.1, AA130548.1, C01658.1, W18282.1, L44352.1, D51291.1, R51070.1, T23439.1, AL139226.14, AC010751.3, AC010688.4, AC014935.1, AC010690.1, AC023065.3, AC021858.2, AL158835.3, AL133230.20, AL353653.5, AL139330.5, AL135907.3, AL353609.2, AC069242.1, AC025177.3, AC025531.2, AC011432.2, AC012277.2, AC023303.2, AL157888.2, AL139237.4,
- 5
- SEQ ID NO.189  
NGO-Br-69  
MK319/T7 3'
- 10 NM\_007186.1, AF049105.1, AL121586.28, AF022655.1, NM\_008383.1, U33198.1, AC004691.1, AE003666.1, AC002503.1, M34989.1, X14428.1, AE003817.1, AE003513.1, AC004931.1, AC005977.3, AC005245.1, AL163304.2, AJ004834.1, AL009174.1, AP001759.1, AP001101.1, X75910.1, NM\_000449.1, AF257304.1, AF257303.1, AC006533.7, AF206287.1, NM\_009307.1, AC007463.3, AE001862.1, AF092918.1, AC003689.1, AC004134.1, AF020554.1, AL161540.2, AL161539.2, AL050135.1, U60780.1, AL031686.2, Z97337.2, Z99122.1, U22062.1, X80301.1, X85786.1, M86250.1, D37793.1, L03208.1, D43752.1, Z92952.1, D85027.1, AL037087.2, A1872306.1, A1811998.1, AI401068.1, AA613882.1, A1687495.1, A1224019.1, AA970425.1, AW083819.1, AA595119.1, AW084657.1, A1817733.1, A1419425.1, A1240622.1, R87989.1, A1204529.1, A1000880.1, AA848087.1, Z40915.1, AA502324.1, AW078517.1, A1699218.1, AA729465.1, T85911.1, R88035.1, AW504249.1, AW133062.1, AW435751.1, AW346610.1, A1534994.1, A1534415.1, A1530805.1, A1519460.1, A1512712.1, A1456969.1, A1455689.1, A1404669.1, A1388686.1, A1388197.1, A1388073.1, A1387697.1, A1387259.1, A1386601.1, A1192646.1, A1135562.1, A1135091.1, A1107565.1, A1063523.1, A1063307.1, AA942336.1, AA941421.1, AA201182.1, AA392346.1, W82939.1, AW784983.1, AW607628.1, AW454537.1, AW029340.1, AW024754.1, A1991341.1, A1937337.1, A1863172.1, A1717513.1, F28098.1, A1523953.1, A1343828.1, A1340266.1, A1032053.1, A1024499.1, AA991616.1, AA937835.1, AA889325.1, AA872357.1, AA812821.1, AA805252.1, AA746136.1, AA722399.1, AA660763.1, AA586676.1, AA532648.1, AA527348.1, AA523469.1, AA504479.1, AA417368.1, AA405813.1, AA262932.1, AA228934.1, AA055130.1, N30852.1, H94195.1, D63281.1, R72540.1, AL139226.14, AL122019.21, AC027740.2, AC022067.2, AC021359.2, AC017441.1, AL162382.2, AP000491.1, AC010759.2, AC046181.1, AC026053.2, AC022262.3, AC024341.2, AC020964.1, AC015349.1, AC020328.1, AC010671.7, AF161326.1, AL162271.2, AC020923.4, AC008906.3, AC008790.4, AC011459.2, AC009544.4, AC053476.1, AC019325.3, AC016841.2, AC011568.3, AC009565.7, AC022047.4, AC021225.3, AC012354.3,
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- 30 AL162234.3, AL157949.2, AL138699.1, AP000451.2, AP001384.1, AP001163.1, AP000666.1,

- SEQ ID NO.190  
NGO-Br-70  
MK061/T3 5'
- 35 Z36816.1, AC008469.4, U91320.1, AL117630.1, Z82205.1, Z50112.1, X82322.1, AB018295.1, AF142100.1, AC008498.3, AE002153.1, AC004830.1, AC004738.1, Z78419.1, AL034397.1, X63598.1, L14017.1, Y13096.1, Y13095.1, X54660.1, Y14051.1, D86934.1, AB033763.2, L14020.1, AL046916.1, AW732487.1, AA088822.1, H50443.1, T65364.1, AA112796.1, F11994.1, R11879.1, AW414271.1, AW414220.1, AA075824.1, AA363903.1, AW786911.1, AA896188.1, AW403711.1, A119785.1, A1197257.1, T65515.1, AW401567.1, AL047058.1, R55598.1, AW143393.1, AW375060.1, A1591958.1, F11904.1, AA742633.1, AA517314.1, W85360.1, T08516.1, AA184178.1, D28616.1, AA000364.1, AW796180.1, AW401580.1, T16871.1, AA739011.1, A1153477.1, W21846.1, AW785749.1, AA053446.1, D21680.1, AW390748.1, AA032616.1, AW401807.1, AW801635.1, AA027649.1, Z45691.1, F08352.1, A1410833.1, AW557036.1, AA895817.1, AW546958.1, AW575180.1, AW640041.1, AW555199.1, AJ397620.1, AA018126.1, AJ397023.1, R09436.1, AW522370.1, AJ395743.1, AJ392332.1, AW269432.1, AW169948.1, A1914378.1, AL046089.1, AV106169.1, A1371352.1, AA922035.1, AA707531.1, N91137.1, R45445.1, AW815118.1, AW163019.1, A1522333.1, AA965117.1, AA317592.1, H10898.1, R16064.1, AC023861.2, AC025415.3, AC067823.2, AC026400.2, AC008785.3, AC020710.4, AC024452.2, AC026821.2, AC021956.3, AC023442.2, AL355499.5, AC023449.3, AC036143.2, AC025544.3, AC011509.5, AC008691.4, AC023020.3, AC048481.1, AC024053.2, AC008703.3, AC027678.1, AC023812.3, AC015900.2, AC009637.3, AC025221.2, AC025565.2, AC019141.3, AC018421.3, AC021603.2, AC023380.1, AC022390.1, AL356215.1, AL355972.2, AL139276.2, AL136989.4, AL161742.3, AL353713.1, AL158204.2, AL158143.1, AL137845.1,
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- SEQ ID NO.191  
NGO-Br-70  
MK061/T7 3'
- 55 AF035296.1, AC010889.2, AF038149.1, Z70685.1, AE003463.1, AC006317.3, AF200688.1, AC008041.5, AC005684.1, AC004601.1, AL133451.1, AL050347.1, X55146.1, Z73987.1, AW471383.1, AW294879.1, A1827389.1, A1433239.1, AW575180.1, AW574507.1, A1936491.1, A1803377.1, AW575276.1, AW574501.1, AW574595.1, AW081903.1, A1017541.1, AW575023.1, AW474843.1, AW269983.1, A1143057.1, AW662466.1, AW149715.1, A1818173.1, AW027629.1, A1129967.1, A1084109.1, AA629401.1, A1032340.1, AA775878.1, A1734859.1, A1688609.1, AA134114.1, AA088684.1, A1537873.1, AW474193.1, AA709474.1, AW087318.1, AA052969.1, T17399.1, AW244157.1, A1198524.1, AA455953.1, AA662286.1, T65434.1, N23103.1, A1500354.1, T77285.1, R48306.1, T87060.1, AW079744.1, T16870.1, AA242771.1, AA364661.1, AA725410.1, AA888835.1, AW183474.1, R48408.1, R55361.1, A1952437.1, A1383126.1, AA772585.1, R17756.1, R53154.1, A1468078.1, T83615.1, AA740428.1, AA989632.1, AA776777.1, AW088969.1,
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-112-

- AA970686.1, AW467672.1, F09551.1, R84473.1, AA053446.1, AW839837.1, AW801635.1, R40543.1, AA242901.1, AW375060.1, W21846.1, AW295371.1, AA485133.1, AA281393.1, AW834883.1, AW426950.1, AW335961.1, AI953843.1, AI935134.1, AI817633.1, AI808163.1, AA924764.1, AI370430.1, AA232269.1, AA224090.1, AP001028.3, AC003094.1, AC025920.8, AC024162.2, AC021006.3, AC020773.3, AC026197.1, AC026181.1, AC020755.2, AC024159.1, AC068063.2, AC026416.2, AC020942.4, AC067757.1, AC008162.2, AC046179.1, AC027654.1, AC019099.3, AC024944.2, AC016453.4, AC013350.6, AC024511.2, AC013816.3, AC023176.3, AC016525.3, AC024911.1, AC023157.4, AC010734.3, AC012167.4, AC008131.1, AC020499.1, AC017700.1, AC006100.1, AL356370.1, AL118519.20, AL138762.5, AL137853.7, AL133388.3, AL354680.4, AL160157.3, AL138848.3, AL353733.1, AL162430.1, AL157826.2, ,
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- SEQ ID NO.192  
NGO-Br-70  
MK231/T3 5'  
Z36816.1, AC006075.1, Z54328.1, AC008469.4, U91320.1, AC003034.1, AF165142.1, AC004987.2, AL137290.1, AL117630.1, Z83849.1, Z93242.1, Z82205.1, Z50112.1, X82322.1, AB018295.1, AF142100.1, AC005137.1, AE002153.1, U89337.1, AC005940.3, AC004738.1, AE000895.1, AL163229.2, AL034397.1, X63598.1, L14017.1, Y13096.1, Y13095.1, X54660.1, Y14051.1, AP001684.1, D86934.1, AB033763.2, AP000705.2, Y11769.1, L14020.1, AL046916.1, AW732487.1, H50443.1, AA088822.1, T65364.1, AA112796.1, F11994.1, R11879.1, AA075824.1, AW403711.1, T65515.1, AW414271.1, AW414220.1, AW786911.1, AA363903.1, AA896188.1, AW401567.1, AL047058.1, R55598.1, H19785.1, AI197257.1, F11904.1, AW143393.1, AW401580.1, AW796180.1, AA517314.1, W85360.1, AA742633.1, AI591958.1, T08516.1, AW375060.1, AW401807.1, AA184178.1, D28616.1, AA000364.1, T16871.1, F08352.1, Z45691.1, AW785749.1, D21680.1, AW390748.1, AA739011.1, AI153477.1, AA032616.1, AA027649.1, AA018126.1, AW403200.1, AW402516.1, W21846.1, AA053446.1, AW402128.1, AI410833.1, AW557036.1, AA895817.1, AW546958.1, AW640041.1, AW555199.1, AJ397620.1, AI254622.1, T31811.1, AJ397023.1, AJ395743.1, AJ392332.1, AW269432.1, AW169948.1, AI914378.1, AL046089.1, AV106169.1, AI371352.1, AA922035.1, AA707531.1, N91137.1, R45445.1, AW815118.1, AW163019.1, AI592661.1, AI522333.1, AI341327.1, AA317592.1, AA184644.1, H10898.1, R16064.1, AC027678.1, AC022390.1, AC023861.2, AC011591.4, AC027683.1, AC015844.4, AC015875.1, AL157397.2, AP001926.1, AP001284.1, AP000764.1, AP000614.3, AC025415.3, AC067823.2, AC019331.3, AC026400.2, AC010324.4, AC020710.4, AC022916.2, AC024452.2, AC027437.2, AC027069.2, AC026008.2, AC022696.3, AC021956.3, AC023954.2, AC023442.2, AC023241.2, AL355860.1,
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- SEQ ID NO.193  
NGO-Br-70  
MK464/T3 5'  
Z36816.1, AK000595.1, Z54328.1, AC006960.1, AC007540.3, Z82205.1, Z50112.1, X82322.1, AF142100.1, AC002380.1, AE002153.1, AC004738.1, AC005371.1, AJ251829.1, Z85996.1, AL034397.1, X63598.1, L14017.1, Y13096.1, Y13095.1, X54660.1, Y14051.1, D86934.1, AB033763.2, L14020.1, AL046916.1, AA075824.1, AW403711.1, H50443.1, T65364.1, AW401567.1, T65515.1, AL047058.1, R55598.1, F11904.1, F11994.1, AW401580.1, AW796180.1, AW732487.1, AW401807.1, AA088822.1, Z45691.1, AW786911.1, AI197257.1, AA896188.1, AW403200.1, AW402516.1, AA018126.1, R11879.1, T16871.1, T08516.1, AA517314.1, W85360.1, H19785.1, AA112796.1, T31811.1, AW414220.1, AW405526.1, AW414271.1, AW143393.1, AA363903.1, AW402128.1, AA027649.1, AA742633.1, AW785749.1, AI592661.1, F08352.1, AI591958.1, D21680.1, AW390748.1, AW402023.1, AA184644.1, AA184178.1, D76728.1, D28616.1, AA000364.1, AW640041.1, AJ397620.1, AJ397023.1, AV106169.1, AW815118.1, AW163019.1, AW159142.1, AW159141.1, AW159140.1, AW158139.1, AW158059.1, AI657929.1, AA317592.1, H10898.1, R16064.1, AC023861.2, AC025415.3, AC067823.2, AC020710.4, AC024452.2, AC011052.4, AC021956.3, AC023442.2,
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- SEQ ID NO.194  
NGO-Br-70  
MK464/T7 3'  
AF035296.1, AE003725.1, AC007053.15, U96104.1, U58920.1, AF038149.1, Z70685.1, D87992.1, AC006317.3, AC008041.5, AC005684.1, AC004601.1, AL133451.1, AL050347.1, X55146.1, Z73987.1, AW575180.1, AA775878.1, AW575276.1, AW574595.1, AW575023.1, AW574501.1, AW574507.1, AW294879.1, AI827389.1, AA629401.1, AW471383.1, AI433239.1, AI936491.1, AI803377.1, AW149715.1, AW081903.1, AI017541.1, AW474843.1, AW269983.1, AW027629.1, AI143057.1, AW662466.1, AI818173.1, AI129967.1, AI084109.1, AI032340.1, AI734859.1, AI688609.1, AA134114.1, AA088684.1, AI537873.1, AW474193.1, AA709474.1, AW087318.1, AA052969.1, T77285.1, TI7399.1, AW244157.1, R53154.1, AI198524.1, AA455953.1, AA662286.1, R48408.1, N23103.1, T65434.1, AI500354.1, AA053446.1, AW801635.1, AW079744.1, R48306.1, T16870.1, T87060.1, AA364661.1, T83615.1, AA242771.1, AA725410.1, AA888835.1, AW183474.1, AI952437.1, AI383126.1, R55361.1, AA772585.1, AW839837.1, R17756.1, AI468078.1, AW375060.1, AW088969.1, AA740428.1, AA989632.1, AA776777.1, W21846.1, AA970686.1, F09551.1, AW467672.1, R84473.1, AA242901.1, D30911.1, R40543.1, AW479983.1, AW834883.1, AW826181.1, AV417825.1, AW557036.1, AW555199.1, AW546958.1, AW527142.1, AW491879.1, AW426950.1, AW335961.1, AI229288.1, AI103583.1, AI155354.1, AI153477.1, AA895817.1, AA739011.1, AA290498.1, AA000364.1, AP001028.3, AC025920.8, AC024162.2, AC021006.3, AC020773.3, AC026197.1, AC026181.1, AC020755.2, AC024159.1, AC017539.1, AC006589.3, AC008141.2, AC068063.2, AC067757.1, AC046179.1, AC027654.1, AC019099.3, AC024944.2,



AC016453.4, AC013350.6, AC024511.2, AC013816.3, AC023176.3, AC016525.3, AC024911.1, AC023157.4, AC010734.3, AC008131.11, AC017700.1, AL356370.1, AL118519.20, AL137853.7, AL133388.3, AL354680.4, AL138848.3, AL353733.1, AL162430.1, AL157826.2,

## 5 SEQ ID NO.195

NGO-Br-71

MK137/T3 5'

- AB025608.1, AB009048.1, D45408.1, AB023029.1, AC005922.1, U64851.1, U92032.1, AJ001535.1, U66525.1, AB008265.1, AP000495.1, AC007187.4, AE003492.1, AC010125.3, AC002088.1, AC003071.1, AE001774.1, 10 AC005509.1, AC005900.1, AE001119.1, AC004063.1, AF040653.1, AL353995.1, AL031466.1, AL132715.2, AL161666.2, U28760.1, AL109609.5, AL031579.1, Z66567.1, Z82211.1, Z99129.1, AL021918.1, AL022159.1, AJ001088.1, AL041831.1, AA911802.1, AI791494.1, AI791283.1, AW639607.1, AW540750.1, AL553588.1, AI194910.1, AW565485.1, AW470837.1, AW440357.1, AW106522.1, AV201819.1, AL037101.1, AV091786.1, AI444814.1, AI114364.1, AI002480.1, AA002743.1, AL355146.4, AL161434.3, AL132673.16, AL356292.1, AC027069.2, 15 AC067734.3, AL161788.4, AC058786.7, AC025936.2, AC046186.2, AC009944.3, AC008459.4, AC026989.2, AC025669.2, AC026505.3, AC026390.1, AC024422.2, AC021696.3, AC018826.3, AC012525.6, AL157785.2, AL355332.1, AC062004.2, AC013244.8, AC007943.2, AC027679.1, AC010429.4, AC027741.2, AC026557.2, AC012349.3, AC020732.3, AC027625.2, AC051630.1, AC026958.2, AC021514.3, AC012148.2, AC022580.2, AC009680.5, AC010993.10, AC010994.9, AC010730.4, AC010101.4, AC012195.2, AC014437.1, AC010843.8, 20 AC018408.1, AC011673.2, AC011114.1, AC010132.2, AC007555.1, AC006799.1, AL356357.1, AL356009.2, AL121954.4, AL139278.2, AL354920.1, AL139397.2, AL162719.1, AL138724.2, AP001954.1, AP001823.1,

SEQ ID NO.196

NGO-Br-71

## 25 MK137/T7 3'

- AC006014.2, AC004705.2, AL035652.5, AC044786.2, AE002147.1, AC004848.1, AC007735.2, AC004907.2, AF107885.2, U67494.1, AL161588.2, AL031986.1, AL022373.1, AI732538.1, AI652638.1, AA505930.1, AA991355.1, AW235448.1, AL041832.1, AI791494.1, AI791283.1, AL041831.1, AV254980.1, AW552644.1, AV267495.1, AV264008.1, AV260689.1, AV259564.1, AV258534.1, AV208825.1, AV260910.1, AV264098.1, AW552124.1, 30 AW317034.1, AA391903.1, AA536375.1, AA536264.1, AV210836.1, AW692176.1, AW438480.1, AJ388903.1, AW210311.1, AI643503.1, AI545190.1, AI394892.1, AI141264.1, AA497287.1, AA404284.1, AA256257.1, AW567217.1, AW361948.1, AV267670.1, AU077746.1, AI906249.1, AI901829.1, AV034590.1, AI621492.1, AI551985.1, AI395360.1, AI179945.1, AU030825.1, AA906203.1, AA894271.1, AA852029.1, AA673655.1, C62664.1, C61515.1, AA445695.1, AA418204.1, AA141341.1, AA104978.1, H11780.1, R13493.1, T81922.1, Z44433.1, AL356292.1, AL355146.4, 35 AL161434.3, AL132673.16, AL136305.5, AC007943.2, AC011078.2, AL133508.2, AL138763.2, Z93245.1, AC011585.3, AC018976.2, AC011939.2, AC014847.1, AC022442.3, AC009820.3, AC026491.3, AC022467.4, AC016221.4, AC021619.3, AL137017.5, AL121715.2, AL133322.3,

SEQ ID NO.197

## 40 NGO-Br-72

MK419/T3 5'

- AK000528.1, NM\_016123.1, AF155118.1, AL161587.2, M63234.1, AL031135.1, AC005868.1, AL096699.11, X98048.1, NC\_001148.1, AF249887.1, AC002392.2, AE003724.1, AF030694.2, NM\_004690.1, AC007313.3, AF164041.1, AC006559.6, AC007102.4, AF104413.1, AF104414.1, AE001409.1, AF015463.1, AC005220.1, U67476.1, AL161573.2, 45 AL161572.2, Z681376.2, AL049662.1, AL121783.1, S46763.1, AL021749.1, AL034558.2, U45981.1, Z70720.1, Z73565.1, Z29667.1, L34028.1, L34027.1, D10606.1, AB011474.1, AB026649.1, M84660.1, M74445.1, U07163.1, H53674.1, AI967314.1, AW560842.1, AW761247.1, AI794934.1, AI812788.1, AI774138.1, AI772185.1, AW876515.1, AW756795.1, AW329262.2, AW329038.2, AW649958.1, AW568064.1, AW496536.1, AW348715.1, AW334566.1, AW094252.1, AI960995.1, AI920205.1, C95693.1, AI594372.1, AA592233.1, H36649.1, T92029.1, T18143.1, AC016143.5, 50 AC021719.3, AC025567.6, AC026763.5, AC010161.5, AL354696.1, AC022507.12, AC023928.3, AC009671.3, AC024954.2, AL354815.1, AL121880.15, AC024886.6, AC022072.8, AC031992.2, AC024244.4, AC067883.1, AC057605.1, AC055596.1, AC055595.1, AC049865.1, AC049836.1, AC048201.1, AC048200.1, AC027086.2, AC021723.3, AC021849.3, AC013809.3, AC019131.3, AC011308.3, AC013549.2, AC006091.9, AC017374.1, 55 AL353592.1,

SEQ ID NO.198

NGO-Br-72

## 60 MK419/T7 3'

- AK000528.1, NM\_016123.1, AF155118.1, AC000118.1, AC004033.3, AC004232.1, AC009509.7, AL049839.3, AC008521.5, AL021546.1, AC003002.1, AC000378.1, AL096791.12, AC007227.3, AF051976.2, AC005859.1, AC002565.1, AL132639.2, AC005581.1, AL035400.13, AP000180.1, AP000104.1, Z85987.13, AC005695.1, AC005563.1, AL049643.12, AC005821.1, AC005088.2, AC005031.1, AL135749.2, AL035249.6, AC004805.1, U52111.1, AL138976.3, AL121985.13, AC005914.1, AL035588.21, AC005081.2, AC005519.2, AC007993.15, AC005486.2, AL031848.11, AC004223.1, AF001550.1, AL022318.2, Z98742.5, U62292.1, D84394.1, AP000313.1, AL163305.2, AL121988.10,



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- AP001760.1, AF030876.1, AC005288.1, AC003663.1, AL121586.28, AC004858.2, AF001549.1, Z98200.8, AC002072.1, AC004887.2, AC002299.1, AC005874.3, AF134471.1, AC004477.1, AC005730.1, AC006061.1, AL021939.1, AJ010770.1, AC011462.4, U47924.1, AL035458.35, AL021937.1, AC008101.15, AC009247.11, AC004771.1, AL031133.1, AL049766.14, AC006115.1, AC002369.1, AL133500.2, AP000168.1, AP000053.1, AP000121.1, AC000134.14, AC005803.1, AC005514.1, AL031281.6, AC004745.1, AL035422.12, AC003007.1, Z95152.1, AC004983.2, AL163282.2, AL163267.2, AP000045.1, AC005745.4, AC011508.4, AL023879.1, AL022399.2, AA114131.1, H78605.1, H78687.1, AA084609.1, H07953.1, AA630854.1, AW023111.1, AA501614.1, T74524.1, AA468505.1, AA614254.1, AI889579.1, AA515939.1, AA515728.1, AA612727.1, N64587.1, AW674631.1, AW069227.1, AI679002.1, AI634187.1, AI457313.1, AA536040.1, AA485328.1, AI925869.1, AA622801.1, AA602906.1, AA228368.1, W02749.1, R98218.1, AI653776.1, AI244157.1, AI708005.1, AI421257.1, AW082104.1, AI962030.1, AA715173.1, AA715075.1, AA664126.1, AA297666.1, AL134940.1, AI733856.1, AA613761.1, AA447247.1, AA347969.1, AA284247.1, C15363.1, T54783.1, AW151824.1, AI290405.1, AA864603.1, T49633.1, AW151201.1, AW090754.1, AI933714.1, AW304536.1, AI446336.1, AI278972.1, AA573213.1, AA456924.1, AA303054.1, R93919.1, AW341978.1, AL118612.1, AA552989.1, AW131356.1, AI754105.1, AA502991.1, T47936.1, AI733523.1, AI310343.1, AA669054.1, AA563770.1, AW844636.1, AW770827.1, AI669421.1, AA847499.1, AW576251.1, AW500684.1, AW192599.1, AI755214.1, AI754567.1, AI569100.1, AI249688.1, AI187148.1, AI080307.1, AI038304.1, AA584862.1, AW188742.1, AI077941.1, AA535216.1, T47324.1, AI817230.1, AI525100.1, AI560085.1, AW510513.1, R66121.1, AI904811.1, AA779075.1, AL043144.2, AA225519.1, AC021719.3, AC016143.5, AL355386.1, AC025262.5, AL356280.2, AL162411.1, AC008760.4, AC016953.5, AC010807.4, AL139252.2, AC026868.2, AC009470.3, AL353743.1, AC002993.1, AC009124.4, AC018942.2, AC022826.3, AC023329.2, AL158196.4, AC025278.2, AC021258.3, AC025395.2, AL158165.3, AL034372.30, AL109806.13, AC037464.2, AC011484.2, AC019194.2, AC016888.4, AL160010.3, AC016073.2, AC034198.2, AC027631.2, AL139807.5, AC007621.13, AC008812.6, AL162611.4, AC005995.2, AL121943.14, AC012014.5, AL355490.3, AC008731.4, AL354864.1, AC019071.3, AC026469.3, AL354720.3, AL158014.4, AC026790.2, AP002016.1, AC008749.4, AC021852.3, AC012236.3, AL121845.18, AL163051.1, AC061979.2, AC012291.3, AC026160.1, AC024380.2, AC018808.3, AL158827.4, AC016554.5, AC022554.2, AC006393.6, AC005867.1, AL162584.2, AL161615.2, AL138788.1, AC010607.4, AC026286.2, AC026817.1, AP001177.1, AC025060.3, AC015714.4, AC011247.3, AL121834.8, AL136450.1, AC013564.3, AC012451.3, AC021510.2, AC016485.2, AL137186.4, AL162595.5, AL137247.3, AL137856.2, AC025695.3, AL158152.3, AC068485.1, AC008555.3, AC020697.3, AC010149.4, AL139255.1, AC011501.5, AC008774.3, AC027551.2, AP001501.1, AC007366.3, AC041047.3, AL136139.5, AP001198.1, AC022410.3,

SEQ ID NO.199

NGO-Br-73

MK642/T3 5'

- AF147338.1, AK000060.1, AE003569.1, AF111426.1, AC007048.4, AC005385.3, U60334.1, AF020802.1, AL163269.2, Z95889.1, Z83317.1, AP001724.1, AP000687.1, AJ229041.1, AC008526.5, AC000122.1, AC005901.1, AL117327.5, AP000377.1, AE003526.1, AC007216.2, AC005249.1, U95742.1, AC006933.3, AC004512.1, AL133419.15, AI692537.1, AW243461.1, AW235223.1, AI671570.1, AW653857.1, AW274251.1, T58078.1, T58198.1, AW485453.1, AW428440.1, AA918819.1, AA017211.1, AA247593.1, AV347965.1, AV103024.1, T27488.1, AV242595.1, AV341902.1, AV346780.1, T11529.1, AV245244.1, AV229602.1, AU030011.1, AW575669.1, AW557886.1, AW529718.1, AW212594.1, AV376787.1, AV374992.1, AV367312.1, AV340052.1, AV273236.1, AV265359.1, AV250828.1, AV221007.1, AV219070.1, AV218774.1, AV206725.1, AW066980.1, AI847479.1, AI837994.1, AI835991.1, AV159366.1, AV169546.1, AV152290.1, AV142949.1, AV141913.1, AV130057.1, AV126713.1, AV117344.1, AV115850.1, AV102420.1, AV095928.1, AV075293.1, AV063673.1, AV057658.1, AV056084.1, AV056034.1, AI747610.1, AV038768.1, AV030316.1, AV004917.1, AI574942.1, AI550786.1, AI463222.1, AI462153.1, C78201.1, AA423250.1, AA259531.1, AC015955.4, AP001033.3, AC017914.1, AC012303.2, AL354863.4, AL139010.6, AC027201.2, AC012893.1, AL161612.4, AL022285.6, Z93065.1, AC017070.3, AC055820.2, AC026195.2, AC016205.4, AC011178.3, AC012584.5, AC017432.1, AL160257.3, AC008784.5, AC010323.4, AC034299.2, AC034282.2, AC016893.3, AC032000.1, AC024010.2, AC023809.6, AC022375.1, AL138904.2, AL354990.1,

SEQ ID NO.200

NGO-Br-73

MK642/T7 3'

- AF147338.1, AK000060.1, X80821.1, U60334.1, AE003480.1, AC000122.1, M96441.1, AC005901.1, AC000044.2, AC000034.2, AC004984.1, L28955.1, AL133367.2, AL080079.1, Z80901.1, AL033377.2, AI692537.1, AW653857.1, AA918819.1, T58078.1, T58198.1, AV349661.1, AV349644.1, AV350717.1, AV328677.1, AW070252.1, AW775904.1, AW792828.1, AW274009.1, AW193700.1, AL121308.1, AW023476.1, AI910455.1, AI765240.1, AI567672.1, AI376609.1, AI351633.1, AI291783.1, AI291446.1, AA652658.1, AA570928.1, AA496039.1, H93102.1, R86033.1, R77622.1, R68550.1, AW774292.1, AW413948.1, AW155190.1, AW029172.1, AW009281.1, AU069485.1, AU030011.1, AI182684.1, AI22141.1, AI096187.1, AA839637.1, AA762941.1, AA691770.1, C72277.1, AA548171.1, AA451530.1, AA423704.1, W29889.1, H44377.1, T11529.1, AC015955.4, AP001033.3, AC021893.10, AC027514.2, AL139010.6, AP001460.2, AC026658.2, AC027061.2, AF235092.1, AC015631.3, AC023680.2, AC010000.2, AC015395.1, AL355377.2, AC024702.3, AC016493.3, AC024681.2, AC024087.3, AC011940.3, AC022734.2, AC011916.1, AC010942.1, AC005000.1, AL161904.2, AL139300.2,

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## SEQ ID NO. 201

NGO-Br-74

MK761/T3 5'

- 5 AE003523.1, AC006257.1, AC005330.1, AL355927.1, U56728.1, AL049766.14, AB037825.1, AK000573.1, AE003832.1, AE003801.1, AE003785.1, AC002087.1, NM\_002172.1, AC004829.2, AC005887.3, U29244.1, AC004293.1, X74470.1, Z11532.1, X72306.1, V00542.1, AA765066.1, R57163.1, AA896010.1, AA178333.1, C80989.1, AW105563.1, AA930992.1, C80990.1, C81381.1, AA612483.1, AA383435.1, AW326797.1, AW447131.1, AA681894.1, AW104025.1, Z36392.1, Z36470.1, AW413469.1, AA684257.1, AW149818.1, AI265028.1, AW781170.1, AI907775.1, AA735139.1, 10 AA371572.1, AA313662.1, AA299963.1, AA148581.1, AA135264.1, AW774261.1, AW609685.1, AW300461.1, AI397692.1, AI069165.1, AI068528.1, AA841557.1, AA755125.1, AA623736.1, AC008795.5, AC008855.4, AC011145.3, AC012122.2, AC055879.2, AC069189.1, AC017022.3, AC022187.2, AC013500.3, AC019563.1, AL162579.4, AC026334.3, AC069079.1, AC069026.1, AC027328.2, AC010337.3, AC010472.4, AC008549.4, AC011448.2, AC026393.2, AC011289.3, AC027094.2, AC025974.2, AC025956.2, AC022823.3, AC017010.2, AC015904.3, AC013370.5, AC007477.5, AC020693.3, AC022302.3, AC007413.4, AC007330.5, AC017049.3, AC022176.1, 15 AC019249.3, AF209070.1, AC018198.1, AC017513.1, AC015178.1, AL353664.3, AL354675.2, AL353690.1, AP001372.1, AP001367.1, AP001103.2, AP001085.2, AP001030.2,

## SEQ ID NO.202

20 NGO-Br-74

MK761/T7 3'

- AC025098.4, AC005560.2, AC027661.1, AC011806.1, AC006257.1, AC005330.1, AL355927.1, U56728.1, AL049766.14, AB037825.1, AK000573.1, AE003801.1, AE003478.1, NM\_006496.1, NM\_002172.1, AC005887.3, AC009465.5, U29244.1, AC005317.1, AC004293.1, AL023518.2, X74470.1, Z11532.1, V00542.1, X54048.1, AK001973.1, 25 AK001746.1, M27543.1, AB014467.1, J03198.1, AA765066.1, R57163.1, AW105563.1, C80989.1, C80990.1, C81381.1, AA896010.1, AA178333.1, AA930992.1, AA612483.1, AA383435.1, AW104025.1, AA681894.1, AW326797.1, AW447131.1, Z36392.1, Z36470.1, AW413469.1, AA684257.1, AI265028.1, AW149818.1, AI453042.1, AW781170.1, AV349095.1, AV248065.1, AI907775.1, AA735139.1, AA371572.1, AA313662.1, AA299963.1, AA148581.1, AA135264.1, AV211122.1, AI829193.1, AV172729.1, AI766084.1, AI620180.1, AI400167.1, AI397692.1, AI356812.1, AI337030.1, AI269102.1, AI261301.1, AI092059.1, AI033551.1, AI033398.1, AA954839.1, AA838238.1, AA766120.1, 30 AA755125.1, AA736929.1, AA706621.1, AA704130.1, AA652992.1, C72329.1, AA587349.1, AA490356.1, AA235987.1, AA085406.1, AC008795.5, AC008855.4, AC011145.3, AC012122.2, AC022061.2, AC016691.4, AC022960.2, AC009831.3, AC055879.2, AC027133.1, AC017022.3, AC019563.1, AL162579.4, AC027328.2, AC015904.3, AC024016.2, AL355310.3, AL353664.3, AL354675.2, AL139802.3,

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## SEQ ID NO.203

NGO-Br-75

MK344/T3 5'

- AL157792.2, AL033380.11, U55042.1, X64070.1, AC006607.1, AC006576.15, AF070718.1, AC004703.1, AL122003.17, AB015752.1, AC011309.4, AF030876.1, NM\_013369.1, U82695.2, AF031075.1, AF194032.1, AF081058.1, AF081057.1, AF081056.1, AF081055.1, AF058419.1, U68299.1, U52112.1, AL163298.2, AL080286.16, AL096677.18, L06231.1, X53705.1, AP001753.1, AP001059.1, X81326.1, X53709.1, X53708.1, D86115.1, AW650954.1, AL119238.1, AW030498.1, AI661495.1, AA831895.1, AW393793.1, AW393785.1, AW213405.1, AV230556.1, AW124066.1, AI931357.1, AV124496.1, AI631758.1, AI585396.1, AA918201.1, AA890172.1, AA882048.1, AA757981.1, AA538210.1, 45 AA474203.1, AA402070.1, AA199109.1, AA053059.1, R82169.1, R23708.1, AC063960.2, AC012053.2, AC020661.4, AC023137.2, AC026045.3, AC034236.1, AC016530.3, AC019068.3, AC015557.1, AL138781.3, AL162151.2, AC062006.2, AC044906.2, AC036174.2, AC021165.3, AC023133.2, AC009677.3, AC021462.3, AL353803.1, AL160268.3,

## 50 SEQ ID NO.204

NGO-Br-75

MK344/T7 3'

- AL049749.2, Z83733.1, AE003545.1, U97009.1, AC005512.1, Z78018.1, AB036794.1, AC008701.5, AC006319.3, AC004160.1, AC005026.1, AL049859.7, Z69637.1, AL035686.12, AE003804.1, AE003275.1, NC\_002387.1, U17009.2, 55 AC002066.1, AJ133269.1, AL030995.1, AI964952.1, AW847510.1, AW453459.1, AW125886.1, AI562053.1, AI180354.1, AI130241.1, AW840570.1, AW840396.1, AW795642.1, AW600573.1, AW588022.1, AW455711.1, AW331252.1, AW306566.1, AI913878.1, AI813344.1, AI767557.1, AI593529.1, AA888474.1, AA603364.1, AA601251.1, AA550370.1, AA428312.1, AA305564.1, D78836.1, Z45190.1, AC063960.2, AC006447.17, AC011085.4, AC023285.2, AP001027.1, AL355358.1, AC025684.2, AC021877.4, AC011243.3, AL160291.2, AC006404.20, AC015424.1, AC019870.1, 60 AC020079.1, AC007835.5, AC010565.3, AC010690.1, AC068007.1, AC062025.1, AC009578.3, AC023820.2, AC015567.3, AL109965.22, AL132671.19, AC069237.1, AC044882.2, AC068593.1, AC064847.1, AC023136.3, AC021555.3, AC026242.3, AC013685.3, AC016808.2, AC017040.3, AC013278.1, AP002000.1, AP001931.1,

## SEQ ID NO.205

## NGO-Br-76

## MK415/T3 5'

- 5 AB033888.1, NM\_009236.1, L35032.1, AF047389.1, AF047043.1, AF017182.1, U66141.1, AJ001029.1, NM\_000346.1, AF116571.1, NM\_006941.1, NM\_005686.1, AF149301.1, AC007461.8, AF006501.4, AF098915.1, AF083105.1, AF029696.1, AL031587.3, S74504.1, Z46629.1, AJ001183.1, L29086.1, U08223.2, NM\_007084.1, NM\_009238.1, NM\_009233.1, NM\_009234.1, NM\_005986.1, AF107044.1, AF061784.1, AF009414.1, AL163672.1, AX001335.1, AX001334.1, U12533.1, AJ004858.1, X96997.1, X70298.1, X94126.1, AB014474.1, D61688.1, M90534.1, D83649.1, AB012236.1, Y13436.1, AA764352.1, AW321606.1, AL043036.2, AL120408.1, AA172336.1, AW533152.1, AW532037.1, AW532030.1, AW529354.1, AW414006.1, AW251615.1, AW060475.1, AI884987.1, AI816765.1, 10 AV116901.1, AI600115.1, AI594348.1, AI569726.1, AA965274.1, AI416080.1, AI406268.1, AI327463.1, AI176078.1, AI137787.1, AA734962.1, AA616534.1, AA521730.1, AA040785.1, AW822773.1, AW506135.1, AW417535.1, AW046996.1, AW015864.1, AI566947.1, AI552551.1, AI359981.1, AL355803.2, AC024914.17, AL137061.2,

## SEQ ID NO. 206

- 15 NGO-St-114 5' combined;

- AC005618.1, X97999.1, NM\_005642.1, U18062.1, Z65840.1, NM\_011901.1, AF144562.1, Z65839.1, AC004540.1, AL137039.1, U20660.1, AE003630.1, U15947.1, AL132889.2, AL132885.1, AE003646.1, AE003605.1, AE003412.1, AF146393.1, AC004058.1, U32788.1, AC004056.1, AL355094.2, AJ131018.1, Z97180.1, AP001821.1, AC005825.3, AC006804.3, AE003778.1, AE003576.1, AE003510.1, AF136829.1, AF081203.1, AC004992.1, AF195611.1, AF195610.1, 20 AC006961.16, AC006581.16, AC005414.2, U68299.1, AF016687.1, U23527.1, L78833.1, U18349.1, AC004267.1, AF047659.1, U09744.1, AL117206.1, AL137080.2, Z81467.1, Z81028.1, Z82180.19, Z77652.2, Z75892.1, AL050305.9, Z77249.1, Z97629.1, AJ250862.1, U55366.1, X06535.1, U40028.1, AP001331.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, AW029214.1, AA622246.1, D59188.1, AI904582.1, AW877796.1, AA595371.1, AA278660.1, AW877790.1, AA894917.1, AA252724.1, AA328618.1, AW402842.1, 25 AW362899.1, H14854.1, AW394189.1, AA312894.1, AW365030.1, T72766.1, AW582369.1, T65190.1, T52076.1, AW609538.1, AW366774.1, AA372836.1, AW380678.1, AA460590.1, F11914.1, AA383821.1, T47333.1, AA336307.1, AW403760.1, AA337398.1, AI951709.1, T34968.1, AA346865.1, AL119477.1, AW816164.1, AA348197.1, AA619797.1, T05543.1, AI158644.1, T83104.1, C03576.1, C03455.1, T86869.1, AV121343.1, AA572579.1, AA095559.1, AA517694.1, AA920998.1, AV205440.1, AA763469.1, AV212370.1, AI117791.1, AV213552.1, AV212700.1, C89279.1, H21207.1, 30 AV216550.1, AV100198.1, AV218081.1, AV214781.1, AW199703.1, AI722257.1, AA336858.1, AA102949.1, AA182987.1, W26005.1, AW645787.1, AW638295.1, AW199696.1, R52386.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AW728753.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AI756661.1, AI755675.1, AC008579.2, AC020971.1, AC025193.1, AC021705.4, AC025256.4, AC068708.2, AC020898.3, AC020907.3, AC009035.5, AC026886.2, 35 AC021271.4, AC025944.2, AC025945.2, AC026220.2, AC007186.8, AC019704.1, AC015613.1, AC007913.1, AL158151.5, AL157888.2, AL136135.2, AL133263.2, Z98857.36, AC026124.3, AC027751.2, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2,

- 40 SEQ ID NO.207

## NGO-St-114

## YS071/T3 5'

- NM\_005642.1, AC005618.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, Z65840.1, AE003630.1, U15947.1, AL132889.2, AL132885.1, AF146393.1, AC004058.1, AJ131018.1, AP001821.1, AE003778.1, AE003576.1, AC004992.1, 45 AC005414.2, AF016687.1, L78833.1, AC004267.1, AF047659.1, Z81028.1, U55366.1, U40028.1, AW029214.1, AU077198.1, AW877796.1, AW877790.1, AA595371.1, AA252724.1, AA894917.1, AA622246.1, AA312894.1, AA328618.1, AA460590.1, AW403760.1, T47333.1, AI904582.1, T72766.1, AA278660.1, AA372836.1, F11914.1, T34968.1, T65190.1, AW673639.1, H14854.1, T05543.1, AA383821.1, AI158644.1, AA315968.1, AA572579.1, AW402842.1, AA517694.1, AW362899.1, AW582369.1, AV121343.1, AA920998.1, AW816164.1, AW394189.1, 50 AV205440.1, C89279.1, AV213552.1, AV212370.1, AW609538.1, AV212700.1, AW365030.1, AA619797.1, AW380678.1, C03576.1, AV216550.1, AV100198.1, AI722257.1, AA182987.1, AV218081.1, AV214781.1, AL119477.1, D59188.1, AW645787.1, AW638295.1, AW199703.1, AW199696.1, AW728753.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AI471179.1, AW375040.1, AW375037.1, AW021363.1, AI976597.1, AV049065.1, C54464.1, C54153.1, C51985.1, AA426143.1, AA406093.1, C11684.1, R74232.1, D27736.1, AC008579.2, AC020971.1, 55 AC025193.1, AC020907.3, AC007186.8, AC019704.1, AL136135.2, AL133263.2, Z98857.36, AC026124.3, AP001863.1, AC068193.4, AC036188.2, AC024947.2, AC025766.3, AC010623.3, AC016558.3, AC008534.3, AC036127.2, AC068579.1, AC009142.4, AC011724.2, AC024698.4, AC022198.2, AC021719.3, AC022788.2, AC010764.3, AC009695.4, AC025532.2, AC021157.3, AC016890.4, AC022273.2, AC016685.4, AC011266.3, AC023349.2, AC018492.3, AC012101.3, AC024158.1, AC012448.3, AC010741.3, AC012387.4, AC017805.1, AC014787.1, 60 AC006937.5, AC006905.1, AL356435.1, AL109955.13, AL135939.9, AL133542.3, AL161790.3, AL162418.2, AL159176.3, AP001993.1,

## SEQ ID NO. 208

## NGO-St-114

-117-

YS071/T7 3'

- NM\_005642.1, AC005618.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AL009178.4, AB016897.1, AL109801.13, AE003618.1, AC007504.3, AC007172.6, AC005834.1, AB007651.1, AE003764.1, AE003738.1, AL078581.11, AL031259.1, Z81455.2, Z82900.1, AB025604.1, Z30211.1, AC012082.6, AC004747.2, AC004521.2, AC024750.1, AF233591.1, AC012099.4, AC003012.1, AC005076.2, AC007269.2, AF121898.1, AC006075.1, AC004583.1, AF042091.1, AL163282.2, AL117191.4, AL121716.16, AL161585.2, AL121754.18, AL008723.8, AL021182.1, AL031429.11, AL035593.11, AL023094.2, U37796.1, X04112.1, X15215.1, AI052691.1, AI346408.1, AW304965.1, AI709369.1, AW190867.1, AW192823.1, AI818211.1, AI434577.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, AW069225.1, AI376092.1, W65333.1, AI804531.1, AI366201.1, AI940448.1, AW860175.1, AW604918.1, AA461518.1, AA063580.1, AA825152.1, AA604623.1, AI278875.1, AA947107.1, AA417019.1, W39724.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, AW607519.1, AA975911.1, AA037065.1, AA838760.1, AW089083.1, AA635906.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, T90567.1, AW519252.1, AW150510.1, R73733.1, AA508614.1, W56065.1, T86870.1, AL118821.1, AA508722.1, AA886319.1, AA577447.1, AA380499.1, AA314905.1, AA854628.1, AA412648.1, H84875.1, AW614384.1, F09561.1, AA326994.1, AA037079.1, AA380870.1, R30839.1, AI287373.1, AI654286.1, R27607.1, T65121.1, H85281.1, N87733.1, AA715623.1, AA946962.1, AA460590.1, AA628285.1, C02002.1, AA894943.1, AA876963.1, AI431981.1, AA585211.1, AI216614.1, AA381394.1, AA278612.1, AA585402.1, AW463162.1, D80075.1, R52386.1, AA036649.1, AA671025.1, AA369696.1, AW057744.1, T86869.1, AA794137.1, AW414681.1, AC020971.1, AC025419.6, AC021297.2, AC020004.1, AC064829.3, AC009954.3, AC011791.3, AC013328.5, AC007819.7, AC009807.3, AC016991.2, AC009345.6, AC008043.3, AC018408.1, AC017738.1, AC018228.1, AL138817.5, AL356212.1, AL133518.3, AL136980.3, AL139294.1, AL031011.20, AP000708.1, Z82169.1, Z95393.1,

SEQ ID NO.209

25 NGO-ST-114

YS081/T3 5'

- AC005618.1, X97999.1, NM\_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AL132889.2, AL132885.1, AE003646.1, AE003605.1, AE003412.1, AC004058.1, AC004056.1, Z97180.1, AP001821.1, AC006804.3, AE003778.1, AE003576.1, AE003510.1, AF136829.1, AC006961.16, AC006581.16, AE001546.1, U68299.1, U18349.1, AC004267.1, AF047659.1, U09744.1, Z77249.1, U55366.1, X06535.1, AP001111.1, AB029433.1, Z95704.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AA312894.1, AW366774.1, AA336307.1, AA337398.1, AI951709.1, AA460590.1, AL119477.1, AA348197.1, T86869.1, AA095559.1, AW029214.1, AW877796.1, AW877790.1, AA595371.1, AA252724.1, AA894917.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, AW622907.1, AW217541.1, AW217534.1, AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AW021363.1, AI976597.1, AI966918.1, AI966929.1, AI964567.1, AV155610.1, AI756661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AA979929.1, AA979727.1, C72737.1, AA426143.1, AA406093.1, AA123407.1, C19565.1, R74232.1, T18355.1, AC008579.2, AC021705.4, AC007186.8, AC019704.1, AC007913.1, AL158151.5, Z98857.36, AC025179.3, AC008814.3, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AL161444.2, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC068193.4, AC012386.9, AC006513.25, AC068979.2, AC036188.2, AC008533.5, AC011367.5, AC011371.4, AC009142.4, AC025796.2, AC021409.3, AC010764.3, AC021373.3, AC011693.4, AC016685.4, AC018862.3, AC018994.3, AC012109.2, AC010741.3, AC012726.1, AC017805.1, AC014787.1, AC006937.5, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL139119.5, AL135939.9, AL355804.2, AL354674.2, AL161790.3, AL159176.3, AL157770.2, AP001993.1, AP001806.1, AP001457.1, AP000881.1, AP000826.1, AP000646.1, AP000621.1,

50 SEQ ID NO.210

NGO-ST-114

YS081/T7 3'

- NM\_005642.1, AC005618.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AE003618.1, AC004927.2, AC007172.6, AC005834.1, AE003738.1, AF165124.1, AL163258.2, AL078581.11, AL031259.1, AL109801.13, Z81455.2, L77246.1, AP001713.1, AP000178.1, AP000033.1, AP000266.1, AP000102.1, Z99115.1, M15318.1, AC004747.2, AE002267.1, AC004828.2, AE001658.1, AC004583.1, AF042091.1, AL355101.2, AL163282.2, AL109985.2, AL049569.13, U37796.1, X76272.1, X04112.1, X15215.1, AB018107.1, AI434577.1, AI371764.1, AA947107.1, AW519252.1, AA776228.1, AW512466.1, AW304965.1, AW264130.1, AI376092.1, AI274749.1, AI090392.1, AI052691.1, AA824551.1, AA635906.1, AA604623.1, AA507377.1, AA417019.1, AA188912.1, AA063580.1, W61316.1, AI346408.1, AA825152.1, AW069225.1, AA037065.1, AI675129.1, AI285611.1, AI278875.1, AI125952.1, AA975911.1, AA613880.1, AA602587.1, AA461518.1, W15503.1, AW089083.1, AW190867.1, T90567.1, W56065.1, AW265444.1, AI356847.1, T86870.1, AA838760.1, AI818211.1, AI366201.1, AA417113.1, AW192823.1, AI709369.1, AW150510.1, AA508614.1, AA886319.1, AA577447.1, AW607519.1, AA380499.1, AA854628.1, H84875.1, AA508722.1, AW614384.1, F09561.1, AI940448.1, AW860175.1, AW604918.1, W65333.1, W39724.1, AA314905.1, AA326994.1, AI804531.1, R73733.1,

-118-

AA412648.1, AI287373.1, AL118821.1, R27607.1, AA037079.1, T65121.1, AI654286.1, AA380870.1, N87733.1, AA715623.1, AA946962.1, C02002.1, AA628285.1, H85281.1, AA460590.1, AA894943.1, AA876963.1, AA585211.1, AI216614.1, R30839.1, AA278612.1, AA585402.1, D80075.1, AA036649.1, AW057744.1, AA794137.1, AA671025.1, AI431981.1, AA381394.1, AA794920.1, AW463162.1, AI607308.1, AA691044.1, AW414681.1, AC020971.1, AC025419.6, AC020004.1, AC064829.3, AC064826.2, AC034126.2, AC016547.5, AC008835.3, AC026466.3, AC009954.3, AC024883.3, AC011791.3, AC016991.2, AC008043.3, AC018408.1, AC017738.1, AL133518.3, AL133472.3, AL031011.20, Z95393.1, AC007834.20, AC007623.20, AC009757.7, AC021171.3, AC010644.5, AC010590.4, AC008825.3, AC027749.2, AC024483.2, AC015533.4, AC027630.4, AC024466.3, AC018737.2, AC024399.2, AC009554.4, AC026890.1, AC026021.1, AC016063.4, AC011781.4, AC016357.6, AC022518.2, AC013478.3, AC015826.2, AL356212.1, AL137140.5, AL136359.4, AL161900.3, AL122125.1, AL139294.1, AP001872.1,

SEQ ID NO.211

NGO-St-114

YS1615/T3 5'

X97999.1, AC005618.1, NM\_005642.1, U18062.1, NM\_011901.1, AF144562.1, U20660.1, U15947.1, AL132889.2, AL132885.1, AF146393.1, AC004058.1, AJ131018.1, AP001821.1, AE003778.1, AE003576.1, AC004992.1, AF195611.1, AF195610.1, AC005414.2, AF016687.1, L78833.1, AC004267.1, AF047659.1, AL117206.1, Z81467.1, Z81028.1, Z82180.19, Z77652.2, Z75892.1, AL050305.9, Z97629.1, U55366.1, U40028.1, AW029214.1, AA622246.1, AI904582.1, AW877796.1, AA595371.1, AW877790.1, AA278660.1, AA894917.1, AA252724.1, AA328618.1, AW402842.1, AW362899.1, H14854.1, T72766.1, AW394189.1, T65190.1, AW365030.1, AA372836.1, AW582369.1, F11914.1, AU077198.1, AW609538.1, AW380678.1, AA383821.1, T47333.1, AW403760.1, T34968.1, AA460590.1, AA312894.1, AW816164.1, AA346865.1, AA619797.1, T05543.1, AI158644.1, AV121343.1, AA572579.1, C03576.1, AA517694.1, T83104.1, C03455.1, AA920998.1, AV205440.1, AV212370.1, AV213552.1, AV212700.1, C89279.1, AA763469.1, H21207.1, AV216550.1, AI117791.1, AV100198.1, AV218081.1, AV214781.1, AW199703.1, AI722257.1, AA182987.1, AA336858.1, AW645787.1, AW638295.1, AW199696.1, AW728753.1, AA102949.1, AI471179.1, AW375040.1, AW375037.1, AV049065.1, C54464.1, C54153.1, C51985.1, C49917.1, C11684.1, D27736.1, AC008579.2, AC020971.1, AC025193.1, AC025256.4, AC020898.3, AC020907.3, AC009035.5, AC015613.1, AL136135.2, AL133263.2, Z98857.36, AC026124.3, AC027751.2, AP001863.1, AC068193.4, AC036188.2, AC024947.2, AC025972.2, AC041033.2, AC026404.4, AC025766.3, AC024583.3, AC010243.3, AC010273.3, AC010302.3, AC010623.3, AC016558.3, AC008534.3, AC036127.2, AC068579.1, AC009171.4, AC009142.4, AC013670.3, AC017106.3, AC018686.4, AC011724.2, AC024698.4, AC022198.2, AC021719.3, AC019033.4, AC022788.2, AC023629.2, AC010764.3, AC021828.2, AC009695.4, AC025532.2, AC021157.3, AC016890.4, AC022273.2, AC016685.4, AC011266.3, AC023349.2, AC018492.3, AC012101.3, AC024158.1, AC012448.3, AC010741.3, AC012387.4, AC017805.1, AC014787.1, AC006937.5, AC006905.1, AC006704.1, AL356435.1, AL355593.3, AL133542.3, AL161790.3, AL162418.2, AL159176.3, Z92842.1, Z92863.2, AP001993.1,

SEQ ID NO.212

NGO-ST-114

YS1615/T7 3'

AC005618.1, NM\_005642.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AL009178.4, AB016897.1, AE003618.1, AC007504.3, AB007651.1, AE003764.1, AE003738.1, AF165124.1, AL078581.11, AL031259.1, Z81455.2, Z82900.1, L77246.1, AB025604.1, Z99115.1, M15318.1, Z30211.1, AC012082.6, AC004521.2, AC024750.1, AE003600.1, AF233591.1, AE001658.1, AF121898.1, AF022814.1, AF042091.1, AF005383.1, AL117191.4, AL121716.16, AC002077.1, AL021182.1, AL031429.11, X76272.1, X04112.1, X15215.1, AI052691.1, AI346408.1, AW304965.1, AW190867.1, AI709369.1, AW192823.1, AI818211.1, AI434577.1, AW264130.1, AA507377.1, AA613880.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, AI376092.1, AW069225.1, AI366201.1, AI804531.1, AA063580.1, AA461518.1, W65333.1, AA825152.1, AA604623.1, AA947107.1, AI278875.1, AA417019.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI940448.1, W39724.1, AI356847.1, AW860175.1, AW604918.1, AA975911.1, AA037065.1, AA838760.1, AA635906.1, AW089083.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, AW519252.1, T90567.1, AW150510.1, AA508614.1, W56065.1, AW607519.1, T86870.1, R73733.1, AL118821.1, AA886319.1, AA508722.1, AA577447.1, AA380499.1, AA854628.1, H84875.1, AW614384.1, F09561.1, AI287373.1, AA314905.1, AA326994.1, R30839.1, R27607.1, T65121.1, AA412648.1, AI654286.1, N87733.1, AA715623.1, AA037079.1, AA946962.1, AA380870.1, C02002.1, AA628285.1, AA894943.1, AA876963.1, AI431981.1, AA460590.1, H85281.1, AA585211.1, AI216614.1, AA278612.1, AA585402.1, D80075.1, AW057744.1, AA381394.1, AA036649.1, AA794137.1, AA691044.1, AA671025.1, AA794920.1, AW414681.1, AW463162.1, AA549454.1, AC020971.1, AC025419.6, AC064829.3, AC064826.2, AC008835.3, AC013328.5, AC009807.3, AC018408.1, AC017738.1, AC018228.1, AL138817.5, AL133472.3, AL136980.3, Z82169.1, AC009757.7, AC060773.2, AC036223.2, AC008825.3, AC027438.2, AC015679.3, AC015964.2, AC021450.3, AC011218.4, AC022625.1, AC006719.1, AL163153.1,

SEQ ID NO.213

NGO-St-114

YS1631/T7 3'

NM\_005642.1, AC005618.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AL009178.4, AB016897.1, AE003618.1,

- AC007504.3, AB007651.1, AE003738.1, AF165124.1, AL078581.11, AL031259.1, AL109801.13, Z81455.2, Z82900.1, L77246.1, AB025604.1, Z99115.1, M15318.1, Z30211.1, AC012082.6, AC004521.2, AC024750.1, AC012099.4, AL121716.16, AL021182.1, AP001037.1, AI052691.1, AW304965.1, AI709369.1, AI346408.1, AW190867.1, AW192823.1, AI818211.1, AI434577.1, AW264130.1, AA507377.1, AA613880.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, AI376092.1, AW069225.1, AI366201.1, AI804531.1, AA461518.1, AA063580.1, W65333.1, AA825152.1, AA604623.1, AA947107.1, AI278875.1, AA417019.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, W39724.1, AA975911.1, AA037065.1, AI940448.1, AW860175.1, AW604918.1, AA838760.1, AW089083.1, AA635906.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, AW519252.1, T90567.1, AW150510.1, AA508614.1, W56065.1, T86870.1, AL118821.1, R73733.1, AA508722.1, AA886319.1, AW607519.1, AA577447.1, AA380499.1, AA854628.1, H84875.1, AW614384.1, F09561.1, AI287373.1, R30839.1, AA326994.1, R27607.1, T65121.1, AA314905.1, AI654286.1, N87733.1, AA412648.1, AA715623.1, AA946962.1, AA628285.1, C02002.1, AA037079.1, AA380870.1, AA894943.1, AA876963.1, AI431981.1, AA585211.1, AI216614.1, AA460590.1, H85281.1, AA278612.1, AA585402.1, D80075.1, AW057744.1, AA794137.1, AA691044.1, AA671025.1, AA794920.1, AW414681.1, AA381394.1, AA036649.1, AI859319.1, AW463162.1, AC020971.1, AC025419.6, AC064829.3, AC064826.2, AC034126.2, AC008835.3, AC013328.5, AC009807.3, AC018228.1, AI133472.3, AI136980.3, AC023599.7, AC068540.2, AC009757.7, AC060773.2, AC036223.2, AC008825.3, AC026083.3, AC027438.2, AC015679.3, AC015964.2, AC011218.4, AC024065.2, AC011647.3, AC013478.3, AC006719.1, AI135842.4,
- 20 SEQ ID NO. 214  
NGO-St-114  
YS1682/T3 5'  
AC005618.1, X97999.1, NM\_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AE003646.1, AE003605.1, AE003412.1, AC004058.1, AC004056.1, AL132889.2, Z97180.1, AL132885.1, AP001821.1, AC004005.2, AC006804.3, AE003778.1, AE003510.1, AF136829.1, AC006961.16, AC006581.16, U68299.1, U18349.1, AF047659.1, U09744.1, Z77249.1, U55366.1, X06535.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AW366774.1, AA336307.1, AA337398.1, AA312894.1, AI951709.1, AL119477.1, AA348197.1, AA460590.1, T86869.1, AA095559.1, AW029214.1, AA252724.1, AW877796.1, AW877790.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AW021363.1, AI976597.1, AI966918.1, AI966929.1, AI964567.1, AI857189.1, AI756661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AA979929.1, AA979727.1, C72737.1, AA426143.1, AA406093.1, C19565.1, R74232.1, T18355.1, AC008579.2, AC021705.4, AC007186.8, AC019704.1, AC007913.1, AL158151.5, AC068193.4, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AL159176.3, Z98857.36, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC012386.9, AC006513.25, AC068979.2, AC036188.2, AC009142.4, AC025796.2, AC021409.3, AC021373.3, AC016685.4, AC012109.2, AC012726.1, AC014787.1, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL135939.9, AL355472.2, AL355804.2, AL354674.2, AL157770.2, AP001993.1, AP001806.1, AP000881.1, AP000826.1, AP000646.1, AP000621.1,
- SEQ ID NO. 215  
NGO-St-114  
YS1743/T3 5'  
AC005618.1, X97999.1, NM\_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AC000003.1, AE003646.1, AE003605.1, AE003412.1, AC004254.1, AC004056.1, AL035448.28, Z97180.1, AC006804.3, AE003758.1, AE003634.1, AE003597.1, AE003510.1, AC007029.3, AF136829.1, AC000064.1, AC002458.1, NM\_004703.1, AC006961.16, AC006581.16, AC007566.1, AC006240.1, U68299.1, AC004148.1, AC005547.1, U18349.1, U73644.1, U09744.1, AL132889.2, Z77249.1, AL132885.1, X06535.1, X77723.1, X91141.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AW366774.1, AA336307.1, AA337398.1, AI951709.1, AA312894.1, AL119477.1, AA348197.1, AA460590.1, T86869.1, AA095559.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI976597.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW374004.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AL120839.1, AW021363.1, AI966918.1, AI966929.1, AI964567.1, AI912789.1, AI857189.1, AI756661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AI372843.1, AA979929.1, AA979727.1, C72737.1, AA551099.1, AA426143.1, AA406093.1, AA203657.1, C19565.1, R74232.1, F06378.1, T18355.1, AC008579.2, AC021705.4, AC015898.4, AC026989.2, AC020553.3, AC015900.2, AC011789.4, AC022373.1, AC007186.8, AC019704.1, AC007913.1, AL158151.5, AL157785.2, AL355332.1, AC026728.3, AC026712.3, AC026384.2, AC024050.6, AC019207.3, AC020725.3, AC023953.2, AC009593.4, AC019835.1, AC014673.1, AC008189.2, AC008159.1, AL109836.17, AP001894.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC012386.9, AC006513.25, AC068979.2, AC063921.4, AC055875.2, AC034211.3, AC008066.3,

-120-

AC020740.4, AC025942.2, AC025796.2, AC021409.3, AC022788.2, AC025525.2, AC025532.2, AC021373.3, AC022247.2, AC017029.4, AC016685.4, AC011566.3, AC012109.2, AC015727.3, AC010741.3, AC009981.5, AC019821.1, AC007984.3, AC012726.1, AF212833.1, AC017607.1, AC014838.1, AC009366.6, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL135939.9, AL355804.2, AL354674.2, AL161790.3, AL157770.2, Z98857.36, AP001993.1, AP001806.1, AP000881.1, AP000841.1, AP000826.1, AP000646.1, AP000621.1,

SEQ ID NO.216

NGO-St-114

YS1751/T7 3'

10 NM\_005642.1, AC005618.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AL121748.6, AL031259.1, Z81455.2, AL009178.4, AB016897.1, AC010227.5, AC008893.4, AC008000.7, AC007172.6, AC004583.1, AF042091.1, AL355094.2, AL163282.2, AL031683.1, X15215.1, AB005246.1, AB005230.1, AW304965.1, AI052691.1, AW190867.1, AI709369.1, AW192823.1, AI346408.1, AI818211.1, AI434577.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI804531.1, AI371764.1, AI285611.1, AI675129.1, AI125952.1, AW069225.1, AI376092.1, AI366201.1, AA947107.1, 15 AA461518.1, AA063580.1, AA825152.1, AA776228.1, AA604623.1, AI278875.1, AI274749.1, AA417019.1, W65333.1, W15503.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, AA975911.1, W39724.1, AA037065.1, AW265444.1, AW089083.1, AA838760.1, AA635906.1, AA824551.1, AA602587.1, AI940448.1, AA188912.1, AW519252.1, AW860175.1, AW604918.1, T90567.1, AW150510.1, W56065.1, T86870.1, AA508614.1, AL118821.1, R73733.1, AA508722.1, AA886319.1, AA577447.1, AA380499.1, AA854628.1, AW614384.1, AW607519.1, H84875.1, F09561.1, 20 AI654286.1, AI287373.1, R30839.1, AA326994.1, T65121.1, R27607.1, AA314905.1, AA946962.1, N87733.1, AA715623.1, AA412648.1, AA628285.1, C02002.1, AA037079.1, AA894943.1, AA876963.1, AI431981.1, AA380870.1, AI216614.1, AA585211.1, AA278612.1, AA585402.1, AA460590.1, H85281.1, AW057744.1, D80075.1, AA794137.1, AA691044.1, AA671025.1, AA794920.1, AW414681.1, AC025419.6, AC015533.4, AC009954.3, AC016357.6, AC021952.4, AL133518.3, AL353600.1, AL031011.20, Z95393.1, AC012600.4, AC012515.11, AC007834.20, 25 AC007623.20, AC021171.3, AC026459.2, AC008952.4, AC010626.4, AC068206.1, AC027630.4, AC044795.2, AC024399.2, AC012600.3, AC016275.2, AC015826.2, AC009615.2, AC004555.2, AL356212.1, AL137140.5, AL136980.3, AL161900.3, AL139294.1,

SEQ ID NO. 217

30 NGO-St-114

YS1771/T3 5'

AC005618.1, X97999.1, NM\_005642.1, U18062.1, Z65840.1, Z65839.1, AC004540.1, AL137039.1, AE003630.1, AL132889.2, AL132885.1, AE003646.1, AE003605.1, AE003412.1, AC004058.1, AC004056.1, Z97180.1, AP001821.1, AC006804.3, AE003510.1, AF136829.1, AC006961.16, AC006581.16, U68299.1, U18349.1, U09744.1, Z77249.1, 35 X06535.1, AP001111.1, AB029433.1, AB003324.1, D00170.1, Y17816.1, AU077198.1, AW673639.1, AA315968.1, D59188.1, T52076.1, AA312894.1, AW366774.1, AA336307.1, AA337398.1, AA460590.1, AI951709.1, AL119477.1, AA348197.1, T86869.1, AA095559.1, AW029214.1, AW877796.1, AW877790.1, AA595371.1, AA252724.1, AA894917.1, AW563125.1, AW563124.1, AW506736.1, AW506735.1, AW506714.1, AW506713.1, AW433456.1, AW330840.1, AW056105.1, AI987345.1, AI519245.1, AI511851.1, AI456317.1, AI455940.1, AA264246.1, AW649858.1, 40 AI239260.1, C93674.1, AW787238.1, AW787237.1, AW597401.1, AW565183.1, AW352495.1, AW331243.1, AW286148.1, AI668513.2, AW021363.1, AI976597.1, AI966918.1, AI966929.1, AI964567.1, AI756661.1, AI755675.1, AV049065.1, AI746131.1, AI711682.1, AI677124.1, AI667849.1, AI665080.1, AI637127.1, AI549172.1, AI461446.1, AI461444.1, AA979929.1, AA979727.1, C72737.1, AA426143.1, AA406093.1, C19565.1, R74232.1, T18355.1, AC008579.2, AC021705.4, AC007186.8, AC019704.1, AC007913.1, AL158151.5, Z98857.36, AC026384.2, AC024050.6, 45 AC019207.3, AC020725.3, AC019835.1, AC014673.1, AC008189.2, AL109836.17, AP001894.1, AP001863.1, AP001548.1, AP001544.1, AP001493.1, AP001282.1, AP000906.2, AC012386.9, AC006513.25, AC068979.2, AC009142.4, AC022198.2, AC025796.2, AC021719.3, AC021409.3, AC022788.2, AC021782.2, AC025321.2, AC010929.2, AC025532.2, AC021373.3, AC016685.4, AC012109.2, AC018879.3, AC010741.3, AC012726.1, AC006871.1, AC006803.2, AL354880.3, AL109955.13, AL135939.9, AL355804.2, AL354674.2, AL161790.3, 50 AL157770.2, AP001993.1, AP001806.1, AP000881.1, AP000826.1, AP000646.1, AP000621.1,

SEQ ID NO.218

NGO-St-114

YS181/T3 5'

55 AC005618.1, X97999.1, NM\_005642.1, U18062.1, Z65839.1, Z65840.1, AC006804.3, AE003512.1, AC002052.8, AC006961.16, AW673639.1, D59188.1, AA315968.1, AU077198.1, T52076.1, AW366774.1, AA348197.1, AA337398.1, AA336307.1, AI951709.1, T86869.1, AA095559.1, AL119477.1, AA312894.1, AI239260.1, AA516747.1, AC008579.2, AC007913.1, AL158151.5, AC017003.2, AC012386.9, AC068979.2, AC026101.6, AC016639.5, AC016632.4, AC034249.1, AC021373.3, AC017624.1, AC010671.7, AC006871.1, AC006803.2, AP001806.1, AP000881.1, 60 AP000826.1, AP000646.1,

SEQ ID NO. 219

NGO-St-114

YS191/T7 3'



AC005618.1, NM\_005642.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AL009178.4, AB016897.1, AE003618.1, AC007504.3, AB007651.1, AE003764.1, AE003738.1, AF165124.1, AL163258.2, AL078581.11, AL031259.1, Z81455.2, Z82900.1, L77246.1, AP001713.1, AP000178.1, AP000033.1, AB025604.1, AP000266.1, AP000102.1, Z99115.1, M15318.1, Z30211.1, AC012082.6, AC004521.2, AC024750.1, AL121716.16, AL109801.13, AL008723.8, AL021182.1, 5 AB018107.1, AB005246.1, AI052691.1, AI346408.1, AW304965.1, AW190867.1, AI709369.1, AW192823.1, AI434577.1, AI818211.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI675129.1, AI371764.1, AI285611.1, AI125952.1, W65333.1, AI376092.1, AW069225.1, AI366201.1, AI804531.1, AA461518.1, AA063580.1, AA825152.1, AA604623.1, AW860175.1, AW604918.1, AI940448.1, AI278875.1, AA947107.1, W39724.1, AA417019.1, AI274749.1, W15503.1, AA776228.1, AW512466.1, W61316.1, AI090392.1, AI356847.1, AA975911.1, AA037065.1, AA838760.1, AW089083.1, 10 AW607519.1, AA635906.1, AA824551.1, AA602587.1, AW265444.1, AA188912.1, AW519252.1, T90567.1, AW150510.1, R73733.1, AA508614.1, W56065.1, T86870.1, AL118821.1, AA508722.1, AA886319.1, AA577447.1, AA380499.1, AA854628.1, H84875.1, AA314905.1, AW614384.1, F09561.1, AA326994.1, AA412648.1, AI287373.1, R30839.1, AA037079.1, R27607.1, AA380870.1, T65121.1, AI654286.1, N87733.1, AA715623.1, AA946962.1, H85281.1, AA460590.1, AA628285.1, C02002.1, AA894943.1, AA876963.1, AI431981.1, AA585211.1, AI216614.1, AA278612.1, 15 AA585402.1, AA671025.1, D80075.1, AW463162.1, AA381394.1, AA036649.1, AA794137.1, AW057744.1, R52386.1, AA794920.1, AA549454.1, AV100160.1, AC020971.1, AC025419.6, AC064829.3, AC064826.2, AC008835.3, AC013328.5, AC009807.3, AC017738.1, AC018228.1, AL133472.3, AL136980.3, AL353600.1, Z82169.1, AC009757.7, AC060773.2, AC036223.2, AC008825.3, AC027438.2, AC015679.3, AC013782.3, AC016693.4, AC024065.2, AC011647.3, AC013478.3, AC006719.1,

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SEQ ID NO. 220

NGO-St-114

YS274/T7 3'

NM\_005642.1, AC005618.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AE003618.1, AC007172.6, AC005834.1, 25 AE003738.1, AF165124.1, AL163258.2, AL078581.11, AL031259.1, Z81455.2, AP001713.1, AP000178.1, AP000033.1, AP000266.1, AP000102.1, AC004747.2, AC004583.1, AF042091.1, AL163282.2, AL163277.2, AL132879.2, X76272.1, X04112.1, AP001732.1, X15215.1, AP001037.1, AB018107.1, AI434577.1, AI371764.1, AA947107.1, AW519252.1, AA776228.1, AW512466.1, AW304965.1, AW264130.1, AI376092.1, AI274749.1, AI090392.1, AI052691.1, AA824551.1, AA635906.1, AA604623.1, AA507377.1, AA417019.1, AA188912.1, AA063580.1, W61316.1, 30 AW069225.1, AI346408.1, AA825152.1, AI675129.1, AI278875.1, AI125952.1, AA975911.1, AA613880.1, AA602587.1, AA461518.1, AA037065.1, AI285611.1, AW089083.1, AW190867.1, W15503.1, T90567.1, W56065.1, AW265444.1, AI356847.1, T86870.1, AI366201.1, AA838760.1, AA417113.1, AI818211.1, AW192823.1, AI709369.1, AW607519.1, AW150510.1, AA508614.1, AA886319.1, AA577447.1, AA380499.1, AA854628.1, AW860175.1, AW604918.1, H84875.1, AA508722.1, AW614384.1, AI940448.1, AA412648.1, F09561.1, AA314905.1, W39724.1, W65333.1, 35 AA326994.1, AI804531.1, R73733.1, AA037079.1, AI287373.1, AL118821.1, AA380870.1, R27607.1, T65121.1, AI654286.1, N87733.1, AA715623.1, AA946962.1, H85281.1, AA628285.1, C02002.1, AA460590.1, AA894943.1, AA876963.1, AA585211.1, AI216614.1, R30839.1, AA278612.1, AA585402.1, AA381394.1, AW463162.1, D80075.1, AA671025.1, AA794137.1, AA036649.1, AW057744.1, AI431981.1, R52386.1, AA794920.1, AA369696.1, AA549454.1, AC020971.1, AC025419.6, AC020004.1, AC064829.3, AC016547.5, AC008835.3, AC009954.3, AC011791.3, 40 AC016991.2, AC008043.3, AC018408.1, AC017738.1, AL133518.3, AL031011.20, Z95393.1, AC007834.20, AC007623.20, AC067724.3, AC009757.7, AC021171.3, AC064826.2, AC027235.2, AC010515.5, AC008825.3, AC027749.2, AC024483.2, AC015533.4, AC027630.4, AC025229.3, AC046169.1, AC044876.1, AC018737.2, AC024399.2, AC026890.1, AC022020.3, AC024424.2, AC016063.4, AC019157.4, AC011781.4, AC016357.6, AC022518.2, AC013478.3, AC015826.2, AL356212.1, AL355305.2, AL139258.3, AL137140.5, AL161900.3, 45 AL122125.1, AL139294.1, AL022594.18, AP001872.1,

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SEQ ID NO.221

NGO-St-114

YS303/T7 3'

NM\_005642.1, AC005618.1, U18062.1, X97999.1, NM\_011901.1, AF144562.1, AC007172.6, AL121748.6, Z81455.2, 50 Z82900.1, AC004521.2, AC012099.4, AC004583.1, AF042091.1, AL163282.2, Z92812.1, X15215.1, AI052691.1, AW304965.1, AI709369.1, AW190867.1, AI346408.1, AW192823.1, AI818211.1, AW264130.1, AA613880.1, AA507377.1, AI434577.1, AI675129.1, AA417113.1, AI371764.1, AI285611.1, AI125952.1, AI804531.1, AW069225.1, AI376092.1, AI366201.1, AA461518.1, AA825152.1, AA604623.1, AI278875.1, AA947107.1, AA063580.1, AI274749.1, 55 AA776228.1, AA417019.1, W15503.1, W65333.1, AW512466.1, AI356847.1, W61316.1, AI090392.1, AA975911.1, AA037065.1, W39724.1, AW089083.1, AA635906.1, AA838760.1, AW265444.1, AA824551.1, AA602587.1, AI940448.1, AA188912.1, AW860175.1, AW604918.1, AW519252.1, T90567.1, AW150510.1, AA508614.1, W56065.1, T86870.1, AL118821.1, AA508722.1, AA886319.1, AA577447.1, R73733.1, AA380499.1, AA854628.1, AW614384.1, AW607519.1, H84875.1, F09561.1, AI654286.1, AI287373.1, R30839.1, AA326994.1, R27607.1, T65121.1, AA946962.1, AA314905.1, 60 AA715623.1, N87733.1, AA412648.1, AA628285.1, C02002.1, AA894943.1, AA876963.1, AI431981.1, AA380870.1, AA037079.1, AI216614.1, AA585211.1, H85281.1, AA460590.1, AA278612.1, AA585402.1, AW057744.1, D80075.1, AW414681.1, AA794137.1, AA671025.1, AA691044.1, AA794920.1, AA036649.1, AW280434.1, AI62830.1, AC020971.1, AC015533.4, AC016357.6, AL138817.5, AL133518.3, AL353600.1, AL031011.20, Z82169.1, Z95393.1,



## SEQ ID NO.222

NGO-St-114

YS305/T7 3'

- 5 NM\_005642.1, AC005618.1, U18062.1, X97999.1, Z81455.2, AL078462.9, AL034349.3, X15215.1, AI052691.1, AW304965.1, AI709369.1, AW190867.1, AI818211.1, AI346408.1, AW192823.1, AI804531.1, AI434577.1, AW264130.1, AA613880.1, AA507377.1, AA417113.1, AI675129.1, AI371764.1, AI125952.1, AI285611.1, AW069225.1, AI376092.1, AI366201.1, AA461518.1, W65333.1, AA825152.1, AA604623.1, AI278875.1, AA947107.1, AA417019.1, AI274749.1, AA776228.1, AA063580.1, W15503.1, AW512466.1, AI090392.1, W61316.1, W39724.1, AI356847.1, AA975911.1, AW089083.1, AI940448.1, AA635906.1, AA037065.1, AW265444.1, AA824551.1, AA602587.1, AA838760.1, 10 AW519252.1, AA188912.1, W56065.1, T86870.1, AW860175.1, AW604918.1, T90567.1, AA886319.1, AA577447.1, AW150510.1, AA854628.1, AA508614.1, R73733.1, AW614384.1, AA380499.1, F09561.1, AW607519.1, AA508722.1, AI654286.1, AL118821.1, H84875.1, AA326994.1, AI287373.1, AA946962.1, AA314905.1, T65121.1, R27607.1, AA412648.1, AA628285.1, C02002.1, R30839.1, N87733.1, AA715623.1, AI216614.1, AA894943.1, AA876963.1, AA380870.1, AA037079.1, AA585211.1, AA278612.1, AA585402.1, AA460590.1, H85281.1, AW057744.1, AI431981.1, 15 D80075.1, AA036649.1, AL031011.20, Z95393.1, AC018923.5, AC036181.2, AC068931.1, AC009440.2, AC027630.4, AC009554.4, AC006286.13, AC011996.3, AC010890.3, AC009528.7, AC007913.1, AL158151.5, AL161785.4,

## SEQ ID NO.223

NGO-St-115

20 YS1641/T7 3'

- L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC006578.5, AC005974.1, AC002416.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AC009396.5, AC007270.2, AC007314.3, AF049850.1, AF016494.1, AL032655.1, U23177.1, D25323.1, D90170.1, D90168.1, M64933.1, AI627646.1, AA641661.1, AI401150.1, 25 AW090508.1, AA701607.1, AI962712.1, AI953614.1, AW131544.1, AI829826.1, AW302357.1, AA042864.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AA501219.1, AA069672.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AI375729.1, AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW425207.1, AW815621.1, AW005947.1, AI982567.1, AI144435.1, AA171398.1, AA788576.1, F33435.1, AI631440.1, AA669918.1, AW815443.1, AW391454.1, AA101255.1, AA676341.1, AW815833.1, 30 AA169326.1, AW815622.1, AW391447.1, AW815635.1, U69195.1, AA101351.1, AA908462.1, AA126685.1, AW815508.1, AW815506.1, AW249892.1, AW815512.1, AW609613.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW801962.1, AW381537.1, R12509.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, AW189578.1, T23713.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, AA705248.1, R19314.1, T70135.1, AW462450.1, AW381476.1, F05151.1, AI206928.1, AW381459.1, AW843169.1, AW610177.1, AW393428.1, 35 AW016196.1, AW009270.1, AA092442.1, AW371229.1, AI658933.1, AI919572.1, AW384329.1, AI708578.1, AI435870.1, AI274998.1, AA969666.1, AA235124.1, W25228.1, AC006391.7, AC016175.1, AL356136.1, AC009423.2, AC017078.3, AC027239.2, AC024155.2, AC021304.2, AL354733.4, AL135938.7, AL353743.1, AP001998.1, AC022816.9, AC021256.4, AC024322.2, AC017144.1, AL162420.3, AC009192.60, AC068789.3, AC051628.10, AC018995.4, AC012480.4, AC035149.2, AC016591.4, AC040893.1, AC023199.2, AC026808.1, AC022926.2, 40 AC015797.2, AC013664.1, AL356260.1, AL118513.14, AL354999.1, AL160035.3, AL159978.2, AL022597.5, AP001532.1, AP001400.1, AP000590.3, Z92865.1, AL022596.1,

## SEQ ID NO. 224

NGO-St-115

45 YS1693/T7 3'

- L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC005974.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AC007270.2, AF049850.1, AF016494.1, X56462.1, D25323.1, D90170.1, D90168.1, M64933.1, X59856.1, AA641661.1, AI627646.1, AI962712.1, AA701607.1, AW090508.1, AI401150.1, AW131544.1, AI953614.1, AI829826.1, 50 AW302357.1, AA042864.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AA069672.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AI023923.1, AA501219.1, T67414.1, AI580826.1, AI375729.1, AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW815621.1, AW005947.1, AI982567.1, AI144435.1, AA171398.1, AA788576.1, AW425207.1, F33435.1, AI631440.1, AA669918.1, AW815443.1, AW391454.1, AA101255.1, AA676341.1, AW815833.1, AA169326.1, AW815622.1, AW391447.1, AW815635.1, U69195.1, AA101351.1, 55 AA908462.1, AA126685.1, AW815508.1, AW815506.1, AW249892.1, AW815512.1, AW609613.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW381537.1, R12509.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, AW189578.1, T23713.1, AW371378.1, AW381482.1, AW381510.1, AW801962.1, AW381496.1, AA705248.1, R19314.1, T70135.1, AW381476.1, F05151.1, AI206928.1, AW462450.1, AW381459.1, AW843169.1, AW610177.1, AW393428.1, AW016196.1, AW009270.1, AA092442.1, AW371229.1, AI658933.1, AI919572.1, 60 AW384329.1, AI708578.1, T79039.1, AW381472.1, F37823.1, AA705236.1, AA895510.1, AC006391.7, AC016175.1, AL356136.1, AC017078.3, AL135938.7, AC016389.2, AC021003.4, AC017144.1, AC016337.1, AL356266.2, AL162420.3, AL161719.6, AL161899.2, AC009192.60, AC068789.3, AC051628.10, AC012480.4, AC022926.2, AC015797.2, AC013664.1, AL137250.3, AL356258.2, AL356260.1, AL354999.1, AL160035.3, AL159978.2, AP001532.1, AP001400.1, AP000590.3,

## SEQ ID NO.225

NGO-St-115

YS1713/T7 3'

- 5 L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, L07873.1, AE003830.1, AC005974.1, AL096770.14, AL021578.1, AB024964.1, AB026048.1, AC012397.3.1, AC010329.3, AC012147.7, AE003603.1, AE002611.1, AC004506.1, AC007270.2, AJ239329.2, D25323.1, AA641661.1, AW090508.1, AI627646.1, AI962712.1, AI953614.1, AI401150.1, AW131544.1, AA701607.1, AW302357.1, AI829826.1, AA501219.1, AI984992.1, AA042864.1, AA640106.1, AA903408.1, 10 AA483607.1, AA069672.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AI375729.1, AI565611.1, AW425207.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW005947.1, AI982567.1, AI144435.1, AA171398.1, AA788576.1, AW815621.1, F33435.1, AI631440.1, AA101255.1, AA676341.1, AA669918.1, AW815443.1, AA169326.1, AW391454.1, AW815833.1, AA101351.1, U69195.1, AA908462.1, AW815622.1, AW391447.1, AW815635.1, AW801962.1, AW249892.1, AA126685.1, AA044415.1, AW815508.1, 15 AW815506.1, AW815512.1, AW609613.1, AA678797.1, AW462450.1, AW381515.1, AW474060.1, AW381537.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, R12509.1, AW189578.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, T23713.1, T70135.1, AW381476.1, AA705248.1, R19314.1, F05151.1, AW381459.1, AI206928.1, AW843169.1, AW009270.1, H19326.1, AW016196.1, R45471.1, AW084668.1, AI916589.1, AI435870.1, AI274998.1, AI095803.1, AA235124.1, AA234950.1, W25228.1, AA092442.1, AI352024.1, AW384329.1, AC006391.7, 20 AC016175.1, AL1356136.1, AL353636.2, AL135938.7, AL158822.4, AC017144.1, AL162420.3, AC069151.1, AC009192.60, AC068789.3, AC041003.2, AC012480.4, AC053495.3, AC020603.3, AC020726.3, AC012297.3, AC018491.7, AC007532.7, AC013956.1, AC015797.2, AC013664.1, AC013097.1, AL356435.1, AL354999.1, AL162418.2, AL160035.3, AL159978.2, AL163639.1, AL139023.1, AP001532.1, AP001400.1, AP000590.3,

## 25 SEQ ID NO.226

NGO-St-115

YS1732/T7 3'

- L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, AE003830.1, AC005974.1, AC007270.2, AF049850.1, AF016494.1, AL117207.1, D90170.1, D90168.1, 30 M64933.1, AI627646.1, AI401150.1, AA701607.1, AA641661.1, AI962712.1, AI829826.1, AW131544.1, AI953614.1, AW302357.1, AA042864.1, AW090508.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AI291840.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI580826.1, AI375729.1, AA069672.1, AI334962.1, AI334964.1, T67414.1, AI669755.1, AI565611.1, N95392.1, AW005947.1, AI144435.1, AI023923.1, AI982567.1, AA788576.1, F33435.1, AW815621.1, AA501219.1, AA171398.1, AI631440.1, AA101255.1, AA676341.1, AA169326.1, AW815443.1, 35 AW391454.1, AW815833.1, AA669918.1, AA101351.1, AA908462.1, AW815635.1, AW815622.1, AW391447.1, AW425207.1, AW249892.1, AA678797.1, AW815508.1, AA044415.1, AW815506.1, AW815512.1, AW609613.1, AA126685.1, U69195.1, AW381515.1, AW189578.1, AW474060.1, AW381537.1, AA156824.1, AA705248.1, AW379059.1, AW371260.1, AI720441.1, AW371378.1, R19314.1, AW381482.1, AW381510.1, T23713.1, AW381496.1, R12509.1, AI206928.1, F05151.1, AW381476.1, AW610177.1, AW393428.1, AW016196.1, AW381459.1, AW843169.1, 40 AI658933.1, AW009270.1, AI919572.1, AW371229.1, T70135.1, AA092442.1, AW801962.1, AW462450.1, AI708578.1, AW384329.1, AW381472.1, AA895510.1, T79039.1, AI401152.1, F37823.1, AC006391.7, AC016175.1, AL356136.1, AC017144.1, AL162420.3, AC068789.3, AC012480.4, AC022263.4, AC021643.7, AC016390.3, AC013664.1, AL354999.1, AL031113.1, AL160035.3, AL159978.2, AL021574.2, AP000590.3, AL020985.1, AL021568.1,

## 45 SEQ ID NO.227

NGO-St-115

YS1792/T7 3'

- L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AC007270.2, AF049850.1, AF016494.1, D25323.1, D90170.1, D90168.1, M64933.1, 50 AI627646.1, AI401150.1, AA701607.1, AA641661.1, AI962712.1, AI829826.1, AW131544.1, AA640106.1, AI953614.1, AA042864.1, AW302357.1, AW090508.1, AI984992.1, AA483607.1, AA903408.1, AW249681.1, AW235086.1, AI381502.1, AI291840.1, AI619912.1, AI580826.1, AA069672.1, T67414.1, AI375729.1, AI023923.1, AI334964.1, AI565611.1, AI334962.1, AI669755.1, N95392.1, AW005947.1, AI144435.1, AI982567.1, AW815621.1, AA788576.1, F33435.1, AA501219.1, AA171398.1, AI631440.1, AA101255.1, AA676341.1, AA669918.1, AW815833.1, AW815443.1, 55 AA169326.1, AW391454.1, AA101351.1, AA908462.1, AW815622.1, AW425207.1, AW391447.1, AW815635.1, AW249892.1, AA678797.1, AW815508.1, AA044415.1, AW815506.1, AW815512.1, AW609613.1, AA126685.1, AW381515.1, U69195.1, AW474060.1, AW381537.1, AW189578.1, AA156824.1, AI720441.1, AW379059.1, AW371260.1, AW371378.1, AA705248.1, AW381496.1, AW381482.1, AW381510.1, R12509.1, T23713.1, AW381476.1, R19314.1, AI206928.1, F05151.1, AW381459.1, AW843169.1, AW610177.1, AW393428.1, AW016196.1, AW009270.1, 60 T70135.1, AI658933.1, AA092442.1, AW371229.1, AI919572.1, AW801962.1, AW462450.1, AI708578.1, AW384329.1, AW381472.1, F37823.1, AA895510.1, AA705236.1, T79039.1, AC006391.7, AC016175.1, AL356136.1, AC010633.4, AC015575.5, AC011760.8, AL162420.3, AC068789.3, AC012480.4, AC019214.2, AL354999.1, AL160035.3, AL159978.2, AP000590.3,

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SEQ ID NO.228

NGO-St-115

YS1801/T3,

5 L07872.1, L34544.1, L34543.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, L07873.1,  
U60094.1, U60093.1, X59130.1, X59129.1, M81869.1, M81874.1, M81870.1, AB003695.1, M81873.1, M81872.1,  
M81875.1, AF085173.1, AE003646.1, AE003411.1, AF047659.1, AC011288.3, AC002338.2, AC007729.2, AE003662.1,  
AC006978.2, AC007082.4, AC006263.1, AF003130.1, Y08501.1, U80814.1, X66728.1, X65871.1, AJ007973.1,  
X58393.1, M94383.1, AE002611.1, AF223391.1, AC024864.1, AC024206.1, AC012329.3, AF104919.1, AL355836.1,  
10 AL157756.2, AL161587.2, AL161492.2, AL132964.2, AL137898.1, AL132962.1, AL035581.1, Z93385.1, Z81086.1,  
AL035445.4, U70855.1, X96762.1, AL031135.1, U69195.1, AW462450.1, AI325751.1, AA935398.1, AW084668.1,  
AI916589.1, AW801962.1, T79039.1, T70135.1, AA501219.1, W25228.1, AI435870.1, AI274998.1, AI095803.1,  
AA235124.1, AA234950.1, R37405.1, AA081973.1, AA101254.1, H19326.1, AW239382.1, AW090508.1, R16902.1,  
F04242.1, AA969666.1, R45471.1, AA232981.1, AI352024.1, AW384329.1, T19153.1, AA233367.1, AI953614.1,  
R44578.1, F01398.1, AA641661.1, T23712.1, AW384317.1, AA101350.1, AI962712.1, AW425207.1, AW249681.1,  
15 AI627646.1, AI401150.1, AA171575.1, AW131544.1, R19314.1, AA817421.1, AI142713.1, AA736032.1, R71133.1,  
AW760949.1, AJ394324.1, AW418568.1, AW221760.1, AW093987.1, AW043304.1, AI995809.1, AV200012.1,  
AV198387.1, AV191304.1, AI779257.1, C65393.1, D73771.1, D69291.1, D68255.1, D37730.1, AL356136.1,  
AC006391.7, AC019747.1, AC015644.3, AC015641.3, AC068980.2, AC021871.8, AC063967.1, AC024734.3,  
AC024447.2, AC006927.22, AC017011.3, AC010780.3, AC025099.1, AC010147.4, AC013569.3, AC017470.1,  
20 AC006714.2, AL353636.2, AL158822.4, AP001377.1, AC012598.9, AC055764.3, AC067725.2, AC025573.4,  
AC024560.5, AC036183.2, AC055790.2, AC069123.1, AC069026.1, AC013610.2, AC068491.1, AC024084.2,  
AC008751.4, AC008749.4, AC005077.2, AC008267.3, AC027094.2, AC034098.1, AC025889.2, AC016462.3,  
AC027268.1, AC025317.2, AC018681.5, AC023815.2, AC018491.7, AC013504.2, AC013097.1, AC006904.2,  
AC006900.1, AC006719.1, AL138904.2, AL354990.1, AP000904.2, AP001455.1, AP000706.1, AL009206.1,

SEQ ID NO.229

NGO-St-115

YS1801/T7 3'

30 L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1,  
U60094.1, M81877.1, M81876.1, AE003627.1, AC005734.1, AE003830.1, AC005974.1, AL021578.1, AB024964.1,  
AB026048.1, AC012397.31, AC012147.7, AC006729.1, AE003603.1, AE003578.1, AC008261.3, AC017118.3,  
AC007270.2, AC005149.1, AF068710.1, AE000051.1, AJ239329.2, D25323.1, AW090508.1, AI627646.1, AA641661.1,  
AI962712.1, AI953614.1, AI401150.1, AW131544.1, AA701607.1, AW302357.1, AI829826.1, AA501219.1, AI984992.1,  
AA042864.1, AA640106.1, AA903408.1, AA483607.1, AA069672.1, AW249681.1, AW235086.1, AI381502.1,  
35 AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AW425207.1, AI375729.1, AI565611.1, AI334962.1,  
AI334964.1, AI669755.1, N95392.1, AW005947.1, AI982567.1, AI144435.1, AA171398.1, AA788576.1, AW815621.1,  
F33435.1, AI631440.1, AA101255.1, AA676341.1, AA669918.1, AW815443.1, AA169326.1, AW391454.1, AW815833.1,  
AA101351.1, U69195.1, AA908462.1, AW815622.1, AW391447.1, AW815635.1, AW801962.1, AW249892.1,  
AA126685.1, AA044415.1, AW815508.1, AW815506.1, AW815512.1, AW609613.1, AA678797.1, AW462450.1,  
40 AW381515.1, AW474060.1, AW381537.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, R12509.1,  
AW189578.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, T23713.1, T70135.1, AW381476.1, AA705248.1,  
R19314.1, F05151.1, AW381459.1, AI206928.1, AW843169.1, AW009270.1, AW016196.1, AW084668.1, AI916589.1,  
AI435870.1, AI274998.1, AI095803.1, AA235124.1, AA234950.1, W25228.1, AA969666.1, AA092442.1, F04242.1,  
R45471.1, AW384329.1, AC006391.7, AC016175.1, AL356136.1, AC010631.4, AC025727.1, AC018490.4, AC020100.1,  
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SEQ ID NO.230

NGO-St-115

YS276/T7 3'

55 L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60094.1,  
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AW302357.1, AA042864.1, AI984992.1, AA640106.1, AA903408.1, AA501219.1, AA483607.1, AA069672.1,  
AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AI375729.1,  
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SEQ ID NO.231

10 NGO-St-115

YS302/T7 3'

L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AC008408.5, AC011422.2, AE003830.1, AC006356.3, AC005974.1, AL021578.1, AB024964.1, AB026048.1, AC012397.31, AC012147.7, AE003578.1, AC007115.1, AC007270.2, U66059.1, AF030179.1, AC005149.1, AF049850.1, AF016494.1, AL133376.6, D25323.1, D90170.1, D90168.1, U07978.1, M64933.1, AI627646.1, AA641661.1, AW090508.1, AI401150.1, AI953614.1, AI962712.1, AW131544.1, AA701607.1, AI829826.1, AA042864.1, AW302357.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AW249681.1, AW235086.1, AI381502.1, AA501219.1, AA069672.1, AI619912.1, AI291840.1, AI023923.1, T67414.1, AI580826.1, AI375729.1, AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW005947.1, AI144435.1, AW815621.1, AI982567.1, AA788576.1, AA171398.1, AW425207.1, F33435.1, AI631440.1, AA669918.1, AW815443.1, AA101255.1, AW391454.1, AA676341.1, AW815833.1, AA169326.1, AW815622.1, AA101351.1, AW391447.1, AW815635.1, AA908462.1, AA126685.1, AW815508.1, AW249892.1, AW815506.1, AW815512.1, AW609613.1, U69195.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW381537.1, AA156824.1, R12509.1, AW801962.1, AW379059.1, AW371260.1, AI720441.1, AW189578.1, AW371378.1, T23713.1, AW381482.1, AW381510.1, AW381496.1, AA705248.1, R19314.1, AW381476.1, F05151.1, AW462450.1, AI206928.1, T70135.1, AW381459.1, AW843169.1, AW009270.1, AA092442.1, AW610177.1, AW393428.1, AW016196.1, AW371229.1, AI658933.1, AI919572.1, R16902.1, HI9326.1, AI708578.1, AA235124.1, AA969666.1, AW384329.1, R45471.1, AC006391.7, AC016175.1, AL356136.1, AC011340.3, AC017144.1, AL162420.3, AC009192.60, AC068789.3, AC012480.4, AC027785.2, AC025508.2, AC012346.3, AC027284.1, AC009659.3, AC021978.4, AC013448.3, AC020022.1, AC015797.2, AC010694.2, AL137160.4, AL354999.1, AL160035.3, AL159978.2, AP001532.1, AP001400.1, AP000590.3,

SEQ ID NO.232

15 NGO-St-115

YS323/T7 3'

L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC005974.1, AC007270.2, AF049850.1, AF016494.1, D25323.1, D90170.1, D90168.1, M64933.1, AA641661.1, AI627646.1, AA701607.1, AI962712.1, AW131544.1, AI401150.1, AW090508.1, AI953614.1, AI829826.1, AA042864.1, AW302357.1, AA640106.1, AI984992.1, AA903408.1, AW249681.1, AW235086.1, AI381502.1, AI619912.1, AI291840.1, AA483607.1, AI580826.1, AA069672.1, AI375729.1, AA501219.1, T67414.1, AI565611.1, AI023923.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AI982567.1, AW005947.1, AI144435.1, AW815621.1, AA788576.1, F33435.1, AA171398.1, AI631440.1, AW815443.1, AA101255.1, AA676341.1, AW391454.1, AW425207.1, AW815833.1, AA169326.1, AA669918.1, AW815622.1, AW815635.1, AW391447.1, AA101351.1, AA908462.1, AW815508.1, AW815506.1, AW249892.1, AW815512.1, AW609613.1, U69195.1, AA126685.1, AA044415.1, AA678797.1, AW381515.1, AW189578.1, AW474060.1, AW381537.1, AA156824.1, R12509.1, AW379059.1, AW371260.1, AI720441.1, AA705248.1, AW371378.1, T23713.1, AW381482.1, AW381510.1, AW381496.1, F05151.1, AW381476.1, AI206928.1, R19314.1, AW801962.1, AW381459.1, T70135.1, AW843169.1, AW610177.1, AW393428.1, AW016196.1, AI658933.1, AA092442.1, AW462450.1, AW009270.1, AI919572.1, AW371229.1, AW384329.1, AI708578.1, AW381472.1, AA895510.1, F37823.1, R45471.1, R16902.1, AC006391.7, AC016175.1, AL356136.1, AC017144.1, AL162420.3, AC068789.3, AC012480.4, AC013664.1, AL354999.1, AL160035.3, AL159978.2, AP000590.3,

SEQ ID NO.233

55 NGO-St-115

YS372/T7 3'

L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, M81876.1, AE003830.1, AC005974.1, AC012397.31, AC007270.2, AF049850.1, AF016494.1, D25323.1, D90170.1, D90168.1, M64933.1, AA641661.1, AI627646.1, AA701607.1, AI962712.1, AW131544.1, AW090508.1, AI953614.1, AI401150.1, AI829826.1, AA042864.1, AW302357.1, AA640106.1, AI984992.1, AA903408.1, AA483607.1, AW249681.1, AW235086.1, AI381502.1, AA069672.1, AI619912.1, AI291840.1, AI580826.1, T67414.1, AI023923.1, AA501219.1, AI375729.1, AI565611.1, AI334962.1, AI334964.1, AI669755.1, N95392.1, AW005947.1, AI144435.1, AI982567.1, AW815621.1, AA788576.1, F33435.1, AA171398.1, AW425207.1, AI631440.1, AA101255.1, AW815443.1, AA676341.1, AW391454.1, AA669918.1, AA169326.1, AW815833.1, AW815622.1, AA101351.1, AW391447.1, AW815635.1, AA908462.1, U69195.1, AW815508.1, AW249892.1, AW815506.1, AW815512.1, AA126685.1, AW609613.1, AA044415.1, AA678797.1, AW381515.1, AW474060.1, AW381537.1, AW189578.1,

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- R12509.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, AW371378.1, AA705248.1, T23713.1, AW381482.1, AW381510.1, AW381496.1, AW381476.1, R19314.1, T70135.1, F05151.1, AI206928.1, AW801962.1, AW381459.1, AW843169.1, AW462450.1, AW610177.1, AW393428.1, AW016196.1, AW009270.1, AA092442.1, AW371229.1, AI658933.1, AI919572.1, AW384329.1, AI708578.1, AW381472.1, F37823.1, T79039.1, AA895510.1, AA705236.1, AC006391.7, AC016175.1, AL356136.1, AC017144.1, AL162420.3, AC009192.60, AC068789.3, AC012480.4, AC010552.3, AC023549.2, AC022931.3, AC022391.2, AL354999.1, AL160035.3, AL159978.2, AP001005.1, AP000590.3,
- SEQ ID NO.234  
NGO-St-115  
YS406/T7 3'
- L34543.1, L07872.1, L34544.1, NM\_015874.1, L08904.1, D14041.1, S63463.1, X17459.1, M81871.1, U60093.1, U60094.1, M81877.1, AE003830.1, AC005974.1, AC007270.2, AF049850.1, AF016494.1, AF035530.1, D25323.1, D90170.1, D90168.1, M64933.1, AA701607.1, AA641661.1, AI627646.1, AI962712.1, AI401150.1, AW131544.1, AW090508.1, AI953614.1, AI829826.1, AA042864.1, AW302357.1, AA640106.1, AI984992.1, AA903408.1, AW249681.1, AW235086.1, AI381502.1, AA483607.1, AI619912.1, AI291840.1, AA069672.1, AI580826.1, T67414.1, AI375729.1, AI023923.1, AI565611.1, AI334962.1, AI334964.1, AA501219.1, AI669755.1, N95392.1, AW005947.1, AI144435.1, AI982567.1, AW815621.1, AA788576.1, F33435.1, AA171398.1, AI631440.1, AA101255.1, AA676341.1, AW815443.1, AA169326.1, AW425207.1, AA669918.1, AW391454.1, AW815833.1, AA101351.1, AW815622.1, AA908462.1, AW815635.1, AW391447.1, AW249892.1, AW815508.1, AA044415.1, AW815506.1, AA678797.1, AA126685.1, AW815512.1, AW609613.1, U69195.1, AW381515.1, AW474060.1, AW381537.1, AW189578.1, AA156824.1, AW379059.1, AW371260.1, AI720441.1, AW371378.1, AW381482.1, AW381510.1, AW381496.1, R12509.1, AA705248.1, T23713.1, AW381476.1, AI206928.1, F05151.1, AW381459.1, R19314.1, AW843169.1, T70135.1, AW801962.1, AW610177.1, AW393428.1, AW016196.1, AW462450.1, AI658933.1, AW009270.1, AA092442.1, AW371229.1, AI919572.1, AI708578.1, AW384329.1, AW381472.1, F37823.1, AI274998.1, AA235124.1, W25228.1, AC006391.7, AC016175.1, AL356136.1, AC022173.4, AC009377.5, AC017144.1, AL162420.3,
- SEQ ID NO.235  
NGO-St-116  
YS1651/T3 5'
- M22382.1, NM\_002156.1, M34664.1, X54793.1, M22383.1, X55023.1, X53584.1, X53585.1, AC006511.5, M34661.1, AF071216.1, M34660.1, M34663.1, M34662.1, AL096817.12, M34562.1, AJ250915.1, AF227510.1, AL163248.2, U68562.1, D16852.1, AF040153.1, U87959.1, AF121264.1, U94594.1, U38963.1, AL031663.1, Y15783.1, AJ235272.1, AF103898.1, AF103897.1, X70868.1, AF075440.1, U96733.1, X56034.1, U20804.1, AJ249625.1, Z66568.2, U72247.1, AJ130947.1, AJ130877.1, AP001297.1, D50609.1, Z11547.1, Z12114.1, AF165812.1, X57520.1, X70867.1, AE003485.1, AF031929.1, U17244.1, Z49766.1, M33301.1, X99341.1, AF192796.1, L11390.2, L10917.1, Z12115.1, Z11546.1, L21006.1, L21008.1, L21007.1, X62578.1, AF076436.1, AF076435.1, AF076434.1, AF076433.1, AC006229.17, AF195273.1, AF062533.1, U45241.1, AF085694.1, AF003957.1, M98257.1, Z15160.1, X68263.1, AE003610.1, U40419.1, AC004721.1, M35600.1, AA186560.1, AA315828.1, AA190505.1, AA101281.1, AA196456.1, AA355063.1, AA220969.1, AL118805.1, AW107008.1, AA313717.1, AA211155.1, AW246390.1, AI133536.1, AA130735.1, AA307775.1, AI956302.1, AI526655.1, AA186742.1, AI876755.1, AI789073.1, AA147407.1, AA314982.1, AA066721.1, AA083150.1, AI049243.1, AA153935.1, AI788452.1, AA314648.1, AW211098.1, AI119103.1, AA073178.1, AI882194.1, AI875338.1, AA182547.1, AA179642.1, AA333493.1, AI663294.1, AA355152.1, AA308780.1, F06480.1, AW012138.1, AA114125.1, AA181753.1, AW258808.1, AI891951.1, AI316009.1, AI787944.1, AI931393.1, AW246054.1, AW045067.1, AA218257.1, AW319430.1, AA407305.1, AA361120.1, AW213301.1, AW259849.1, AW012331.1, AA415608.1, AI874815.1, AA375302.1, AA199785.1, AJ398447.1, AW229516.1, AA341141.1, AA355963.1, AW259968.1, R58784.1, AW258893.1, AA355415.1, C89446.1, AA314047.1, AA184322.1, AA087600.1, AA413960.1, AW260552.1, W41752.1, AA333568.1, AA793425.1, AA215942.1, AW773213.1, AL117921.1, AA026155.1, AW784168.1, AA158695.1, AA346637.1, AI980165.1, AI524820.1, N84903.1, AA537973.1, AI709970.1, AA027070.1, N88468.1, AA409877.1, AA096333.1, AA067313.1, AA530483.1, AA301042.1, AA093803.1, AW803755.1, AW803695.1, AC024884.6, AC032001.2, AF252831.1, AF252830.1, AF202031.1, AF189745.1, AC027473.2, AL354869.1, AL160258.3, AC020550.3, AF260011.1, AC008821.4, AC008840.3, AC008511.4, AC009077.5, AC016517.4, AP001561.1, AP000641.1, AL121980.6, AC010746.3, AC018953.5, AC007521.11, AC017670.1, AC023505.8, AC009800.6, AC024321.3, AC053499.2, AC009702.4, AC027301.3, AC007716.2, AC024986.2, AC006440.8, AC013618.3, AC026185.1, AC018811.3, AC018494.3, AC013802.2, AL138997.6, AL158054.5, AL139821.2, AL138683.2, AC068767.2, AC068639.3, AC068036.3, AC044841.2, AC011008.3, AC007996.3, AC010275.4, AC068576.1, AC027239.2, AC023275.2, AC021876.3, AC055878.1, AC047627.1, AC044783.1, AC008709.2, AC015911.4, AC013744.3, AC022484.3, AC011693.4, AC018862.3, AC019325.3, AC023375.2, AC009939.2, AC021304.2, AC019197.3, AC022069.1, AC017455.1, AL356107.2, AL121996.5, AL356059.1, AL133227.11, AL353707.1, AL161661.1, AP001998.1, AP001197.1, AP001096.2,
- SEQ ID NO.236  
NGO-St-116  
YS1651/T7 3'

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SEQ ID NO.237

NGO-St-116

30 YS1701/T3 5'  
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SEQ ID NO.238

NGO-St-116

YS1701/T7 3'

M22382.1, NM\_002156.1, M34664.1, AJ250915.1, AC006511.5, M22383.1, X53585.1, X54793.1, X53584.1,



AC004220.1, M34663.1, AL096817.12, AF227510.1, AL163248.2, X55023.1, U68562.1, M34662.1, M34661.1, M34660.1, M34562.1, AF025468.2, AF069298.1, AL161494.2, L36035.1, AE001727.1, X02895.1, AF240627.1, AF197942.1, AL109763.2, U58764.1, AC024848.1, AC011594.8, AE001112.1, AE000808.1, Z81571.1, X79205.1, AP000183.1, AP000038.1, AP000107.1, M74012.1, AC007320.2, AC011592.5, AC008122.15, U67599.1, U67521.1, 5 AL161505.2, AL133396.1, Z35719.1, AL118497.9, Z82253.1, Z70272.1, AL021367.1, AP001115.1, AA630404.1, AA826248.1, AI832486.1, AI609776.1, AI926703.1, AI627740.1, AA769669.1, AW004895.1, AI619432.1, AI570191.1, AW246607.1, AW131404.1, AI818534.1, AI922978.1, AI827012.1, AW102810.1, AI690942.1, AW573149.1, AA565131.1, AI961421.1, AI221866.1, AW276236.1, AI924961.1, AI956156.1, AA448453.1, AW177563.1, AI683208.1, AW469262.1, AI885544.1, AW410099.1, AI985757.1, AI678654.1, AA564099.1, AA102391.1, AI325539.1, AI189669.1, 10 AW304695.1, AW780292.1, AA595763.1, AW071129.1, AW157717.1, AW276334.1, AI217363.1, AW439804.1, AW117832.1, AA629677.1, AA600146.1, AA603962.1, AW156968.1, AW246632.1, AI801296.1, AI582821.1, AA167738.1, AI609928.1, AI571107.1, AA948019.1, AW513062.1, AA609838.1, AW675607.1, AA515520.1, AI565115.1, AI285386.1, AA617879.1, AW068921.1, AI521493.1, AI284071.1, AA847770.1, AI335167.1, AA577528.1, AA218869.1, AA181826.1, AW572206.1, AA978125.1, AA583474.1, AI023089.1, AW419186.1, AI075218.1, 15 AI983518.1, AA605126.1, AI612727.1, AW104022.1, AW084921.1, AA774671.1, AA479788.1, AI30632.1, AW516994.1, AW513837.1, AI744383.1, AA970442.1, AA196514.1, AI168478.1, AW085863.1, AI573195.1, AA219578.1, AA164508.1, AW236411.1, AW192162.1, AW572335.1, AA133938.1, AW674312.1, AC010746.3, AC024884.6, AC027473.2, AC032001.2, AL136079.3, AL138760.4, AC026299.2, AL354869.1, AC063980.1, AF252831.1, AF252830.1, AF202031.1, AF189745.1, AC008821.4, AC008840.3, AC008511.4, AL137180.3, AL160258.3, 20 AF260011.1, AC026746.3, AC016645.3, AC026750.2, AC026809.1, AC016517.4, AP001561.1, AP000641.1, AP000799.1, AC006909.1, AC009600.11, AC055839.2, AC013509.3, AL121980.6, AC008506.6, AC026610.2, AC021592.3, AC018406.2, AC021065.3, AL137072.1, Z93927.3, AC009822.3, AC068191.1, AC027003.2, AC016458.2, AC022269.3, AC018740.2, AC005308.6, AC011267.2, AF188028.1, AC012670.2, AC016998.1, AL356112.2, 25 AL136358.4, AL158839.2, AL109808.2,

## SEQ ID NO.239

NGO-St-116

YS1731/T7 3'

M22382.1, NM\_002156.1, M34664.1, AJ250915.1, AC006511.5, M22383.1, X53585.1, X54793.1, X53584.1, 30 AC004220.1, AL096817.12, M34663.1, AF227510.1, AL163248.2, X55023.1, U68562.1, M34662.1, M34660.1, M34661.1, M34562.1, AF025468.2, AF069298.1, AL161494.2, L36035.1, AF240627.1, AF197942.1, AL163218.2, AL109763.2, U58764.1, AC024848.1, AC011594.8, AC004038.1, AE000808.1, Z81571.1, AL096701.14, X79205.1, AP000183.1, AP000038.1, AP000107.1, M74012.1, AC007320.2, AF214118.1, AC005200.1, U67521.1, AL034429.1, AL161505.2, AL133396.1, Z35719.1, Z82253.1, Z70272.1, AP001115.1, AB019234.1, AA630404.1, AA826248.1, 35 AI832486.1, AI609776.1, AW246607.1, AA769669.1, AI818534.1, AA565131.1, AW573149.1, AI221866.1, AA448453.1, AI619432.1, AW177563.1, AI827012.1, AW004895.1, AI926703.1, AI924961.1, AW276236.1, AI627740.1, AW410099.1, AW102810.1, AI961421.1, AI956156.1, AW131404.1, AI570191.1, AI325539.1, AW157717.1, AI690942.1, AA564099.1, AI922978.1, AI189669.1, AW469262.1, AI217363.1, AI985757.1, AI885544.1, AI801296.1, AW780292.1, AW276334.1, AA629677.1, AA600146.1, AA595763.1, AW439804.1, AW117832.1, AI609928.1, AA603962.1, AA102391.1, 40 AW156968.1, AW071129.1, AW246632.1, AI678654.1, AI582821.1, AW304695.1, AA948019.1, AA167738.1, AW513062.1, AI683208.1, AI571107.1, AW675607.1, AA609838.1, AI285386.1, AA515520.1, AW068921.1, AI284071.1, AA617879.1, AI335167.1, AA847770.1, AA218869.1, AW572206.1, AI565115.1, AA577528.1, AA978125.1, AA181826.1, AW419186.1, AA583474.1, AI983518.1, AI023089.1, AW104022.1, AI521493.1, AA605126.1, AI075218.1, AA774671.1, AA479788.1, AA130632.1, AW516994.1, AW513837.1, AW084921.1, AI612727.1, AA970442.1, 45 AI744383.1, AA196514.1, AI168478.1, AI573195.1, AA219578.1, AA164508.1, AW572335.1, AW085863.1, AW674312.1, AA970965.1, AW192162.1, AA133938.1, AC010746.3, AC024884.6, AC027473.2, AC032001.2, AL136079.3, AL138760.4, AL354869.1, AC026299.2, AF252831.1, AF252830.1, AF202031.1, AF189745.1, AC008821.4, AC008840.3, AC008511.4, AC063980.1, AL137180.3, AL160258.3, AF260011.1, AC026746.3, AC016645.3, AC026750.2, AC026809.1, AC016517.4, AP001561.1, AP000641.1, AP000799.1, AC006909.1, AC055839.2, 50 AC008506.6, AC025073.2, AC026610.2, AC021592.3, AC018406.2, AC021065.3, AL137072.1, Z95311.10, Z93927.3, AC009822.3, AC068191.1, AC016458.2, AC018740.2, AC011267.2, AF188028.1, AC012670.2, AL356112.2, AL158839.2, AL158012.2, AL109808.2,

## SEQ ID NO.240

55 NGO-St-116

YS1784/T7 3'

AJ250915.1, M22382.1, NM\_002156.1, M34664.1, AC006511.5, M22383.1, X54793.1, X53585.1, X53584.1, 60 AC004220.1, AL096817.12, M34663.1, AF227510.1, AL163248.2, M34662.1, M34660.1, U68562.1, X55023.1, M34661.1, M34562.1, AF025468.2, AF069298.1, AL161494.2, L36035.1, AF197942.1, U58764.1, AC024848.1, AC011594.8, AC004195.1, AC005960.1, AE000808.1, Z81571.1, X79205.1, AP000510.2, AP000183.1, AP000038.1, AB023060.1, AP000107.1, M74012.1, AC007320.2, AC004921.1, AC008122.15, AC000108.1, U67521.1, AL161505.2, AL133396.1, Z35719.1, AL118497.9, Z82253.1, Z70272.1, AP001115.1, AA630404.1, AA826248.1, AI609776.1, AW246607.1, AI818534.1, AI832486.1, AW573149.1, AA769669.1, AA565131.1, AI221866.1, AA448453.1, AW410099.1, AW157717.1, AI325539.1, AI609928.1, AW131404.1, AW177563.1, AI217363.1, AW276236.1,

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AW117832.1, AI961421.1, AI926703.1, AI627740.1, AI189669.1, AW469262.1, AI985757.1, AI690942.1, AA600146.1, AI924961.1, AI619432.1, AI570191.1, AW513062.1, AW246632.1, AW102810.1, AI582821.1, AA564099.1, AW004895.1, AI922978.1, AI827012.1, AA603962.1, AA629677.1, AA102391.1, AW276334.1, AI956156.1, AW304695.1, AI678654.1, AI285386.1, AA948019.1, AW156968.1, AW780292.1, AW439804.1, AW071129.1, AI885544.1, AA595763.1, AI683208.1, AI801296.1, AI571107.1, AA515520.1, AW675607.1, AI284071.1, AW068921.1, AI335167.1, AA167738.1, AA617879.1, AA609838.1, AW572206.1, AA847770.1, AA218869.1, AW419186.1, AI565115.1, AA583474.1, AA978125.1, AA181826.1, AI023089.1, AA577528.1, AI983518.1, AA605126.1, AW104022.1, AA774671.1, AW513837.1, AA479788.1, AA130632.1, AW516994.1, AI521493.1, AI075218.1, AI612727.1, AA970442.1, AI573195.1, AI744383.1, AI168478.1, AA219578.1, AA164508.1, AW572335.1, AI196514.1, AI192162.1, AW104912.1, AA970965.1, AW236411.1, AA133938.1, AW674312.1, AC010746.3, AC024884.6, AC027473.2, AC032001.2, AL136079.3, AL138760.4, AL354869.1, AC026299.2, AF252831.1, AF252830.1, AF202031.1, AF189745.1, AC008821.4, AC008840.3, AC008511.4, AL137180.3, AL160258.3, AC063980.1, AF260011.1, AC026746.3, AC016645.3, AC026750.2, AC026809.1, AC016517.4, AP001561.1, AP000799.1, AP000641.1, AC006909.1, AC055839.2, AC008753.7, AC026610.2, AC018406.2, AC021065.3, AL137072.1, AC009822.3, AC068191.1, AC064839.3, AC022269.3, AC018740.2, AC005308.6, AC011267.2, AC013285.5, AF188028.1, AC012670.2, AC006875.1, AL356112.2, AL136358.4, AL159970.7, AL158839.2, AL109808.2,

SEQ ID NO.241

NGO-St-116

20 YS1796/T7 3'  
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- 35 SEQ ID NO.244  
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- 60 SEQ ID NO.245  
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YS025/T7 3'

-131-

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NGO-St-117  
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NM\_006117.1, AF153612.1, AF069301.1, AF244138.1, AF257175.1, NM\_011868.1, AF153613.1, AL163270.2, AP001725.1, AP000689.1, AB003151.1, U11419.1, NM\_012574.1, NM\_008171.1, NM\_000834.2, AC005232.1, AC011915.3, AC007535.3, U88963.1, AF111103.1, AC005304.1, U11287.1, U90278.1, M91562.1, D10651.1, AE003498.1, AC007000.2, AC004843.1, AC006014.2, AC004955.2, AC005488.2, AC004878.2, AC007786.1, AC002082.1, AC005071.2, AC006504.1, AC005355.1, U72724.1, AE000665.1, AL121767.3, AL133233.2, AB022216.1, AF260700.1, AC011525.4, AF182322.1, AC004953.1, AC006487.7, AC005796.1, AL352976.2, AL353820.1, AJ239322.3, AJ239318.3, Z75955.1, AJ009632.2, AP001342.1, AP001135.2, M16512.1, M80474.1, M13968.1, X79424.1, AI870279.1, AI807002.1, AL036852.1, AI565595.1, AI564314.1, W67775.1, AW270727.1, AI610377.1, AW662848.1, AA617696.1, AA934587.1, AI096931.1, AA628682.1, AW731836.1, AA913577.1, AI391743.1, AW474447.1, AI363079.1, AI336097.1, AI432577.1, AI352108.1, AI352327.1, AA969876.1, AA995606.1, W74527.1, AA622402.1, AI085901.1, AA027090.1, AI307399.1, AI287814.1, AA620556.1, AW194674.1, W79046.1, AW182085.1, AA085733.1, AA187157.1, AI625204.1, AI031865.1, AW591699.1, AA897169.1, AA972318.1, AI349588.1, AI674578.1, AI659404.1, AW302400.1, F36532.1,
- 55
- 60

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- AI371256.1, AA733183.1, AA531124.1, AA365494.1, F30300.1, AI370734.1, T90909.1, Z25096.1, AA027130.1, AA115569.1, T71475.1, AI432578.1, AW088726.1, AA721771.1, AA115089.1, T49643.1, R00622.1, T83325.1, AA426250.1, N93780.1, T83700.1, AA393863.1, AA282967.1, AI872750.1, R00626.1, AI471045.1, AW750808.1, AW369701.1, R08138.1, N74066.1, AI370415.1, AA658299.1, T55344.1, AA003997.1, AW744236.1, AW742885.1, AA250467.1, AW557746.1, AW208617.1, AA968175.1, AW322345.1, AI500088.1, AA260498.1, AA848318.1, AA958697.1, AI877303.1, AA397074.1, AA008542.1, AA036229.1, AW456866.1, AI931743.1, AA253686.1, AW743789.1, AI411403.1, AL033383.25, AL136309.3, AL355594.3, AC021873.7, AC068763.2, AC022912.3, AC034235.2, AC025224.3, AC025502.2, AC024325.2, AC019078.3, AL137142.8, AL133407.4, AL139254.3, AL354955.1, AP000916.2, AP001804.1, AC055832.2, AC004166.10, AC020947.5, AC010246.4, AC010348.3, AC009061.8, AC067929.1, AC025127.2, AC005073.2, AC007003.2, AC004867.2, AC027394.2, AC012350.3, AC010947.3, AC025740.1, AC018553.2, AC013532.2, AL355552.1, AL139294.1,
- SEQ ID NO.248  
NGO-St-117  
YS286/T7 3'
- NM\_006117.1, AF153612.1, AF069301.1, AF257175.1, AF244138.1, NM\_011868.1, AF153613.1, AP000689.1, AB003151.1, U11419.1, NM\_012574.1, NM\_008171.1, NM\_000834.2, AC005232.1, AC011915.3, U88963.1, AF111103.1, AC005304.1, U11287.1, U90278.1, M91562.1, D10651.1, AE003498.1, AC007000.2, AC004843.1, AC006014.2, AC005488.2, AC004878.2, AC007786.1, AC002082.1, AC005071.2, AC006504.1, AC005355.1, AC005273.1, U72724.1, U17243.1, AL121767.3, AL133233.2, AB022216.1, AC011525.4, AF024504.2, AC004953.1, AC007773.1, AC006487.7, AC005796.1, AL352976.2, AJ239322.3, Z75955.1, AP001342.1, AP001135.2, AI870279.1, AI807002.1, AL036852.1, AI564314.1, AI565595.1, W67775.1, AW270727.1, AI610377.1, AW662848.1, AA617696.1, AA934587.1, AI096931.1, AA628682.1, AW731836.1, AA913577.1, AI391743.1, AW474447.1, AI363079.1, AI336097.1, AI432577.1, AI352108.1, AI352327.1, AA969876.1, AA995606.1, W74527.1, AA622402.1, AI085901.1, AA027090.1, AI307399.1, AI287814.1, AA620556.1, W79046.1, AW194674.1, AW182085.1, AA085733.1, AA187157.1, AI625204.1, AI031865.1, AW591699.1, AA897169.1, AA972318.1, AI349588.1, AI674578.1, AI659404.1, AA365494.1, AW302400.1, F36532.1, AI371256.1, AA733183.1, AA531124.1, AA027130.1, AA115569.1, F30300.1, AI370734.1, T90909.1, Z25096.1, T71475.1, AI432578.1, AA426250.1, AW088726.1, T83700.1, AA393863.1, AA721771.1, AA115089.1, T49643.1, AA282967.1, R00622.1, T83325.1, N93780.1, AW750808.1, AI872750.1, R00626.1, R08138.1, AI471045.1, AW369701.1, N74066.1, AI370415.1, AA658299.1, AA003997.1, AW744236.1, AA250467.1, T55344.1, AA848318.1, AA968175.1, AW742885.1, AW322345.1, AW208617.1, AW557746.1, AI877303.1, AI500088.1, AA260498.1, AA958697.1, AA397074.1, AA008542.1, AA036229.1, AW456866.1, AI931743.1, AA253686.1, AI411403.1, W67774.1, AL033383.25, AL136309.3, AL355594.3, AC021873.7, AC068763.2, AC022912.3, AC034235.2, AC025224.3, AC025502.2, AC024325.2, AC019078.3, AL133293.18, AL137142.8, AL133407.4, AL139254.3, AL354955.1, AP000916.2, AP001804.1, AC055832.2, AC004166.10, AC020947.5, AC010246.4, AC010348.3, AC061712.2, AC009061.8, AC005073.2, AC010139.3, AC004867.2, AC027394.2, AC012350.3, AC011039.4, AC010947.3, AC025740.1, AC013532.2, AC005143.1, AL355487.1,
- SEQ ID NO.249  
NGO-St-118  
YS1802/T7 3'
- NM\_001655.1, X81198.1, AF111103.1, AF111102.1, S74341.1, AF151870.1, NM\_016049.1, AE003475.1, AL136295.2, U32692.1, AF019376.1, Z70680.1, AE003528.1, AC004931.1, AE000604.1, AC006050.1, AL117667.2, AL096862.18, Z46793.1, AL035250.17, AL031224.1, Z99289.1, AL109798.19, AL112548.1, L29789.1, AA412680.1, AI755123.1, AA102578.1, AA206349.1, AW055098.1, AA293170.1, AW439825.1, AW269634.1, AI076926.1, AI025067.1, AI700509.1, AI078164.1, AI697821.1, AA705915.1, AI160192.1, AI093354.1, AA165600.1, AA705055.1, AA527537.1, AA192464.1, AI653666.1, AI264667.1, AI650293.1, AI091869.1, AA506760.1, AI950897.1, AI380068.1, AI264617.1, AI125887.1, AA047461.1, AI890839.1, AI683902.1, N24749.1, N32156.1, AI302074.1, AA088764.1, N26132.1, AI040426.1, AI358017.1, AI141871.1, AW474078.1, AI523696.1, N32947.1, AA688242.1, AI961853.1, AI446329.1, AI002397.1, AA993720.1, AA707731.1, AA422132.1, H99310.1, AI879755.1, AI918396.1, AA804436.1, AA928305.1, AW168784.1, AA719418.1, AI087106.1, AI024105.1, AW129693.1, W15326.1, H94333.1, AI962023.1, W42458.1, N21273.1, AW194030.1, AA856562.1, AI758429.1, AA243440.1, AA434593.1, W85810.1, AI079791.1, H99597.1, N67805.1, AA808672.1, AW303758.1, AI769314.1, R76982.1, AI754941.1, N42618.1, H98545.1, AA599213.1, AI832336.1, AA811624.1, H88780.1, AI886101.1, AI474209.1, H88997.1, N94593.1, AI888666.1, AA055972.1, AA788790.1, AA491237.1, AI401139.1, H96031.1, T99642.1, AA598401.1, AA026110.1, Z40496.1, AI658990.1, AP000941.2, AP000846.1, AP000869.1, AC019068.3, AC019509.1, AC010015.3, AC036149.2, AC027187.2, AC025241.2, AC026015.2, AC027724.1, AC012532.3, AC015914.3, AC022658.3, AC024732.2, AC016276.2, AC002317.1, AL163952.1, AL135929.4, AC000380.1, AL135909.3, AC020636.4, AC023892.11, AC010856.3, AC055864.2, AC023156.3, AC068590.1, AC025079.3, AC021269.3, AC013670.3, AC021378.3, AC060765.1, AC058803.1, AC021150.5, AC013386.4, AC019162.3, AC027521.1, AC018425.3, AC012274.2, AC024231.3, AC025978.1, AC013331.4, AC016418.4, AC023018.2, AC021567.2, AC011783.3, AC012436.4, AC020636.3, AC010066.5, AC011892.3, AC014423.1, AL121919.13, AL353638.2, AL160285.5, AL139284.3, AL356033.1, AL354000.2, AL354985.2, AL161451.4, AL157950.3, AL353774.1, AL160290.3, AL139003.1, AP001393.1,

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## SEQ ID NO.250

NGO-St-119

YS334/T3 5'

- 5 NM\_003146.1, M86737.1, S50213.1, L08814.1, L08815.1, U84139.1, AB004793.1, AE003462.1, X68408.1, L08825.1, AL031904.1, AL035653.12, AC007058.2, U40759.1, NC\_001145.1, AE002662.1, AE002914.1, AE003202.1, AE002711.1, AC007285.3, AL163298.2, AL163002.1, S74619.1, Z48622.1, AP001753.1, AB001517.1, AP001055.1, Z79396.1, AW247262.1, AA258912.1, AA443507.1, AA085435.1, AA312302.1, F07281.1, AA359039.1, D55248.1, D54571.1, D54563.1, D54952.1, D54973.1, AW802206.1, D53930.1, AA355756.1, AA404188.1, AI556014.1, AA104553.1, AL138347.1, AW489221.1, AA253486.1, AW320565.1, AA088369.1, H10266.1, AW401443.1, D77299.1, AW381661.1, 10 AA993395.1, AA464881.1, AA036329.1, AI913779.1, AA476079.1, AA306252.1, AA590151.1, AW748405.1, AW366265.1, AA130307.1, AI789443.1, AW378315.1, AW269617.1, AW370347.1, AW480897.1, AA497585.1, AW536819.1, AW536546.1, AU060291.1, AA162184.1, W07230.1, AP000781.2, AC020482.1, AC009182.3, AL139094.5, AC044849.2, AC020624.5, AC016588.5, AC010741.3, AL161790.3, AC068888.2, AC013552.4, AC022413.3, AC011472.5, AC068473.1, AC024176.4, AC019023.3, AC019286.4, AC024462.2, AC020561.2, AC016441.4, 15 AC022770.4, AC025303.1, AC006286.13, AC021638.5, AC018018.1, AC018205.1, AC003656.1, AL356318.1, AL355178.2, AL133463.8, AL160401.4, AL139816.4, AL158160.1, AL118500.5,

## SEQ ID NO.251

NGO-St-119

20 YS334/T7 3'

- NM\_003146.1, M86737.1, S50213.1, U84139.1, L08814.1, AC007967.3, AC017111.4, AC026237.4, AC005313.2, AF130357.1, AC004918.1, AF131217.2, AF165124.1, AL163247.2, AL021938.1, AL035534.1, AB037738.1, AI200891.1, AI832834.1, AI694393.1, AI597819.1, AA773470.1, AA640958.1, AI989881.1, AI954549.1, AA669346.1, AL043692.1, AA872063.1, AW771391.1, AI653466.1, AA488456.1, AI770053.1, AI719199.1, AA181676.1, AI768076.1, AW250844.1, 25 AI769368.1, AI326218.1, AI292284.1, AA102606.1, AW583325.1, AA630377.1, AW246563.1, AI803290.1, AW469194.1, AW072040.1, AI801767.1, AA129398.1, AA129437.1, N47701.1, AW055203.1, AA204842.1, AA403256.1, AW162590.1, AW873160.1, N47715.1, AA428207.1, AI802539.1, AW474265.1, AW517489.1, AA155636.1, AA187844.1, AI708178.1, AI298177.1, AA084865.1, AW196881.1, AI802262.1, AA223606.1, AA188417.1, AW182589.1, AW601976.1, AI125376.1, AA983384.1, AI669267.1, AA047175.1, AI369594.1, AA640599.1, 30 AA629829.1, AA506517.1, AA426576.1, AI034453.1, AI927125.1, AI198409.1, AA088196.1, AA644298.1, AA172185.1, AI024913.1, AA282185.1, AW772651.1, AA418911.1, AA679982.1, AA232539.1, AA928645.1, AI421368.1, AW516350.1, AI249088.1, AA770296.1, AL042406.1, AI913779.1, AA102637.1, W92454.1, AW732257.1, AW194956.1, AI433062.1, AA203343.1, AA581113.1, T29388.1, AA258817.1, AA173277.1, AW873703.1, AI569301.1, AA522909.1, H10212.1, AW138326.1, AI630694.1, AI475149.1, AA367901.1, AP000781.2, AC068719.1, AL355364.3, AC021659.7, 35 AC008383.4, AC010757.2, AC009475.3, AC012291.3, AC027118.2, AC023547.2, AC026245.1, AC011808.3, AC007856.6, AC015665.2, AL136227.4, AL356094.1,

## SEQ ID NO.252

NGO-St-120

40 YS357/T3 5'

- NM\_013285.1, L05425.1, U69600.1, AL034379.8, AL021571.1, AB015478.1, X99436.1, AC024751.1, AC006920.10, NM\_009722.1, NM\_001681.1, AC006581.16, AJ223584.1, AJ131821.1, AL121578.1, AL008715.1, X52496.1, X02814.1, M23115.1, M23114.1, Z11500.1, J04703.1, AF235167.1, AE003511.1, AC002045.1, AC007216.2, U95742.1, AC002299.1, AF196970.1, AC007283.3, AF013149.1, AF152363.1, AC005844.7, AC005841.3, AF001549.1, 45 AC000385.1, AL049988.1, AL109865.36, Z50082.1, Z68325.1, Z82204.1, AL049849.1, S75106.1, AK000019.1, AB020863.1, X07653.1, AA373618.1, AW245855.1, AW161434.1, AW409934.1, AW163245.1, AA126101.1, AA690847.1, AW362598.1, AW377646.1, AA858436.1, AL024316.1, AW377648.1, AW427911.1, H35824.1, AI112354.1, AI573674.1, AA684606.1, AI035443.1, AA316055.1, AA171883.1, AV125438.1, AI853194.1, AA308223.1, AW326870.1, AV125326.1, AA692026.1, AV138378.1, AA303227.1, AA581348.1, AW765532.1, AA989948.1, 50 C70491.1, AW773907.1, D23001.1, AV442312.1, AW650351.1, AI994797.1, AI488290.1, N38238.1, T80141.1, AW736578.1, AI077091.1, AI908898.1, AI847850.1, AI776439.1, AI467314.1, AI382397.1, AI290588.1, AI091365.1, AA414121.1, AA409715.1, AA038677.1, AW738493.1, AI709211.1, AI661426.1, AI482631.1, AI114591.1, D78236.1, AA742179.1, AA744826.1, AA663314.1, AA594218.1, AA452237.1, AA410224.1, AA298534.1, AA199847.1, H74324.1, R99587.1, AC023077.3, AC027731.2, AL355880.2, AC011124.3, AC018953.5, AC023502.3, AC026155.3, AC024905.7, 55 AC067611.1, AC064107.1, AC056245.1, AC033416.1, AC027813.1, AC021828.2, AL138975.1, AC026677.2, AC022164.4, AC022147.4, AC023398.2, AC027006.2, AC025043.3, AC017041.2, AC016838.3, AC023448.2, AC021481.3, AC019325.3, AC023958.2, AC025279.1, AC022408.3, AC016492.1, AP001767.1, AP001120.1,

## SEQ ID NO.253

60 NGO-St-120

YS357/T7 3'

- NM\_013285.1, L05425.1, AL034379.8, U69600.1, AC007020.4, AF085279.1, L39991.1, AF176688.1, AC006200.2, AE003829.1, NM\_010393.1, NM\_006574.1, NM\_002824.1, AF126482.1, AF125444.1, AF059274.1, AF088905.1, AC005515.1, AF016684.1, AL121748.6, Z72514.1, U20374.1, U47326.1, X16423.1, X16203.1, X16197.1, U07055.1,

X64053.1, X16481.1, X65748.1, X00246.1, Y13586.1, Y10211.1, M24398.1, M27134.1, M23445.1, L29190.1, M27034.1, J00393.1, M63790.1, AC000365.1, NM\_010398.1, AC007281.3, AF041855.1, AF057279.1, AF082510.1, U88154.1, U88153.1, U96752.1, U91424.1, Z68106.1, AL020997.1, AL110509.2, X16198.1, X16424.1, AB021155.1, M11284.1, L00606.1, AW157242.1, AA902387.1, AI925558.1, AI628921.1, AW070650.1, AA401208.1, AW409935.1, AW162279.1, 5 AA722289.1, AW172793.1, AA126418.1, AA780182.1, AA857353.1, AW804193.1, AW156969.1, AW183614.1, AI376281.1, AI826742.1, AA582490.1, AA446557.1, AW246802.1, AI474094.1, AA483614.1, AA934590.1, AA846248.1, AI253092.1, AA888018.1, AW804232.1, AI699045.1, AI954511.1, AA171554.1, AI867001.1, AI760439.1, AW804255.1, AI763044.1, AW804270.1, AI825244.1, AI671605.1, AA126000.1, AI702310.1, AA766044.1, AI798554.1, AW250835.1, W81287.1, AW768894.1, AA635139.1, AW002316.1, AW362969.1, AW118384.1, AA493881.1, AI470650.1, 10 AA659293.1, AA863491.1, AA196109.1, AA831455.1, AI244063.1, AA659297.1, N32569.1, AI245761.1, AA515590.1, AI909114.1, T27737.1, AA524198.1, AW607751.1, AI345764.1, AW301566.1, AI310849.1, AI310651.1, AW268086.1, AI589981.1, AA056760.1, AW268169.1, AA403201.1, AL135350.1, AA614309.1, AI907635.1, AW529039.1, AI112872.1, AI060050.1, AA546717.1, AW532741.1, AW557260.1, AV220510.1, AI646349.1, AI536459.1, AW653179.1, AI853259.1, AV090573.1, AI058723.1, AV310274.1, AV236721.1, AV236719.1, AV167761.1, 15 AW111676.1, AV311465.1, AV296078.1, AV225966.1, AA646750.1, AA472792.1, AA111295.1, AC027731.2, AL355880.2, AC023077.3, AC026348.3, AC068683.1, AC022553.2, AC023000.2, AC010058.5, AC013019.1, AC010195.7, AC026992.2, AC027820.2, AC021884.2, AC022388.2, AC022937.3, AC019056.4, AC017422.1, AC015232.1, AC007438.6, AC006086.7, AC006087.12, AC002490.1, AL159141.1, AC044907.2, AC022558.3, AC044814.2, AC025036.6, AC051623.1, AC012145.3, AC021523.3, AC021296.2, AC007477.5, AC021959.4, 20 AC006279.6, AC015535.4, AC020585.5, AC025110.1, AC010009.4, AC016767.3, AC019749.1, AC018050.1, AC016210.1, AC015148.1, AC009454.1, AL136090.10, AL135840.7, AL133341.9, AP001390.1, AP001120.1,

SEQ ID NO.254

NGO-St-121

25 YS363/T3 5'

AF098638.1, NM\_004703.1, X77723.1, X91141.1, U70777.1, D85844.1, D86066.1, AB001750.1, D88828.1, D38038.1, Y08613.1, AF164343.1, AC000021.1, AB022176.1, AL031003.1, AC011309.4, AC002089.1, AC013454.4, AC003019.1, U58108.1, L78833.1, AF051934.1, AL163268.2, AC000119.1, AL022476.2, S86117.1, AJ229042.1, AB018418.1, AC010151.3, AC024080.2, AC008444.4, AC002340.2, AE003833.1, AE003798.1, AF035218.1, AC006249.1, 30 AC004657.1, AF027868.1, AL031661.28, AL161587.2, AL117188.1, AL049845.7, AL031431.8, AL022239.1, U22110.1, D90899.1, Z79479.1, AB020865.1, Z34519.1, Z99114.1, AW501546.1, W28259.1, W27092.1, AW371635.1, AL042125.1, AA611522.1, AA614931.1, AW748799.1, AA110819.1, Z28809.1, AW304131.1, AI371714.1, AW450989.1, AV162434.1, AI024379.1, AI288155.1, H24233.1, H16513.1, AW371421.1, AW496353.1, R40226.1, AA208526.1, AA075857.1, AA543909.1, AW501200.1, AW385206.1, AW760996.1, AW558606.1, AW558583.1, AW298142.1, AW294127.1, AI874594.1, AI835959.1, AI788080.1, AV100560.1, AI537352.1, AI411951.1, AI410456.1, AA858493.1, AI309599.1, 35 AI194657.1, AI182965.1, AI152676.1, AI144668.1, AI060676.1, AI046764.1, AA959394.1, AA940384.1, AA797665.1, AA763173.1, AA717573.1, AA710050.1, AA709538.1, AA561671.1, AA408328.1, AA285493.1, AA270256.1, AA241245.1, AA230889.1, AA213293.1, AA104682.1, AA104275.1, AA104274.1, AA087023.1, AA062156.1, AA061500.1, AA031128.1, AA028486.1, AA011772.1, W63860.1, W34388.1, W18032.1, W09805.1, AW694402.1, 40 AW691053.1, AV213344.1, AV007100.1, AA892832.1, AA489256.1, T76002.1, AC015727.3, AC006338.3, AC007248.2, AC007039.3, AC006990.3, AC006983.2, AC053490.1, AC006982.1, AC036236.1, AC026852.1, AC020855.2, AC021307.3, AC010089.2, AC024353.2, AC011753.2, AC020562.1, AC013575.1, AC011900.1, AL163760.1,

SEQ ID NO. 255

45 NGO-St-121

YS363/T7 3'

AC004148.1, AL157499.1, AL050211.1, AC009275.5, AC008154.6, AE003690.1, AE003653.1, AC005524.1, Z47358.1, X98238.1, AI972322.1, AA193309.1, AA528241.1, AW235706.1, AA527684.1, AI436191.1, AA890512.1, AW299850.1, AA767452.1, AI580941.1, AI056055.1, AI130923.1, AA283713.1, AI418205.1, AI056706.1, AI808670.1, AW137415.1, 50 AI400431.1, AW295892.1, AA846649.1, AA960854.1, AI222234.1, AI084465.1, AA479888.1, AA917434.1, AA960792.1, AA290870.1, AW089851.1, AI090024.1, AI078176.1, AA683232.1, AI023887.1, AA706411.1, AA040801.1, AI632800.1, AI367258.1, AA693619.1, W15394.1, T03894.1, AI955173.1, AI269900.1, AA218890.1, AI669191.1, AA760918.1, AI826582.1, AI910510.1, AW082288.1, N52967.1, Z39660.1, Z28661.1, W58520.1, AA954763.1, R50797.1, AA041239.1, H90518.1, AI349313.1, AI301633.1, AA412174.1, AI800039.1, F26651.1, AW235792.1, AA621533.1, AA194263.1, 55 AI932942.1, H09347.1, AI953061.1, R40788.1, AW752307.1, AA216603.1, AW351827.1, H73642.1, Z28597.1, AW137802.1, H51737.1, N45966.1, AW576920.1, Z20686.1, Z28596.1, Z24941.1, AA425331.1, N44279.1, AA766379.1, AI742337.1, AA426446.1, AI696486.1, Z72398.1, D20547.1, AA778438.1, AV331582.1, AW046470.1, AA472952.1, AA120705.1, AV357525.1, AA409778.1, AC016370.4, AC026940.2, AC026455.2, AC015932.4, AC019267.3, AC018853.3, AC009074.2, AC009201.3, AC022549.1, AC014455.1, AC017510.1, AC006491.23, AC011631.1, 60 AL157823.3, AP001847.1, Z92859.1,

SEQ ID NO.256

NGO-St-122

YS1742/T3 5'

-135-

NM\_005089.1, D49677.1, U51224.1, D49676.1, AC004106.1, NM\_009453.1, D45205.1, NM\_011663.1, S69507.1, D26474.1, D17407.1, U92882.1, Z74476.1, AC002530.1, U80017.1, AL031767.13, AL133100.1, AL096854.5, Z99279.1, M83200.1, AP000002.1, AK000538.1, NC\_001139.1, AC005250.1, AC003074.1, AC004451.1, AC004882.2, AC007402.3, AC009992.5, AC004947.2, AF098999.1, AL121754.18, U60414.1, U62631.1, U57971.1, AB013003.1, AB013004.1, AP000173.1, AP000333.1, AW866867.1, AI417175.1, AW371109.1, AW137848.1, AI200960.1, N80309.1, AA845804.1, AA320008.1, AA028127.1, AA028151.1, AA814970.1, AA814962.1, AA920561.1, AA331011.1, AW364105.1, AI598939.1, AW144684.1, AW356771.1, AW805221.1, AI472111.1, AW345188.1, AW535394.1, AI576737.1, AI454541.1, AI112465.1, AA601026.1, AI112441.1, AI663887.1, AA388471.1, AW383892.1, AV357914.1, AW826265.1, AW613523.1, AW514825.1, AV331731.1, AW117909.1, AV149324.1, AV124185.1, AV036810.1, AA841469.1, AA771282.1, AA507133.1, AA199064.1, Z74661.1, W27716.1, AV440680.1, AW671805.1, AW569275.1, AV359278.1, AV212567.1, AW039499.1, AI989107.1, AI946720.1, AI868501.1, AV117593.1, AI763597.1, AV062802.1, AI755024.1, AV032630.1, AI648156.1, AI594159.1, AI466310.1, AI452794.1, AI412501.1, AI381209.1, AI232722.1, AI101718.1, AI011347.1, AI266800.1, AI114436.1, AI058893.1, AA807323.1, AA763112.1, AA709977.1, AA600133.1, AA545349.1, AA519216.1, AA452591.1, AA424001.1, AA329479.1, AA326345.1, Z81248.1, AA078585.1, C07041.1, C06862.1, C06853.1, H34402.1, AC008536.5, AC008461.4, AC008812.6, AC008763.4, AC017027.4, AC016287.3, AC011257.3, AL136314.4, AC025259.4, AC068227.1, AC020985.4, AC018429.3, AC019244.2, AL139113.4, AL137004.2, AC069141.1, AC063954.2, AC046141.3, AC007641.10, AC067960.2, AC018728.2, AC009245.8, AC027495.2, AC025669.2, AC044808.1, AC023841.2, AC023421.2, AC026513.2, AC015916.3, AC019049.2, AC016814.3, AC011985.3, AC018671.5, AC016503.2, AC021329.3, AC021563.1, AC011094.2, AL121983.7, AL157361.6, AL139419.1, AP000654.1,

SEQ ID NO.257

NGO-St-122

YS1742/T7 3'

NM\_005089.1, AC004106.1, D49677.1, U51224.1, D49676.1, NM\_011663.1, NM\_009453.1, S69507.1, D45205.1, D26474.1, D17407.1, AL031317.1, AL139078.2, AB026659.1, AW194326.1, AW089584.1, AI991464.1, AI828556.1, AA430135.1, AA723697.1, AI634052.1, AW237119.1, T67521.1, AA377829.1, AW515964.1, AA569819.1, T67543.1, AA601026.1, AA669459.1, AW609046.1, AI663908.1, AI663887.1, AI893901.1, AI636519.1, AI632192.1, H41170.1, AC008536.5, AC008461.4, AC008451.3, AC040954.1, AC007569.8, AC027671.2, AC016823.4, AC021594.3, AL138881.4, AP001641.1,

SEQ ID NO.258

NGO-St-123

YS1702/T7 3'

U40705.1, AF043911.1, NM\_003218.1, U74382.1, AF003001.1, AC006572.2, AL163204.2, NM\_009352.1, U65586.1, X93511.1, U70993.1, L63545.1, AC004484.2, AC004617.1, U47029.1, D83257.1, Y17297.1, AC011738.4, AE003685.1, NM\_009263.1, AL033534.1, Z47809.1, S78177.1, X13986.1, X51834.1, X16151.1, J04806.1, NC\_001145.1, AC004667.2, AE003478.1, AE003432.1, AC002080.1, AC004964.2, AC007285.3, Z36238.1, Z48618.1, AL036326.1, AA467901.1, N68057.1, AW772242.1, AI394003.1, AA135978.1, AA135764.1, AA467846.1, T76958.1, AA463246.1, AW152089.1, F13251.1, AW088675.1, R70911.1, AW860774.1, AA468251.1, AL046407.1, AI347136.1, AA317158.1, AI524143.1, Z45971.1, AI144010.1, AA207271.1, T63517.1, AI802125.1, AA468235.1, AI689994.1, AI680979.1, AW003979.1, AA529658.1, R68526.1, AI125634.1, AW197488.1, AI088591.1, AA204808.1, AI989793.1, Z19923.1, AI553354.1, R25990.1, AI313657.1, AI313655.1, AW367580.1, AI653818.1, AA982217.1, AW822952.1, AW413558.1, AW413468.1, AW412565.1, AW412480.1, AW411784.1, AW261735.1, AW260247.1, AW260085.1, AW259661.1, AW240668.1, AW240555.1, AW215800.1, AW212687.1, AW209307.1, AW209207.1, AW209119.1, AW208838.1, AW113907.1, AI987812.1, AI929854.1, AI891858.1, AI875465.1, AI875197.1, AI847805.1, AI839505.1, AI802541.1, AI790405.1, AI788611.1, AV017671.1, AV001287.1, AI648742.1, AI647513.1, AI528600.1, AI325605.1, AI282135.1, AI182295.1, AI132382.1, AU021551.1, AI043071.1, AI043053.1, AI042865.1, AI035296.1, AA986704.1, AA980925.1, AA839469.1, AA798241.1, AA789592.1, AA591084.1, AA563324.1, AA537448.1, AA145872.1, AA122501.1, AA073811.1, W08572.1, AL137013.3, AL050303.2, AC022893.2, AF164115.1, AC011941.4, AC012670.2, AL162851.3, AC068925.1, AC023087.3, AC011904.2, AC024067.3, AC024095.6, AC021771.2, AC018453.3, AC015364.1, AC017348.1, AC008172.1, AC055808.2, AC011346.3, AC017014.3, AC026903.2, AC016486.4, AC012288.2, AC012602.2, AC014153.1, AL139162.3, AL009027.1,

55 SEQ ID NO. 259

NGO-St-124

YS033/T3 5'

AF039690.1, AF161348.1, AC006041.2, AC004636.1, AE003598.1, AE003485.1, NM\_007186.1, AC005694.3, AC005529.7, AC005527.3, AC006221.1, AC004755.1, AF049105.1, AF022655.1, AL121586.28, Z47074.1, AP000965.2, U48937.2, AE003029.1, AF163441.1, AF123008.1, AF123007.1, AF122994.1, AF092091.1, AL137686.1, Z82185.1, AL035070.3, AJ011930.1, AP001068.1, AP001067.1, M98498.1, W29097.1, AI092201.1, AA690806.1, AA155014.1, AV127431.1, AA089195.1, AI967815.1, AI865255.1, AV359357.1, AV328696.1, AV287587.1, AV313495.1, AV272703.1, AV233789.1, AV233050.1, AA143515.1, AW708128.1, AW368913.1, AV338709.1, AV332139.1, AV290604.1, AV323766.1, AV027087.1, AI240775.1, AI170252.1, AI038890.1, AW679928.1, AW584240.1,



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AW581584.1, AW581582.1, AW573270.1, AW518642.1, AW516804.1, AW436684.1, AW369753.1, AW341252.1, AV354655.1, AW134807.1, AI969272.1, AI949771.1, AI948870.1, AI924168.1, AI914290.1, AI892918.1, AI871649.1, AI832248.1, AI830664.1, AI824895.1, AI819076.1, AI819130.1, AL037429.1, AI796870.1, AI769675.1, AI717994.1, AI708155.1, AI700048.1, AI697939.1, AI697687.1, AI689763.1, AI660476.1, AI655335.1, AU059236.1, AI621281.1, AI394537.1, AI379706.1, AI341342.1, AI304914.1, AI301627.1, AI300957.1, AI299037.1, AI298964.1, AI292090.1, AI290292.1, AI224563.1, AI167134.1, AI146249.1, AI140672.1, AI089910.1, AI039908.1, AI016407.1, AA995707.1, AA973566.1, AA967806.1, AA938631.1, AA907234.1, AA780678.1, AA742364.1, AA682624.1, AA591111.1, AA452630.1, AA252245.1, AA252941.1, AA242923.1, AA153891.1, W65797.1, W05501.1, N70619.1, D81647.1, AC024509.2, AL355978.2, AC019168.3, AC023267.2, AC024691.2, AC009011.2, AC034307.2, AC022983.2, AC015865.1, AC013902.1, AC017166.1, AC006839.13, AL139226.14, AC035146.2, AC007640.2, AC012411.3, AC021822.3, AC013829.4, AC021670.2, AL162453.4,

SEQ ID NO. 260

NGO-St-124

YS033/T7 3'  
AF039690.1, U79271.1, AL117525.1, AC009479.3, AC005358.1, AF136378.1, AC005081.2, AF045555.1, AL031650.21, AC006919.5, AC010967.2, AC008056.6, NM\_012776.1, AC005386.1, NM\_001619.2, U42580.2, AC007538.5, S81843.1, U08438.1, Z68282.1, AL121757.7, AL049544.4, AL031681.13, S48813.1, U39674.1, L23127.1, M34073.1, M80776.1, X61157.1, AB025639.1, M74822.1, M87854.1, X53421.1, AI735499.1, AW028371.1, AI445418.1, AI266387.1, AI288955.1, AW193663.1, AI298467.1, AI168222.1, AI148323.1, AI140814.1, AI089322.1, AA879456.1, AA843811.1, AA829894.1, AA102109.1, AA029201.1, W72147.1, N51485.1, AI808317.1, AI033069.1, AA161465.1, AA812519.1, N64528.1, H99906.1, AA886109.1, R71679.1, AI970343.1, AA744290.1, AW021346.1, AA099913.1, AW195719.1, AI267979.1, AA083859.1, AI038590.1, N51277.1, AA883684.1, R07471.1, H98684.1, R36854.1, F25334.1, R39448.1, AA083954.1, R54092.1, H09074.1, AA346369.1, AA910762.1, AW873705.1, N21975.1, D59844.1, AW195087.1, H11525.1, AA971254.1, W77907.1, W29097.1, AW057648.1, AL041060.1, AI659852.1, AA878973.1, AW392482.1, AI057361.1, AA715235.1, F35739.1, AW427844.1, AW022199.1, AI963422.1, AA860455.1, AA026096.1, T26899.1, AI481147.1, N71178.1, AW413553.1, AW046739.1, AI529534.1, AI661769.1, AA269966.1, AI614472.1, AA026516.1, AI713205.1, AI575014.1, AI112396.1, AI073194.1, AI651890.1, AI575171.1, AA466212.1, AW181975.1, AI888595.1, AV162955.1, AI452798.1, AI167638.1, AW495689.1, AI397450.1, AW547034.1, AW479264.1, AC024079.2, AC022960.2, AL161723.3, AP001333.1, AC044855.2, AC060801.2, AC018648.2, AC068004.1, AC009623.3, AC013699.2, AC021912.3, AC018685.5, AC016675.4, AF202962.1, AL139349.16, AL132661.15, AL117190.2, AC010798.6, AC037488.2, AC036143.2, AC034212.3, AC008377.3, AC018640.1, AC009444.2, AC025803.2, AC021417.3, AC026750.2, AC024242.2, AC026809.1, AC022882.3, AC016721.4, AC024342.2, AC009923.3, AC022828.2, AC023002.1, AC011237.3, AC017078.3, AC011290.2, AL080314.29, AL163540.3, AL162632.1, AL353713.1, AL158068.4, AL159973.2, AL133501.1, AP001586.1, AP001023.1, AP000425.1,

SEQ ID NO.261

NGO-St-124

YS173/T3 5'  
AF039690.1, AF161348.1, AC006615.1, AC006041.2, AC004636.1, AB006709.1, AE003598.1, AC005070.1, AC007632.4, AC005041.2, AC006221.1, Z47074.1, U48937.2, AC007019.4, AC011751.2, AF145727.1, AF164622.1, AF163441.1, AF204231.1, AC010870.4, AC005589.1, AC008072.3, AF092091.1, AF009623.1, AC004048.1, AC004257.1, AL163300.2, AL137686.1, U88309.1, AL021492.1, Z46787.1, Z94057.1, AL035070.3, AP001819.1, AJ011930.1, AP001068.1, AP001067.1, AB029041.1, AB020662.1, D84549.1, M98498.1, AI092201.1, AA155014.1, W29097.1, AW150169.1, AV127431.1, AA089195.1, AI606060.1, AI967815.1, AV359357.1, AV328696.1, AV287587.1, AV313495.1, AV272703.1, AV233789.1, AV233050.1, AA690806.1, AW708128.1, AV338709.1, AV332139.1, AV290604.1, AV323766.1, AV027087.1, AI240775.1, AI170252.1, AW679928.1, AW584240.1, AW581584.1, AW581582.1, AW369753.1, AV354655.1, AL044559.1, AL037429.1, AU059236.1, AA780678.1, D81647.1, AC024509.2, AL355978.2, AC019168.3, AC023267.2, AC024691.2, AC018403.4, AC009011.2, AC012473.5, AC012487.3, AC006724.1, AP001523.1, AC037470.2, AC040171.2, AC009636.3, AC025660.2, AC022983.2, AC023750.1, AC015865.1, AC016040.2, AC017166.1, AL354654.1, AL138479.1,

SEQ ID NO.262

NGO-St-124

YS173/T7 3'  
AF039690.1, U79271.1, AL117525.1, AF136378.1, AL031650.21, X79703.1, AC006919.5, AC008056.6, NM\_012776.1, NM\_001619.2, AF193021.1, AC007538.5, S81843.1, AF121782.1, AF064857.1, AL163281.2, AL133283.9, U08438.1, Z50044.1, Z68282.1, AL121757.7, AL049544.4, AL031681.13, S48813.1, U39678.1, U39674.1, L23127.1, M34073.1, M80776.1, X61157.1, M74822.1, M87854.1, X53421.1, AI735499.1, AW028371.1, AI445418.1, AI266387.1, AI288955.1, AW193663.1, AI298467.1, AI168222.1, AI148323.1, AI140814.1, AI089322.1, AA879456.1, AA843811.1, AA829894.1, AA102109.1, AA029201.1, W72147.1, N51485.1, AI808317.1, AI033069.1, AA161465.1, AA812519.1, N64528.1, H99906.1, AA886109.1, R71679.1, AI970343.1, AA744290.1, AW021346.1, AA099913.1, AW195719.1, AI267979.1, AA083859.1, AI038590.1, N51277.1, AA883684.1, R07471.1, H98684.1, R36854.1, R39448.1, F25334.1, AA083954.1, R54092.1, H09074.1, AA346369.1, AA910762.1, AW873705.1, N21975.1, W29097.1, D59844.1, AW195087.1, H11525.1,

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AA971254.1, W77907.1, AW057648.1, AL041060.1, AI659852.1, AA878973.1, AW392482.1, AI057361.1, AA715235.1, F35739.1, AW022199.1, AW427844.1, AA860455.1, AI963422.1, AA026096.1, AI481147.1, T26899.1, AW413553.1, AW046739.1, AI529534.1, AI661769.1, AA269966.1, N71178.1, AI614472.1, AI713205.1, AI575014.1, AI112396.1, AI073194.1, AA026516.1, AI651890.1, AI575171.1, AA466212.1, AV162955.1, AA690806.1, AI397450.1, AC022960.2, AP001333.1, AC044855.2, AC060801.2, AC018648.2, AC068004.1, AC013699.2, AC026224.1, AC021912.3, AC018685.5, AF202962.1, AL139349.16, AL132661.15, AL117190.2,

SEQ ID NO.263

NGO-St-125

10 YS3710/T3 5'

AF099990.1, AF068261.1, D88190.1, AC005950.1, AC001228.1, D64137.1, NM\_002840.1, AF099988.1, AL137556.1, Y19224.1, Y00815.1, NM\_000076.1, AC024753.1, AE003481.1, AE003458.1, NM\_002653.1, AF109719.2, AC004367.1, AF009648.1, AL157480.1, Z83844.5, U48869.1, U22398.1, AB018791.1, NM\_014961.1, AE003669.1, AF112221.1, AC005811.10, AF082296.1, AC004466.1, AL008583.1, AK000911.1, AB020678.1, M63356.1, AE003487.1, AF047034.2, AF071810.1, AC004797.1, U09808.1, AE003663.1, U90653.2, NM\_012699.1, AC022517.1, AF071813.1, AC004876.2, AC005259.1, L81775.1, X95703.1, X98993.1, X62681.1, AF189262.1, NM\_014341.1, AF176006.3, AF192559.3, NM\_013024.1, AF189289.1, AF071815.1, NM\_009453.1, NM\_006460.1, AC007395.3, AF139177.1, U86410.1, M83196.1, U40628.1, U40627.1, X00618.1, AL031107.1, J02675.1, AB021179.1, D45205.1, D83484.1, X00254.1, X76232.1, M63348.1, U03771.1, AF255552.1, AF168787.1, AC007774.1, AC006486.1, AJ004801.1, Z77662.1, AL136295.2, U14656.1, AW070197.1, AI873022.1, AW575715.1, AW271726.1, AW172297.1, AW170107.1, AI524194.1, AI652188.1, AI623209.1, N95583.1, AA283710.1, AA573499.1, AI674687.1, AA694439.1, AI760975.1, AA731091.1, AI230984.1, AA805306.1, AA927565.1, AW369632.1, AI425458.1, AI578926.1, AI043684.1, AA851538.1, AA221745.1, AW028244.1, AI873396.1, AI492967.1, AI192683.1, AI854240.1, AI850380.1, AI575971.1, AI461919.1, AW047118.1, AA997145.1, AI008247.1, AA408914.1, AA408939.1, AA402099.1, C11942.1, AA305260.1, AW869895.1, AJ272945.1, AI429741.1, AW595481.1, AI595277.1, AI327425.1, AA481582.1, AA061204.1, W98922.1, AV408902.1, AW696319.1, AW677099.1, AW513114.1, AW280634.1, AW280527.1, AW243892.1, AW193511.1, AI852364.1, AI803180.1, AI784610.1, AI671129.1, AI640998.1, AA998163.1, AA964571.1, AI159402.1, AW244421.1, AW624533.1, AW593458.1, AW574954.1, AW149459.1, AW092856.1, AI987240.1, AI876971.1, AI356089.1, AI225774.1, AI166942.1, AA791749.1, AA544523.1, W16147.1, W18003.1, W13961.1, N42977.1, H19168.1, AC013791.3, AC010216.4, AC008470.3, AC023467.2, AL355519.2, AC025716.1, AC008350.3, AC010714.3, AC020195.1, AC008232.3, AC006903.1, AC006727.1, AC006751.1, Z98864.1, AC008406.5, AC014744.1, AC024725.3, AC026968.2, AC021248.3, AC014187.1, AC014191.1, AL035406.22, AC021024.3, AC009570.7, AC034220.3, AC021091.2, AC009061.8, AC027682.2, AC011430.4, AC007732.2, AC026759.1, AC009911.9, AC010848.12, AC011707.7, AC021618.3, AC019638.1, AC014137.1, AC014975.1, AC010024.2, AC007831.1, AL121908.11, AC024215.7, AC068810.1, AC010648.5, AC022274.4, AC015462.5, AC022307.7, AC024047.2, AC024708.2, AC010003.5, AC009369.5, AC011244.3, AC010703.2, AL122034.8, AL137066.5, AL354940.3, AL157708.2, AC027810.3, AC027796.3, AC058789.9, AC026270.2, AC016631.5, AC011514.2, AC027800.2, AC067434.1, AC026167.2, AC027040.2, AC019234.3, AC012236.3, AC009915.4, AC024159.1, AC023852.1, AC013273.2, AC020327.1, AC020433.1, AC020525.1, AC007925.4, AC017941.1, AC018090.1, AC008228.2, AC013124.1, AC013189.1, AC013210.1, AC014106.1, AC014400.1, AC015146.1, AC007822.3, AL031258.10, AL355153.1, AL080247.3,

SEQ ID NO.264

NGO-St-126 combined

AC067976.1, AC010763.2, AC067721.3, AC063926.3, AC026210.1, AC022240.2, AC025076.3, AP001541.1, AP000614.3, AC009543.4, AC026325.3, AC026317.5, AC026311.4, AC025580.3, AC012112.2, AC022926.2, AC020012.1, AC018212.1, AL137864.6, AL356371.1, AL356260.1, AC040919.1, AC044905.2, AC036192.2, AC023648.3, AC068679.1, AC027464.2, AC021200.4, AC012512.2, AC012164.10, AC017097.2, AC013273.2, AC012352.3, AC022183.2, AC011018.2, AC018224.1, AC015182.1, AC009742.3, AF181895.1, AF128834.1, AL355143.4, AL354814.1, Z92852.20, AL021149.3, AP002000.1, AP001361.1, AP000786.1, AP000785.1, AL021347.1, AI469428.1, AW004984.1, AW675448.1, AW780423.1, AW239395.1, AW651755.1, AA535069.1, AI378367.1, AA879433.1, AA971454.1, AI394371.1, AI564549.1, AA446421.1, AW553616.1, AA928053.1, N78225.1, AI431285.1, AA870109.1, AW674657.1, AI364000.1, AA305698.1, AA760173.1, AW674987.1, AW087890.1, N59764.1, AW548602.1, AW881866.1, AA897396.1, AW673412.1, AW674408.1, AA056907.1, AI202011.1, AA213076.1, AI047089.1, AW392852.1, AI747290.1, T36030.1, AW544283.1, AI131751.1, AW340239.1, TI9014.1, T96204.1, R94457.1, AA518752.1, AI115877.1, AI119061.1, AA123206.1, AI753769.1, AI787898.1, AA765346.1, AI715715.1, AA999172.1, AA221877.1, AI460161.1, T81090.1, C03806.1, N86797.1, AW079585.1, AW672700.1, AW527002.1, AU076916.1, AI741285.1, R00722.1, AI892500.1, R00723.1, AA644165.1, AI916149.1, AI482319.1, AI325806.1, T81139.1, AA438060.1, AA561307.1, AI873729.1, AA561305.1, AV040805.2, AV235074.1, AV220284.1, AI614757.1, AW275744.1, AV265274.1, AV248478.1, AV245335.1, AV263802.1, AV270362.1, AV043755.2, AV048190.1, AV370590.1, D25791.1, AV114853.1, AV111421.1, AV256037.1, AI795876.1, AV374021.1, AV261192.1, AV320489.1, AV252321.1, AV366822.1, AV299835.1, AV312541.1, AA450537.1, AC067976.1, AC010763.2, AC067721.3, AC063926.3, AC026210.1, AC022240.2, AC025076.3, AP001541.1, AP000614.3, AC009543.4, AC026325.3, AC026317.5, AC026311.4, AC025580.3, AC012112.2, AC022926.2, AC020012.1, AC018212.1, AL137864.6, AL356371.1, AL356260.1, AC040919.1, AC044905.2, AC036192.2, AC023648.3, AC068679.1, AC027464.2, AC021200.4, AC012512.2, AC012164.10, AC017097.2, AC013273.2, AC012352.3, AC022183.2, AC011018.2, AC018224.1, AC015182.1, AC009742.3, AF181895.1, AF128834.1, AL355143.4, AL354814.1, Z92852.20, AL021149.3, AP002000.1, AP001361.1, AP000786.1, AP000785.1, AL021347.1, AI469428.1, AW004984.1, AW675448.1, AW780423.1, AW239395.1, AW651755.1, AA535069.1, AI378367.1, AA879433.1, AA971454.1, AI394371.1, AI564549.1, AA446421.1, AW553616.1, AA928053.1, N78225.1, AI431285.1, AA870109.1, AW674657.1, AI364000.1, AA305698.1, AA760173.1, AW674987.1, AW087890.1, N59764.1, AW548602.1, AW881866.1, AA897396.1, AW673412.1, AW674408.1, AA056907.1, AI202011.1, AA213076.1, AI047089.1, AW392852.1, AI747290.1, T36030.1, AW544283.1, AI131751.1, AW340239.1, TI9014.1, T96204.1, R94457.1, AA518752.1, AI115877.1, AI119061.1, AA123206.1, AI753769.1, AI787898.1, AA765346.1, AI715715.1, AA999172.1, AA221877.1, AI460161.1, T81090.1, C03806.1, N86797.1, AW079585.1, AW672700.1, AW527002.1, AU076916.1, AI741285.1, R00722.1, AI892500.1, R00723.1, AA644165.1, AI916149.1, AI482319.1, AI325806.1, T81139.1, AA438060.1, AA561307.1, AI873729.1, AA561305.1, AV040805.2, AV235074.1, AV220284.1, AI614757.1, AW275744.1, AV265274.1, AV248478.1, AV245335.1, AV263802.1, AV270362.1, AV043755.2, AV048190.1, AV370590.1, D25791.1, AV114853.1, AV111421.1, AV256037.1, AI795876.1, AV374021.1, AV261192.1, AV320489.1, AV252321.1, AV366822.1, AV299835.1, AV312541.1, AA450537.1, AC067976.1, AC010763.2, AC067721.3, AC063926.3, AC026210.1, AC022240.2, AC025076.3, AP001541.1, AP000614.3, AC009543.4, AC026325.3, AC026317.5, AC026311.4, AC025580.3, AC012112.2, AC022926.2, AC020012.1, AC018212.1, AL137864.6, AL356371.1, AL356260.1, AC040919.1, AC044905.2, AC036192.2, AC023648.3, AC068679.1, AC027464.2,



AC021200.4, AC012512.2, AC012164.10, AC017097.2, AC013273.2, AC012352.3, AC022183.2, AC011018.2, AC018224.1, AC015182.1, AC009742.3, AF181895.1, AF128834.1, AL355143.4, AL354814.1, Z92852.20, AL021149.3, AP002000.1, AP001361.1, AP000786.1, AP000785.1,

## 5 SEQ ID NO. 265

NGO-St-126

YS136/T3 5'

NM\_003875.1, U10860.1, X87562.1, AL139077.2, AB033168.1, AC007956.5, AE003718.1, NM\_004879.2, AC004877.1, AF010313.2, AC006052.5, AL035671.5, NC\_001139.1, AC020580.9, AC002382.1, AC006064.9, AC005895.1, Z72999.1, AL022328.21, AL049781.4, AL133068.1, AL133399.1, M88277.1, X59698.1, X78987.1, D90899.1, AB037724.1, AK001986.1, AB023482.2, U03425.1, AB009050.1, AW239395.1, AW651755.1, AW672700.1, AU076916.1, AI119061.1, AW527002.1, AI787898.1, AI115877.1, AI614757.1, AA123206.1, AA450537.1, AI892500.1, AI325806.1, AW372007.1, AW367352.1, AI930281.1, AA561307.1, AA561305.1, AW732597.1, AW732373.1, AW248209.1, AV300605.1, AW163311.1, AV204617.1, AI550018.1, AW699234.1, AW653532.1, AW653462.1, AW336984.1, AW163624.1, AI929457.1, AI739490.1, AI069011.1, R58474.1, R57620.1, R46363.1, R14654.1, T38036.1, T33110.1, Z43008.1, 15 AC010763.2, AC026210.1, AC044905.2, AC023648.3, AC019035.5, AC018958.2, AC013273.2, AC012669.2, AC018224.1, AC009742.3, AC012522.7, AC068285.2, AC021891.2, AC008692.4, AC010373.4, AC011116.3, AC018696.3, AC024931.3, AC018996.3, AC009621.4, AC022213.3, AC021265.3, AC022930.2, AL133416.3, AL137161.3, AL137855.2, AL135924.10, AL080247.3,

## 20 SEQ ID NO.266

NGO-St-126

YS136/T7 3'

NM\_003875.1, U10860.1, AC006380.2, AF006203.1, AC009396.5, Z50794.1, U21627.1, AI469428.1, AW004984.1, AI564549.1, AW675448.1, AA535069.1, AI378367.1, AW780423.1, AA879433.1, AI394371.1, AA971454.1, AI431285.1, 25 AA928053.1, AW674657.1, AI364000.1, AA305698.1, AW674987.1, AW087890.1, AW673412.1, AI202011.1, N59764.1, AW674408.1, AI741285.1, AA056907.1, AA897396.1, AW340239.1, AW553616.1, AW548602.1, AA870109.1, AW544283.1, AI131751.1, AI753769.1, AI460161.1, AA765346.1, AI715715.1, AA999172.1, AA221877.1, N78225.1, T81090.1, AW079585.1, R00723.1, AI747290.1, AI482319.1, AA446421.1, AI873729.1, AW275744.1, T96204.1, AV263802.1, AV235074.1, AV248478.1, AW881866.1, D25791.1, AV245335.1, AV370590.1, AV265274.1, 30 AV220284.1, AV040805.2, AV114853.1, AV111421.1, R94457.1, AV261192.1, AV320489.1, AV048190.1, AV043755.2, AV270362.1, AV256037.1, AV374021.1, AV312541.1, AV366822.1, AV352771.1, AV299835.1, AV261104.1, AV337229.1, AV254627.1, AV257886.1, AV252321.1, AV261234.1, AV255806.1, AV380586.1, AV281906.1, AV283090.1, AW681473.1, AV279890.1, R00722.1, AV359752.1, AA218130.1, AV351363.1, T81139.1, AW634678.1, 35 AW634655.1, AV263948.1, AW766970.1, AW460442.1, BB001634.1, AW198719.1, AW148282.1, AV228798.1, AC067976.1, AC067721.3, AC024615.2, AC009550.3, AC037444.2, AC037467.2, AC027003.2, AC010679.3,

## SEQ ID NO.267

NGO-St-126

## 40 YS1613/T3 5'

NM\_003875.1, U10860.1, U67598.1, U39471.1, U28733.1, M64282.1, AE003537.1, AB012242.1, AC008993.3, AE003781.1, AC008063.2, AC005061.2, AC004605.1, AC007090.3, AE001176.1, AF067215.1, AL161532.2, AF016678.1, Z93778.1, Z30215.1, AC002109.1, AL078621.19, AL050399.1, U42844.1, AC000120.1, Z94044.1, AL035447.3, AP002067.1, X60691.1, M93038.1, M14115.1, M16632.1, M59809.1, M59810.1, M59808.1, M14707.1, 45 AA760173.1, AI047089.1, AA518752.1, N86797.1, C03806.1, AA644165.1, T36030.1, T19014.1, AA438060.1, AI916149.1, AA213076.1, AI795876.1, AA123206.1, AA561308.1, AA561307.1, AA561305.1, AW392852.1, AW651755.1, AI325806.1, AI892500.1, AI878306.1, AI119061.1, R94029.1, AV346184.1, AW154885.1, AW031455.1, AW725845.1, AW271459.1, AW201020.1, AV376365.1, AI990909.1, AV174444.1, AI353515.1, AA909030.1, T70524.1, AC063926.3, AC067721.3, AC022240.2, AC009543.4, AC012112.2, AC022926.2, AL137864.6, AL356371.1, 50 AL356260.1, AC025076.3, AC027464.2, AC015773.4, AC012512.2, AC020668.4, AC012352.3, AC015182.1, AF181895.1, AF128834.1, AP001541.1, AP000614.3,

## SEQ ID NO.268

NGO-St-126

## 55 YS1613/T7 3'

NM\_003875.1, U10860.1, AC006380.2, AF134842.1, AC002127.1, NM\_004849.1, AL022067.1, Y11588.1, AC004450.2, AC009396.5, AC006145.2, AC003953.1, Z50794.1, X97212.1, AI469428.1, AW004984.1, AW675448.1, AW780423.1, AA535069.1, AI378367.1, AA879433.1, AA971454.1, AI394371.1, AI564549.1, AA928053.1, AI431285.1, AW553616.1, AW674657.1, AI364000.1, AA870109.1, AA305698.1, AW674987.1, AW087890.1, N59764.1, AW548602.1, 60 AA897396.1, AW673412.1, AA056907.1, AW674408.1, N78225.1, AI202011.1, AW544283.1, AI131751.1, AW340239.1, AI753769.1, AI715715.1, AA765346.1, AI747290.1, AA999172.1, AA221877.1, AI460161.1, AA446421.1, T81090.1, AW079585.1, AI741285.1, AW881866.1, T96204.1, R00723.1, R94457.1, AI482319.1, AI873729.1, AV040805.2, AV235074.1, AV220284.1, AW275744.1, AV265274.1, AV248478.1, R00722.1, AV245335.1, AV263802.1, AV270362.1, AV043755.2, AV048190.1, AV370590.1, D25791.1, AV114853.1, AV111421.1, AV256037.1, AV374021.1, AV261192.1,

- AV320489.1, AV252321.1, AV352771.1, AV366822.1, T81139.1, AV299835.1, AV312541.1, AW681473.1, AV254627.1, AV261104.1, AV337229.1, AV261234.1, AV257886.1, AV255806.1, AV283090.1, AV281906.1, AV279890.1, AV380586.1, AW634678.1, AW634655.1, AV359752.1, AV351363.1, AV280423.1, AA218130.1, AV263948.1, AW460442.1, AW766970.1, W88512.1, AW484561.1, AI705688.1, AA112455.1, N94345.1, AC067976.1, AC067721.3, AC025580.3, AL355980.2, AL162491.3, AC044895.1, AC021200.4, AL133509.7, AL138917.3, AP001361.1, AP000786.1, AC044809.3, AC026450.2, AC034188.2, AC025241.2, AC027415.1, AC026201.1, AC023147.3, AC024449.2, AC022004.2, AC022219.2, AC010987.4, AL136109.3, AL139230.6, AP001828.1, AP000653.1, AP000595.2,
- 10 SEQ ID NO.269  
NGO-St-126  
YS1722/T3 5'  
NM\_003875.1, U10860.1, AE003669.1, AE003647.1, AE003413.1, AC006574.1, U39471.1, U28733.1, M64282.1, AF125313.1, AF101305.1, U85195.1, Z46935.1, AE000658.1, AL136297.2, AL035091.2, AP000064.1, AB012242.1, AC007964.3, AE003566.1, NM\_004849.1, AC005061.2, AF125961.1, AC005988.1, AE001176.1, U69730.1, AL161532.2, AL050399.1, AL133305.2, U97001.1, AL022342.6, AL022067.1, Z99127.1, Y11588.1, Z59557.1, AA446421.1, AW392852.1, AA213076.1, T36030.1, T19014.1, AW881866.1, N78225.1, R94457.1, AI469428.1, AI916149.1, T96204.1, AA760173.1, R00722.1, T81139.1, AI047089.1, AI747290.1, AW004984.1, AW553616.1, AA518752.1, AA870109.1, AW675448.1, AI564549.1, AW780423.1, AA446419.1, AW548602.1, AA644165.1, AA438060.1, AI353445.1, AA305698.1, AI378367.1, AA879433.1, AA535069.1, AW681473.1, AW127943.1, AI394371.1, AI431285.1, AA971454.1, AW674987.1, AW674657.1, AW673412.1, AI364000.1, AI131751.1, AW544283.1, AI715715.1, AA999172.1, AI878306.1, AI239160.1, AA221877.1, AW846110.1, AW846072.1, AV346184.1, AW826474.1, AV376365.1, AW088646.1, AI622981.1, AI489164.1, AA909030.1, AA703095.1, AA676931.1, AA157391.1, AA112455.1, W01474.1, N94345.1, N36362.1, AC067721.3, AC067976.1, AC063926.3, AC025076.3, AP001541.1, AP000614.3, AC009543.4, AC026325.3, AC026317.5, AC026311.4, AC012112.2, AC020012.1, AC018212.1, AL137864.6, AL356371.1, AC040919.1, AC068679.1, AC011172.4, AC017097.2, AC022183.2, AC011018.2, AL355143.4, AP002000.1, AP001361.1, AP000786.1, AP000785.1, AL021347.1, AC032026.3, AC024978.3, AC024402.3, AC024628.3, AC007777.3, AC068800.3, AC025243.3, AC041049.2, AC034110.2, AC068811.4, AC010738.3, AC046201.2, AC025433.3, AC022124.3, AC008857.4, AC008390.6, AC016596.4, AC055724.1, AC068079.1, AC009406.3, AC016336.3, AC025549.3, AC009420.2, AC021811.2, AC022213.3, AC016379.3, AC016563.2, AC020963.1, AC024396.1, AC022272.2, AC016833.2, AC022864.1, AC013363.3, AC013014.1, AC012050.1, AL138849.6, AL161641.3, AL133509.7, AL353655.2, AL355076.1, AL353623.2, AL138917.3, AP001166.1, AP000945.2, AP000940.2,
- 25
- 30
- 35 SEQ ID NO.270  
NGO-St-126  
YS377/T3 5'  
NM\_003875.1, U10860.1, X87562.1, AL139077.2, U67598.1, AE003718.1, AC004877.1, AC006052.5, Z93021.2, AL035671.5, Z83313.1, AC011508.4, AC002382.1, AF199339.1, AC005083.1, AC009525.3, AL049634.8, Z19155.1, AL163275.2, AL136167.8, AL049781.4, AL133399.1, Z83827.1, AL035447.3, X59698.1, X78987.1, D90899.1, AP001730.1, AP001433.1, AB037724.1, AP000158.1, AP000014.2, U03425.1, AW651755.1, AW239395.1, AI115877.1, AI119061.1, AI787898.1, AA123206.1, AW527002.1, AI892500.1, AI325806.1, AA561307.1, AA561305.1, AI614757.1, C03806.1, AW672700.1, AA450537.1, AA561308.1, N86797.1, AW372007.1, AU076916.1, AW367352.1, AI930281.1, AI878306.1, AI045575.1, AV300605.1, AV204617.1, AI550018.1, AW699234.1, AW653532.1, AW653462.1, AW361093.1, AW163624.1, AV160657.1, AI069011.1, AA813333.1, AA772484.1, AA751742.1, AA227692.1, N28842.1, R58474.1, R57620.1, R46363.1, R14654.1, T33110.1, Z43008.1, AC010763.2, AC008011.8, AC044905.2, AC046144.3, AC023648.3, AC027464.2, AC012164.10, AC013273.2, AC012352.3, AC018224.1, AC009742.3, AF181895.1, AF128834.1, AL354814.1,
- 40
- 45
- 50 SEQ ID NO.271  
NGO-St-127  
YS263/T3 5'  
NM\_014753.1, D80009.1, AC024843.1, AF093673.1, AC009784.2, AF063097.1, AL031386.1, NM\_007187.1, AC006004.1, AC007007.2, AF157835.1, AC007202.2, AC005275.1, AC005833.1, AF071185.1, AC005221.1, AL161496.2, AL031634.1, AL121754.18, AL118516.10, AL022345.2, AL050321.8, AJ238786.1, AK001557.1, AK000979.1, AB018116.1, AJ012750.1, W23168.1, AI733771.1, AA129555.1, AI906333.1, AA659526.1, AA905330.1, AV189348.1, C65491.1, AI166512.1, AW871663.1, AW497693.1, AW463327.1, AW463204.1, AV404894.1, AW352454.1, AW255263.1, AI954303.1, AI728334.1, AI668682.1, AI376662.1, AI090140.1, AA999519.1, AA668944.1, AA509065.1, AA503500.1, AA427376.1, AA417429.1, N88168.1, AL023808.2, AL022344.1, AL031601.2, AC037447.2, AC022400.4, AL135925.3, AC025039.3, AC025268.2, AC055809.2, AL136982.1, AC024946.4, AC006888.2, AC009719.2, AC024379.2, AC027182.1, AC022939.2, AC020868.1, AC016788.4, AC024127.1, AL133383.6, AC021024.3, AC068787.3, AC068757.2, AC023600.13, AC027645.3, AC021104.2, AC067748.3, AC027108.2, AC023155.4, AC017090.3, AF252826.1, AC025385.2, AC027211.1, AC024073.2, AC023178.3, AC021839.3, AC024722.2, AC021114.3, AC018443.5, AC017001.4, AC021761.3, AC023873.2, AC023854.2, AC010672.4,
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AC022566.1, AC016042.2, AC012559.6, AF215848.1, AC007689.12, AC016158.2, AC010911.1, AC010073.1, AL158143.2, AL158089.6, AL354975.4, AL136079.3, AL355530.1, AL354857.2, AL161775.3, AL158217.3, AL157877.5, AP001827.1, AP000643.1, Z96803.1,

## 5 SEQ ID NO.272

NGO-St-127

YS263/T7 3'

- 10 NM\_014753.1, D80009.1, AE003451.1, AC011294.3, Z85996.1, AC007244.2, AJ271079.1, M22462.1, AE003815.1, AE003364.1, AC004963.2, AF153352.1, AC007068.17, AE001389.1, Z78067.1, AP000419.1, L15320.1, AC007042.2, AC006544.19, AF135026.1, AE003557.1, AE003528.1, AC003060.1, AF228703.1, U91325.1, AC004832.3, AC004876.2, AC007368.11, AC007461.8, AC004950.2, AC005033.1, AC003065.1, AC005548.1, U21933.1, AF010237.1, AC004167.1, AC004104.1, AC002324.1, AE001032.1, AL050342.42, Z98949.1, Z77662.1, Z50015.1, AL022315.1, AL121723.36, AL157498.1, AL137325.1, U31447.1, AL023800.1, L19655.1, AP000475.3, M73822.1, AP001111.1, AP000023.1, AB028621.1, D87018.1, AB029018.1, AC006481.3, AF050157.1, AL121656.2, AL022310.1, AB016885.1, AW237092.1, AW237137.1, AI935281.1, AW467637.1, AI963620.1, AI650475.1, AI628080.1, AA927690.1, AI338027.1, AI590556.1, AA604575.1, AA203521.1, AI281023.1, AI609068.1, AI689223.1, AW058425.1, AA483799.1, AW473973.1, AA278635.1, AW083923.1, AA915891.1, AA766731.1, AI984984.1, AW803966.1, AI281118.1, AI131367.1, AI537394.1, AI278563.1, AA159506.1, AI304815.1, AI033401.1, AI049943.1, AW004875.1, AA047286.1, T87897.1, AW029023.1, AA480172.1, AI285145.1, AA252803.1, AA261816.1, AI867812.1, AA554061.1, AI753409.1, W81534.1, AI015310.1, AA099000.1, T87990.1, AI184520.1, R00576.1, AI824434.1, AL047806.1, W81533.1, T79535.1, AA047147.1, R33795.1, AA864952.1, AI149983.1, R00680.1, AI810930.1, AW263579.1, AI866914.1, T97738.1, AW796065.1, AA278634.1, AI802574.1, AI651401.1, AW004034.1, AW175987.1, AI005967.1, AA793158.1, H62063.1, AA571438.1, AI376279.1, AA623849.1, AW194865.1, AW428271.1, AW175972.1, AA616918.1, AW205363.1, AA762572.1, AA223495.1, H61156.1, AA421215.1, AA411512.1, AA405999.1, AA293345.1, AA555719.1, T97844.1, AA914529.1, AA726890.1, AA262513.1, AA058106.1, AW910545.1, AW416674.1, AW416666.1, AI406390.1, AA421216.1, AA411513.1, AA399425.1, AA523356.1, AL022344.1, AL023808.2, AC036220.3, AC023099.2, AC022264.2, AC011753.3, AC023723.2, AC014984.1, AC009785.4, AC011191.3, AC013532.2, AC025638.3, AC010033.7, AC068739.2, AC034244.3, AC008481.6, AC027517.2, AC036185.1, AC015925.3, AC015724.4, AC019168.3, AC017420.1, AC013378.3, AC007107.1, AC025011.2, AC022061.3, AC012431.6, AC015990.5, AC058333.2, AC020904.5, AC011543.3, AC011491.4, AC018880.2, AC021111.3, AC024638.2, AC022297.7, AC017059.2, AF215848.1, AL158846.3, AL139404.2, AL139110.2, AL121828.8, AL161618.5, AP001102.2, AP001005.1, AP000813.1,
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## SEQ ID NO.273

NGO-St-127

YS324/T7 3'

- 35 NM\_014753.1, D80009.1, AE003451.1, Z85996.1, AC007244.2, AJ271079.1, M22462.1, AC004963.2, AF153352.1, AC007068.17, Z78067.1, Z83844.5, AL078477.5, AP000419.1, L15320.1, AC007042.2, AC006544.19, AF135026.1, AC027657.1, AE003557.1, AF228703.1, AC004832.3, AC004876.2, AC005003.2, AC006371.2, AC008078.11, AC008010.10, AC007368.11, AF134488.1, AC004961.2, AC007461.8, AC006432.15, AC004950.2, AC002082.1, AC005033.1, AC003065.1, U21933.1, AF010237.1, AC004167.1, AC002324.1, AE001032.1, Z98949.1, Z77662.1, Z50015.1, U93037.1, AL022315.1, AL121723.36, AL031767.13, AL049838.3, AL157498.1, AL137325.1, U31447.1, AL023800.1, AL031665.18, L19655.1, AB040962.1, M73822.1, AP001111.1, AP000023.1, AB028621.1, AB005049.1, AB029018.1, NM\_001702.1, NM\_013146.1, AL121656.2, AL022310.1, U18419.1, X54171.1, AB005297.1, AI963620.1, AW467637.1, AW237092.1, AW237137.1, AI628080.1, AI935281.1, AI650475.1, AI338027.1, AA604575.1, AA927690.1, AI609068.1, AI590556.1, AI281023.1, AW058425.1, AI689223.1, AA203521.1, AA483799.1, AW473973.1, AA278635.1, AA915891.1, AW083923.1, AA766731.1, AI984984.1, AI281118.1, AI131367.1, AI537394.1, AI278563.1, AA159506.1, AI304815.1, AI049943.1, AI033401.1, AW004875.1, AI285145.1, AA047286.1, AW803966.1, AW029023.1, T87897.1, AA480172.1, AA252803.1, AA261816.1, AI753409.1, AI867812.1, W81534.1, AA554061.1, AI015310.1, AA099000.1, AI184520.1, R00576.1, AI824434.1, T87990.1, AA047147.1, AI866914.1, AA864952.1, R33795.1, AI149983.1, AI810930.1, T79535.1, AI802574.1, AW263579.1, T97738.1, R00680.1, W81533.1, AW004034.1, AL047806.1, AW194865.1, AI376279.1, AI651401.1, H62063.1, AW205363.1, AW428271.1, H61156.1, AA421215.1, AA411512.1, AA405999.1, AA293345.1, AA223495.1, AW796065.1, AA278634.1, T97844.1, AA421216.1, AA411513.1, AA399425.1, AA455122.1, AA402812.1, AA402916.1, AA402630.1, AW523356.1, AW522183.1, AW469155.1, AW469154.1, AW469148.1, AI406390.1, AW910545.1, AI005967.1, AA623849.1, AA408648.1, W77672.1, AA914529.1, AA793158.1, AA571438.1, AL022344.1, AL023808.2, AC036220.3, AC023099.2, AC022264.2, AC011753.3, AC023723.2, AC014984.1, AC009785.4, AC011191.3, AC013532.2, AC010033.7, AC068739.2, AC034244.3, AC008481.6, AC036185.1, AC025473.2, AC015925.3, AC015724.4, AC023857.2, AC025011.2, AC022061.3, AC012431.6, AC015990.5, AC009757.8, AC018634.2, AC058333.2, AC040949.2, AC021893.10, AC012640.4, AC011491.4, AC026040.3, AC021111.3, AC025749.2, AC009899.5, AC013391.3, AC018679.5, AC022297.7, AC023325.2, AC022908.2, AC017059.2, AC011329.5, AC014174.1, AC010826.2, AC011098.1, AL158846.3, AL139404.2, AL137004.3, AL137793.2, AL133402.10, AL121828.8, AL161618.5, AL161739.2, AL161448.3, AP001936.1, AP001102.2, AC009857.2, AC026077.3, AC022258.3, AC021240.3, AC023451.2, AC013609.2, AC014418.1, AC007118.1, AC003115.1, AC003118.1, AL138846.3,
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-141-

SEQ ID NO.274

NGO-St-127

YS345/T7 3'

- 5 NM\_014753.1, D80009.1, AE003451.1, AC011294.3, Z85996.1, AC007244.2, AJ271079.1, M22462.1, AE003815.1, AE003418.1, AC004963.2, AF153352.1, AC007068.17, AE001389.1, Z78067.1, AL132792.2, AP000419.1, L15320.1, AC007042.2, AC006544.19, AF135026.1, AC027657.1, AE003557.1, AE003528.1, AC003060.1, AF228703.1, U91325.1, AC004832.3, AC008078.11, AC007368.11, AF134488.1, AC007461.8, AC004950.2, AC002082.1, AC005033.1, AC003065.1, AC005548.1, U21933.1, AF010237.1, AC004167.1, AC004104.1, AC002324.1, AE001032.1, AE0050342.42, Z98949.1, Z77662.1, Z50015.1, AL022315.1, AL121723.36, AL031767.13, AL157498.1, AL137325.1, U31447.1, 10 AL023800.1, L19655.1, AB040962.1, AP000475.3, M73822.1, AP001111.1, AP000023.1, AB028621.1, AB005049.1, AB029018.1, AC006481.3, AF050157.1, AL121656.2, AL022310.1, AB016885.1, AW237092.1, AW237137.1, AI935281.1, AI628080.1, AW467637.1, AI650475.1, AI963620.1, AI338027.1, AA927690.1, AA604575.1, AI281023.1, AI590556.1, AA203521.1, AI609068.1, AI689223.1, AW058425.1, AA483799.1, AW473973.1, AA766731.1, AA278635.1, AW083923.1, AA915891.1, AI984984.1, AI281118.1, AI131367.1, AI537394.1, AI278563.1, AA159506.1, AI304815.1, AW803966.1, AI033401.1, AI049943.1, AW004875.1, AA047286.1, T87897.1, AW029023.1, AA480172.1, AI285145.1, AA252803.1, AA261816.1, AI867812.1, AA554061.1, AI753409.1, W81534.1, AI015310.1, AA099000.1, AI184520.1, R00576.1, T87990.1, AI824434.1, AA047147.1, R33795.1, AA864952.1, T79535.1, AI149983.1, AI810930.1, AI866914.1, AW263579.1, T97738.1, W81533.1, R00680.1, AL047806.1, AI802574.1, AI651401.1, AW004034.1, H62063.1, AI376279.1, AW194865.1, AW796065.1, AW428271.1, AA278634.1, AW205363.1, AA223495.1, H61156.1, 20 AA421215.1, AA411512.1, AA405999.1, AA293345.1, T97844.1, AW175987.1, AI005967.1, AA793158.1, AA623849.1, AA914529.1, AA571438.1, AI406390.1, AA421216.1, AA411513.1, AA399425.1, AA455122.1, AA402812.1, AA402916.1, AA402630.1, AW910545.1, AW469155.1, AW469154.1, AW469148.1, AW523356.1, AW175972.1, AW522183.1, AL022344.1, AL023808.2, AC036220.3, AC023099.2, AC022264.2, AC011753.3, AC023723.2, AC014984.1, AC009785.4, AC011191.3, AC013532.2, AC025638.3, AC010033.7, AC068739.2, AC008481.6, AC027517.2, AC036185.1, AC015925.3, AC015724.4, AC019168.3, AC017420.1, AC020219.1, AC013378.3, 25 AC007107.1, AC025011.2, AC022061.3, AC012431.6, AC015990.5, AC058333.2, AC036174.2, AC020904.5, AC011543.3, AC011491.4, AC026658.2, AC021111.3, AC022297.7, AC012664.3, AC017059.2, AF215848.1, AC011098.1, AL158846.3, AL139404.2, AL139110.2, AL121828.8, AL161618.5, AL157699.2, AP001936.1, AP001005.1, AP000813.1, AC024232.2, AC008060.3, AC026077.3, AC021240.3, AC022518.2, AC023451.2, AC013609.2, 30 AC014418.1, AC006738.1, AC003118.1, AL138846.3, AL136371.2,

SEQ ID NO.275

NGO-St-128

YS1714/T3 5'

- 35 D83327.1, D83077.1, D84296.1, D84295.1, D84294.1, NM\_009441.1, AB008516.1, AJ001866.1, AL163273.2, AP001728.1, AP001429.1, AP000150.1, D83253.1, AP000009.2, AP000151.1, AF099914.1, AL132992.2, AL132977.1, AC006017.2, AC010170.3, U67510.1, AL021684.1, X60399.1, D64005.1, AB018108.1, AC008865.3, AE003786.1, AE003627.1, AE003085.1, AF198444.1, AC006367.3, AC005666.1, AC004053.1, Z82058.1, Z82278.1, Z19156.1, AL034408.2, AL049643.12, X69058.1, AB030387.1, X16640.1, AW510696.1, AW130658.1, AI955031.1, AI365371.1, 40 AW272845.1, AI655615.1, AI651380.1, N75792.1, N22573.1, R49365.1, T65109.1, AA733976.1, AL044710.1, AA968229.1, AI834826.1, AI956999.1, AI935572.1, AA226473.1, F11111.1, AI462554.1, AV373371.1, AV349801.1, AV348118.1, AA226308.1, BB006439.1, AV172670.1, AV348357.1, AA387528.1, AA822624.1, N45260.1, AV331075.1, AI580340.1, H83303.1, AA612013.1, AA054190.1, AI508671.1, AW691731.1, AW690698.1, AW637870.1, AW446918.1, AI662108.1, AI528491.1, AU033435.1, N50729.1, AC020718.3, AC009801.3, AC026848.2, AF206725.1, AC025470.3, 45 AC026616.2, AC011632.3, AL161426.3, AC068145.2, AC009685.3, AC024156.2, AC021196.3, AC011260.4, AC015861.5, AC021000.3, AC007728.1, AC021983.1, AP001378.1, AC025412.3, AC068288.2, AC008905.5, AC026474.3, AC009131.4, AC034282.2, AC067842.1, AC015971.3, AC011726.3, AC009671.3, AC024525.2, AC019359.3, AC025009.2, AC013450.4, AC009746.10, AC018485.6, AC016129.10, AC010667.9, AC023015.2, AC020798.2, AC025338.1, AC020183.1, AC012419.2, AL356317.1, AL133326.8, AL355392.2, AL356017.1, 50 AL161745.5, AL162505.3, AL133241.3, AL117187.2, AL117331.1, AL031011.20, Z98859.1,

SEQ ID NO. 276

NGO-St-128

YS1714/T7 3'

- 55 D83077.1, D84296.1, D84295.1, D84294.1, D83327.1, AL163273.2, AP001728.1, AP001429.1, AP000151.1, D83253.1, AP000009.2, NM\_009441.1, AB008516.1, AC007023.3, AL022395.2, AF037454.1, NM\_008395.1, AC010283.5, AC007198.6, AC020717.3, AC005310.2, AC007955.4, AF090190.1, AC005008.2, AC005034.1, AF131865.1, AF064058.1, AF032967.1, U42213.1, AC005571.1, AC005224.1, AC005304.1, AL049832.2, L28005.1, AB017653.1, AP000463.1, AB025607.1, AB023656.1, AB011163.1, AI336910.1, AI337091.1, AW665117.1, AI885338.1, AL042620.1, 60 AA722789.1, AA743347.1, AA887657.1, AI678227.1, AI318428.1, AW772752.1, AA515769.1, AW341881.1, AA554904.1, AA112857.1, AA083921.1, AW803145.1, AI568131.1, AW237011.1, AI657054.1, AI653679.1, AL040434.1, AW612699.1, AA470557.1, AA662541.1, AA470510.1, AA502576.1, AA852823.1, AW629888.1, R13859.1, AL039361.2, AA021274.1, AW352731.1, AA722688.1, AI003122.1, AW488299.1, AA669782.1, H31610.1, AW525528.1, AA997915.1, AW743421.1, AI646427.1, AI145984.1, W50656.1, AW108450.1, AA794421.1, AI019132.1, H06584.1,

- AI666638.1, AA270792.1, AA417656.1, AW296426.1, AI838089.1, AW466371.1, AA308558.1, AI839685.1, AA048256.1, AV170771.1, AV136593.1, AI846084.1, Z42452.1, AI412296.1, AV278830.1, AV319373.1, AV332268.1, AV327734.1, AV259825.1, AV157173.1, AV378262.1, AV341338.1, AW245310.1, AW822071.1, AV326279.1, AA155001.1, AI812831.1, AA543759.1, AW923586.1, AW921274.1, AW908406.1, AW760328.1, AW349130.1, AW310768.1, AW258283.1, AW202374.1, AI957871.1, AI931902.1, AI790763.1, AA940042.1, AA839623.1, AA758570.1, AA739484.1, AA739481.1, AA387131.1, AA110637.1, AC012032.1, AL139409.3, AL356276.1, AC019259.3, AC025596.1, AC021573.4, AC068169.1, AL161450.4, AC026096.2, AC021484.3, AC012528.2, AC024127.1, AC019061.3, AL139134.4, AL355876.2, AC025076.3, AC037466.3, AC046139.4, AC012506.4, AC025541.4, AC051657.2, AC010256.3, AC018539.4, AC026993.2, AC009654.3, AC025060.3, AC026080.2, AC023271.3, AC019312.3, AC026058.2, AC021552.2, AC012571.3, AC025075.2, AC011170.3, AC009699.6, AC021042.3, AC026842.1, AC021914.3, AC013779.3, AC021694.2, AC008418.1, AC023168.6, AC023000.2, AC013266.3, AC011239.2, AC007373.1, AL136124.8, AL356216.1, AL356055.1, AL137126.4, AL162375.4, AL161640.6, AL160234.1, AP001541.1, AP000945.2, AP000940.2, AP000914.2, AP000614.3,
- 15 SEQ ID NO.277  
NGO-St-128  
YS223/T3 5'  
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- 30 SEQ ID NO.278  
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- 50 SEQ ID NO.279  
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45 SEQ ID NO.281

NGO-St-129  
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## 5 SEQ ID NO.282

NGO-St-129

YS1772/T3 5'

U90236.1, Z35331.1, NM\_004999.1, AB002387.1, NM\_008662.1, U49739.1, AF017303.1, AL096862.18, AE003650.1, AE003436.1, AE003415.1, AL161595.2, AL078620.2, NC\_001146.1, AE003764.1, AC018833.3, AF221108.1, 10 AJ251914.1, X13464.1, X03975.1, Z71468.1, M14045.1, D37977.1, X78287.1, X78286.1, AW629832.1, AA129385.1, AA577227.1, AA028987.1, AW300529.1, AA889126.1, AA037700.1, AI093634.1, AA790620.1, AW660315.1, AW449252.1, AI747845.1, AW741450.1, AI413054.1, AW831515.1, AW663829.1, AW594845.1, AJ392575.1, AW316711.1, AW235712.1, AI863551.1, AI829419.1, AI698448.1, AI366126.1, AI310303.1, AA910369.1, AA696342.1, AA542732.1, AA523580.1, AA522566.1, AL136093.4, AC021058.7, AC061984.2, AC018880.2, AC021861.3, 15 AC017680.1, AC014098.1, AC008577.4, AC009070.5, AC058782.1, AC032032.1, AC025687.2, AC012269.2, AC026206.1, AC013547.2, AC022011.2, AC018835.3, AC023575.2, AC022381.1, AC018878.1, AC013398.2, AC013527.2, AC015353.1, AL355972.3, AL139002.4, AL139814.5, AL354743.1, AL162852.3, AP001087.2, AP001272.1,

## SEQ ID NO. 283

20 NGO-St-129

YS1772/T7 3'

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## SEQ ID NO. 284

40 NGO-St-129

YS1781/T7 3'

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55

## SEQ ID NO. 285

NGO-St-130

YS111/T3 5'

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- AA907496.1, AA728511.1, AA570698.1, AA041001.1, R65462.1, Z34628.1, AC048367.2, AL138904.2, AL354990.1, AC068561.1, AC065048.1, AC062150.1, AC058723.1, AC035761.1, AC024413.3, AC012403.5, AC016964.5, AC022169.2, AC024287.3, AC027418.2, AC016498.4, AC024433.2, AL356266.3, AL157813.3, AL354698.2, AP001004.2, AP001130.1, AC009179.15, AC009386.6, AC024905.7, AC023600.13, AC024523.2, AC025446.3, AC011537.6, AC036127.2, AC067715.1, AC066596.1, AC040168.1, AC020779.3, AC018827.4, AC009659.3, AC016890.4, AC022475.2, AC011266.3, AC022978.3, AC016853.4, AC007495.3, AC010043.4, AC018976.2, AC022048.1, AC020151.1, AL161660.6, AL133318.4, AL137779.1, AP000895.2, AP001578.1,
- 5
- SEQ ID NO.286  
NGO-St-130  
YS111/T7 3'
- 10
- NM\_001981.1, AF052132.1, Z29064.1, U07707.1, AF119858.1, AC007504.3, AF235098.1, AF191069.1, AC003092.1, AF096876.1, AL163252.2, AL115814.1, AP001707.1, AC007376.8, AL021811.1, Z69729.1, AC002113.1, AL031767.13, M22886.1, AC010143.3, AC010971.3, AF002223.1, AF063866.1, AC003665.1, AC005808.1, AL035079.14, AL163232.2, X71844.1, AP001687.1, AP000459.3, AL043535.1, AA781358.1, AI692447.1, N32153.1, AI453034.1, AI813894.1, AA115267.1, AI288222.1, N25318.1, AA534309.1, AA115291.1, AI718641.1, AI978915.1, AI208237.1, AW169456.1, AI275885.1, AW769406.1, AI693511.1, AA886343.1, AA150461.1, N49086.1, AA825660.1, AW075886.1, AA813360.1, AW614630.1, AI520942.1, AA534862.1, Z44586.1, AA164418.1, AA702296.1, AA485200.1, N66885.1, AI920898.1, AW087764.1, N78949.1, R68155.1, N25787.1, AW813048.1, R62156.1, T10010.1, AA478744.1, AI810955.1, F10989.1, AA748186.1, T28758.1, H13536.1, AA644498.1, AW769677.1, AI472645.1, AA385221.1, AI472603.1, AW188171.1, W17317.1, H13535.1, AA585349.1, R59914.1, AA300847.1, AA251517.1, F03176.1, AW050401.1, AA485087.1, AI267611.1, AW366454.1, T25018.1, D19928.1, Z46052.1, AA251530.1, R63487.1, X85627.1, AI060900.1, AA833154.1, AA119303.1, AV361642.1, C80702.1, AV251200.1, AW053510.1, AA630896.1, W02559.1, N48143.1, N38997.1, AW804902.1, AW776207.1, AW775801.1, AW362615.1, AV368479.1, AI452571.1, AI309292.1, AA845594.1, AA505330.1, AA287832.1, AA287578.1, D48726.1, AC048367.2, AC055751.2, AC020941.3, AC017093.2, AC025170.3, AC008488.6, AC019332.3, AC026475.3, AC068066.1, AC015876.3, AC011112.3, AC018392.3, AL354712.2, AL354760.1, AC048389.3, AC068130.2, AC024164.2, AC004898.2, AC027226.2, AC058798.1, AC011152.4, AC010104.2, AL139125.3, AL133282.13, AL035554.1, AP001590.1,
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- SEQ ID NO.287  
NGO-St-130  
YS383/T3 5'
- 35
- NM\_001981.1, U07707.1, Z29064.1, NM\_007943.1, L21768.1, NM\_002396.1, Z95117.1, AP002054.1, U00021.1, M55905.1, AE003677.1, NM\_007944.1, AC004862.1, AF111169.2, AC007543.4, AF131768.1, AC005758.1, AC004476.1, Z35601.1, AL133299.2, AL096802.11, U29156.1, AB027020.1, AI936583.1, AA837424.1, AW340591.1, AA832056.1, AI663323.1, AA642291.1, AL043493.1, AI151900.1, AA637559.1, AA877097.1, AA140007.1, AI584949.1, AW503469.1, AI979367.1, AW372581.1, AU051615.1, AA625121.1, AA490194.1, AA442710.1, AA229914.1, AA229604.1, T70290.1, AW765795.1, AV406101.1, AW186947.1, AI324049.1, C44114.1, R54352.1, R52338.1, F06891.1, F05583.1, T34448.1, Z43889.1, AL138904.2, AL354990.1, AC026989.2, AC026390.1, AC022373.1, AL157785.3, AL162716.4, AL355332.1, AC040919.1, AC046143.3, AC009078.4, AC021477.3, AL136170.3, AL139022.1, AP001845.1, AC037471.3, AC024404.3, AC046166.2, AC012212.4, AC067723.2, AC024891.8, AC025243.3, AC005883.9, AC068054.2, AC068389.1, AC026821.2, AC021585.3, AC023102.2, AC025339.1, AC016044.4, AC008094.4, AC021901.2, AC021342.2, AC022837.1, AC020679.2, AC014595.1, AL136121.5, AL356133.2, AL355176.1, AP001542.1, AL008872.1,
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- 45
- SEQ ID NO.288  
NGO-St-130  
YS383/T7 3'
- 50
- NM\_001981.1, AF052132.1, Z29064.1, U07707.1, AF119858.1, AC007504.3, AF235098.1, AF191069.1, AC003092.1, AF096876.1, AL163252.2, AL115814.1, AP001707.1, AC007376.8, AL021811.1, Z69729.1, AC002113.1, AL031767.13, M22886.1, AC010143.3, AC010971.3, AC002479.1, AF002223.1, AF063866.1, AC003665.1, AC005808.1, AL035079.14, AL163232.2, AL035458.35, X71844.1, AP001687.1, AP000459.3, AL043535.1, AA781358.1, AI692447.1, N32153.1, AI453034.1, AI813894.1, AA115267.1, AI288222.1, N25318.1, AA534309.1, AA115291.1, AI718641.1, AI978915.1, AI208237.1, AW169456.1, AI275885.1, AW769406.1, AI693511.1, AA886343.1, AA150461.1, N49086.1, AA825660.1, AW075886.1, AA813360.1, AW614630.1, AI520942.1, AA534862.1, Z44586.1, AA164418.1, AA702296.1, AI920898.1, AA485200.1, N66885.1, AW087764.1, N78949.1, R68155.1, N25787.1, AW813048.1, R62156.1, T10010.1, AA478744.1, AI810955.1, F10989.1, AA748186.1, T28758.1, H13536.1, AA644498.1, AW769677.1, AI472645.1, AA385221.1, AI472603.1, R59914.1, AA585349.1, AA300847.1, AA251517.1, AA485087.1, AW050401.1, F03176.1, AI267611.1, AW188171.1, W17317.1, H13535.1, AW813048.1, AW366454.1, T25018.1, D19928.1, AA251530.1, X85627.1, AI060900.1, AA833154.1, AA119303.1, AV361642.1, C80702.1, AV251200.1, AW053510.1, AA630896.1, W02559.1, N48143.1, N38997.1, AW776207.1, AW775801.1, AW362615.1, AV368479.1, AI452571.1, AI309292.1, AA845594.1, AA505330.1, AA287832.1, AA287578.1, AC048367.2, AC020941.3, AC017093.2, AC025170.3, AC008488.6, AC008948.5, AC019332.3, AC026475.3, AC015876.3, AC011112.3, AC018392.3, AL354712.2, AL354760.1, AC068130.2, AC024164.2, AC004898.2, AC027226.2, AC011152.4, AC010104.2,
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-146-

AL139125.3, AL133282.13, AP000793.1,

SEQ ID NO.289

NGO-St-131

5 YSI61/T3 5'

AB002318.1, NM\_011602.1, X56123.1, AF177198.1, NM\_006289.1, AF078828.1, AB028950.1, AF178534.1, AC009044.3, AE003535.1, AF224669.1, U41384.1, X59601.1, Z66108.1, Z66107.1, NM\_016559.1, AC020610.6, AE003745.1, AC002044.1, NM\_011027.1, AC005145.1, AC005544.1, U51243.1, AL080195.1, AL021918.1, AB032593.1, AB032592.1, Z57921.1, AJ009823.1, AI751285.1, AW900719.1, AA452483.1, AA387755.1, AW336094.1, W17774.1, AA474115.1, AA718262.1, AI593159.1, AA657201.1, AA615519.1, AI331130.1, R17242.1, AW437322.1, AW654277.1, AW336729.1, AA015516.1, AA013971.1, R54389.1, AW640826.1, AW403043.1, AL042809.1, AL047970.1, AI343291.1, D31413.1, T27372.1, T06850.1, AI691500.1, AW137249.1, AI980726.1, AI387487.1, AA748793.1, AA737559.1, AC026030.2, AC068233.1, AL133410.11, AC009122.5, AC011056.3, AC024491.4, AC009696.5, AC018797.3, AC026049.2, AC024629.1, AC015146.1, AP002018.1,

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SEQ ID NO.290

NGO-St-131

YSI61/T7 3'

AB002318.1, AF085910.1, AL137080.2, NM\_016761.1, AC005825.3, AF221104.1, AF221103.1, AF221102.1, AF110520.1, AC003958.1, AL031276.1, AL008627.1, D49544.1, AI823644.1, AW629480.1, AI751284.1, AA290619.1, AA290618.1, AW136798.1, AW195082.1, AI566119.1, AI866810.1, AI307663.1, AI417845.1, AW242353.1, AI479172.1, AI311003.1, AI522054.1, AI952372.1, R99633.1, AI249792.1, AI366767.1, AW469603.1, AA854194.1, AA582699.1, AI380822.1, AW303332.1, R99089.1, AW902895.1, AW136171.1, AW902834.1, AI985231.1, T16297.1, AI985222.1, T17377.1, AA291006.1, T32600.1, AA291005.1, AW902806.1, AI142264.1, W22495.1, T20064.1, AW898163.1, AW251506.1, AA998450.1, AI072764.1, AI851526.1, AI787438.1, AI465290.1, AA967834.1, AA718676.1, AA039087.1, AA511363.1, AV252009.1, AV272145.1, D80367.1, D80366.1, D80352.1, D80351.1, D80339.1, D80331.1, D80330.1, D80314.1, D80261.1, D80254.1, D80253.1, D80252.1, D80251.1, D59773.1, D59717.1, AI705776.1, AV175623.1, D80293.1, D59809.1, AV249990.1, AW488444.1, AW389528.1, AW218598.1, AI507221.1, C85503.1, AA709996.1, W83532.1, AC026030.2, AC016814.4, AC022910.2,

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SEQ ID NO.291

NGO-St-131

YSI01/T3 5'

AB002318.1, NM\_011602.1, X56123.1, AF177198.1, NM\_006289.1, AF078828.1, AB028950.1, AF065739.1, AF178534.1, AC005145.1, AC009044.3, AF224669.1, U41384.1, X59601.1, Z66108.1, Z66107.1, NM\_016559.1, AC020610.6, NM\_011027.1, AC005544.1, U51243.1, AL080195.1, AL021918.1, AB032593.1, AB032592.1, Z57921.1, AJ009823.1, AI751285.1, AW900719.1, AA452483.1, AA387755.1, AW336094.1, W17774.1, AA474115.1, AA718262.1, AI593159.1, AA657201.1, AA615519.1, AI331130.1, AW437322.1, R17242.1, AW654277.1, AW336729.1, R54389.1, AW640826.1, AA015516.1, AA013971.1, T06850.1, AW403043.1, AL042809.1, AL047970.1, AI343291.1, D31413.1, T27372.1, AW137249.1, AI980726.1, AA748793.1, AA737559.1, AC026030.2, AC068233.1, AC009122.5, AL133410.11, AC024491.4, AC009696.5, AC018797.3, AC026049.2, AC024629.1, AP002018.1, AC026959.3, AC025148.3, AC007653.4, AC012337.3, AC009772.4, AC021650.9, AC011827.3, AC064839.3, AC010074.6, AC013614.4, AC013733.3, AC013405.1, AC021095.1, AC020569.1, AC008076.8, AL355819.2, AL117336.18, AP001007.1,

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SEQ ID NO.292

NGO-St-131

YSI01/T7 3')

AB002318.1, AF085910.1, AF011399.1, AF011398.1, AL137080.2, NM\_016761.1, AC005825.3, AF221104.1, AF221103.1, AF221102.1, AF110520.1, AC003958.1, AL031276.1, AL157416.1, AL138642.1, AL008627.1, D49544.1, AI823644.1, AW629480.1, AI751284.1, AA290619.1, AA290618.1, AW136798.1, AW195082.1, AI566119.1, AI866810.1, AI307663.1, AI417845.1, AW242353.1, AI479172.1, AI311003.1, AI522054.1, AI952372.1, R99633.1, AI249792.1, AI366767.1, AW469603.1, AA854194.1, AA582699.1, AW303332.1, R99089.1, AW136171.1, AI380822.1, AW902895.1, AW902834.1, AI985231.1, T16297.1, AI985222.1, T17377.1, AA291006.1, T32600.1, AA291005.1, AW902806.1, AI142264.1, AW898163.1, W22495.1, T20064.1, AW251506.1, AA998450.1, AI072764.1, AA718676.1, AI851526.1, AI787438.1, AI465290.1, AA967834.1, AA039087.1, AA511363.1, AV252009.1, AV272145.1, AI705776.1, D80367.1, D80366.1, D80352.1, D80351.1, D80339.1, D80331.1, D80330.1, D80314.1, D80261.1, D80254.1, D80253.1, D80252.1, D80251.1, D59773.1, D59717.1, D80293.1, D59809.1, AV175623.1, AV249990.1, AA370498.1, AW488444.1, AW389528.1, AW218598.1, AI507221.1, AA960722.1, AA960721.1, C85503.1, AA709996.1, W83532.1, L38220.1, AC026030.2, AC016814.4, AC022910.2,

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SEQ ID NO.293

NGO-St-132

YS011/T3 5'

NM\_000346.1, AC007461.8, S74506.1, Z46629.1, AF029696.1, AF006571.1, U12533.1, AB012236.1, AB035888.1,

-147-

AB035887.1, AF106572.1, AB006448.1, D83256.1, NM\_006941.1, AF006501.4, AL031587.3, AJ001183.1, AF191325.1, AF164104.1, AF226675.1, Z99757.12, AF047389.1, AF047043.1, AF017182.1, U66141.1, U66105.1, AJ001029.1, AE002049.1, AL135162.1, AW701461.1, AW323770.1, AW232285.1, AA220077.1, T18789.1, AW924151.1, AW747248.1, AW746893.1, AW746873.1, AW746213.1, AW681012.1, AW680640.1, AW677948.1, AW677800.1, 5 AW672276.1, AW672019.1, AW665912.1, AW471059.1, AW384568.1, AW384558.1, AW384516.1, AW384461.1, AW371943.1, AW286733.2, AW406345.1, AW321606.1, AW298118.1, AW290875.1, AW289095.1, AW245072.1, AW161855.1, AW161352.1, AW103014.1, AW007471.1, AI885013.1, AL035821.1, AI682325.1, AI539787.1, AI497991.1, AI410380.1, AI351117.1, AI350368.1, AI338712.1, AI335760.1, AI286186.1, AI266340.1, AI186949.1, AI167245.1, AI144319.1, AI134312.1, AI062232.1, AA973886.1, AA906673.1, AA904015.1, AA873306.1, AA836977.1, 10 AA688139.1, AA634800.1, AA630304.1, AA592961.1, AA472666.1, AA449553.1, AA449122.1, AA443810.1, AA314988.1, AA287892.1, AA243383.1, W57682.1, T49849.1, AC040983.1, AC009041.5, AC012004.3,

SEQ ID NO.294

NGO-St-132

15 YS1637/T3 5'  
NM\_000346.1, Z46629.1, AF029696.1, AB012236.1, U12533.1, AC007461.8, S74505.1, AF106572.1, AF265207.1, AF061784.1, NM\_006941.1, AJ001183.1, S74504.1, AB035887.1, AF226675.1, AF006501.4, AL031587.3, S74506.1, U66141.1, AJ001029.1, AF047389.1, AF047043.1, AF017182.1, AF006571.1, Z18958.1, X79250.1, AF164104.1, AB035888.1, Z99757.12, AF152356.2, AJ245601.1, AB006448.1, AF191325.1, Z18957.1, Z18959.1, D83256.1, 20 U70441.1, NM\_011441.1, D49474.1, D49473.1, L29085.1, NM\_005986.1, AX001335.1, Y13436.1, NM\_007084.1, AF107044.1, AB033888.1, X65664.1, U31967.1, NM\_011443.1, NM\_009233.1, NM\_009234.1, AF009414.1, AX001334.1, AX001333.1, X96997.1, X94127.1, X94126.1, AB011802.1, L29086.1, NM\_003107.1, NM\_009236.1, L35032.1, X70683.1, AF116571.1, NM\_009238.1, NM\_005686.1, AF098915.1, X70298.1, Z31560.1, AB014474.1, L07335.1, S69429.1, NM\_006942.1, AC007421.12, U12532.1, D50603.1, AB006867.1, AF193760.2, L12010.1, 25 AJ004858.1, M86315.1, AB026622.1, AE003776.1, AJ251580.1, AJ001730.1, NM\_011446.1, NM\_009237.1, U12467.1, X94125.1, AB023419.1, AB011803.1, M86335.1, X73038.1, AF001047.1, L12022.1, L12020.1, X65660.1, L12013.1, M86313.1, AI594348.1, AA616534.1, AL120408.1, AW321606.1, AW153579.1, AW184648.1, AV116901.1, AW343046.1, AV120409.1, AW231213.1, AW227743.1, AW210917.1, AW513608.1, AW152310.1, AI935610.1, AI821650.1, AI758881.1, AI743736.1, AI743707.1, AI739667.1, AI732705.1, AI635063.1, AI073502.1, AA260278.1, 30 AI765094.1, AI087935.1, AW048216.1, AA434433.1, AA427400.1, AA405793.1, AW434258.1, AW045442.1, AI574719.1, AI137262.1, AI136910.1, AA799800.1, AA959594.1, AI009328.1, AA411418.1, AW533591.1, AW533022.1, AW532784.1, AW526351.1, AI716553.1, AI029515.1, AI029109.1, AA956282.1, AA956131.1, AA924900.1, AA924896.1, AA875101.1, AI145897.1, AI136894.1, AI112078.1, AI102567.1, AA943207.1, AW244680.1, AI828016.1, AI817673.1, AI240186.1, AW766057.1, AW615144.1, AW532037.1, AW414006.1, AW235281.1, AW131791.1, 35 AW131705.1, AW071909.1, AW055151.1, AW044044.1, AW028031.1, AW005368.1, AI990431.1, AI971611.1, AI631443.1, AI611652.1, AI571299.1, AI566261.1, AI480221.1, AI423139.1, AI421743.1, AI421119.1, AI418146.1, AI373018.1, AI364349.1, AI356682.1, AI327463.1, AI292258.1, AI199308.1, AI151028.1, AI146406.1, AI146367.1, AI137787.1, AI097136.1, AI096977.1, AI094794.1, AI056908.1, AI052267.1, AI717565.1, AA405899.1, AC009041.5, AC012004.3, AF215846.1, AL355803.2, AL137061.2, AL136179.11, AL117346.16, AC024914.17, AC020788.4, 40 AC015652.6, AC008220.4, AC007975.6, AC008318.6, AC012822.1, AC020509.1, AC055113.1, AL137016.10, AC024915.10, AC058787.7, AC024069.15, AC007588.3, AC017264.1, AL121747.21, AC068951.1, AC011649.3, AC026244.2, AC021051.3, AC027243.2, AC040983.1, AC027700.1, AL162584.3, AC022980.3, AC016156.7, AC068986.3, AC022499.5, AC026376.7, AC011544.5, AC008569.5, AC021881.2, AC022532.2, AC022917.3, AC023096.1, AC022606.2, AC005528.25, AC010665.4, AC010575.3, AC023011.1, AC010892.3, AC019870.1, 45 AC013906.1, AC014152.1, AC014782.1, AC009485.2, AL139246.4, AL034405.13, AL159992.3,

SEQ ID NO.295

NGO-St-132

YS1637/T7 3'

50 NM\_000346.1, AC007461.8, S74506.1, Z46629.1, AF029696.1, AC007070.4, U61951.2, AB023041.1, AB006448.1, AC022521.4, AC007196.4, AC005169.2, AE003780.1, AC012392.1, AF162444.1, AC006240.1, AL161548.2, AL161502.2, NC\_001142.1, AC004669.2, AC004411.2, AC002329.2, AC018363.6, AC008134.3, AC007259.4, AC005508.1, AC004562.1, AF058914.1, AC002539.1, AL163814.1, AL163812.1, AL161561.2, AL049655.2, AL049171.1, AL022023.1, AL021637.2, Z35596.1, AL078637.1, AL132960.2, AL132970.2, AL132965.1, AL049538.8, 55 U39674.1, AP001313.1, Z20656.1, AP000367.1, AP000371.1, AW005563.1, AA576678.1, AI934455.1, AI382146.1, AA527295.1, AI870355.1, AI380233.1, AI681309.1, AI299871.1, AA913619.1, AW087477.1, AA912521.1, AA778589.1, AI453423.1, AW360836.1, AA331097.1, H90100.1, AA469143.1, AA420856.1, AW075227.1, AA884178.1, AA420456.1, AA657762.1, AI348085.1, AA333065.1, AW888412.1, AW142661.1, AI985948.1, AA400739.1, AA955408.1, AI008321.1, AW213674.1, AI852411.1, AI548994.1, W24710.1, AW360293.1, AW323128.1, AV021074.1, AW897800.1, 60 AI599999.1, AV281945.1, AV220920.1, AV144700.1, AV008800.1, AV233902.1, AA469215.1, AV360627.1, AV165338.1, AV220098.1, BB004489.1, AV349732.1, AV302326.1, AW228243.1, AW360802.1, AI504553.1, AV280305.1, BB003834.1, AV305178.1, C15879.1, AV163514.1, AW381053.1, AV305177.1, AV318841.1, AW829173.1, AV361282.1, AV248007.1, R30640.1, AW900425.1, AW892801.1, AW776398.1, AW697226.1, AW690623.1, AW586197.1, AW586064.1, AW559610.1, AW267726.1, AW218488.1, AU061986.1, AI164072.1,

AI162251.1, AA825782.1, AA411689.1, H63328.1, T48235.1, AV424751.1, AC013323.5, AC007194.1, AC025309.2, AC006755.1, AC024521.3, AC013645.3, AC011065.4, AC024527.3, AC010190.7, AC024104.4, AC011491.4, AC026623.2, AC021142.4, AC034285.1, AC025724.1, AC015854.3, AC021507.2, AC008258.3, AL078597.4, AL163642.1, AL021576.1,

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SEQ ID NO.296

NGO-St-133

YS102/T3 5'

- 10 NM\_014820.1, AB018262.1, Z19158.1, AP000007.1, AF102137.1, Z80789.1, AB030817.1, L14331.1, AC006840.17, AC004606.1, AL031012.1, AP001425.1, AB025414.1, AC016752.2, AE003801.1, AE003726.1, AE003616.1, AE003485.1, AE003420.1, AF127577.2, AC015450.3, AC008040.7, AC006596.2, AC006050.1, AL035331.1, AL078611.1, AL163243.2, Z71182.1, AP001698.1, Z79997.1, AP000208.1, AP000247.1, AP000130.1, AW468485.1, W76094.1, AA449405.1, AW230655.1, AA313460.1, AI325788.1, AI892481.1, AA116789.1, AA076346.1, AA373986.1, AV145606.1, AW227769.1, AW320879.1, AI535287.1, Z19251.1, AW765531.1, AW281101.1, AA985348.1, AW656932.1, AW481973.1, AW410280.1, AW356980.1, AW336895.1, AW200321.1, AW050865.1, AI834977.1, 15 AL048825.1, AI646136.1, AI478830.1, AA345311.1, AA278482.1, AA203592.1, R10075.1, T99341.1, T81329.1, AC015462.5, AC023782.2, AC025607.3, AC018351.8, AC068119.1, AC026858.2, AC016229.3, AC012437.3, AL138879.3, AP001901.1, AC036213.3, AC010464.4, AC026644.2, AC011615.3, AC008293.1, AL354734.3, AL353707.1, AL162311.1, AL157757.1, AC012413.4, AC023891.7, AC026770.3, AC011960.3, AC027067.2, 20 AC015595.3, AC017094.5, AC007521.11, AC015996.2, AC012972.1, AL157905.3, AL354800.3,

SEQ ID NO.297

NGO-St-133

YS102/T7 3'

- 25 NM\_014820.1, AB018262.1, AF010516.1, AC005406.2, Z70268.1, AC009044.3, AE003547.1, NM\_006021.1, Z74035.1, X95549.1, AL022722.1, AL109925.11, AJ243368.2, Z70688.1, Y15228.1, AP000382.1, AE003736.1, AL049612.11, AI769448.1, AI581514.1, AW471382.1, AI671783.1, AW044465.1, AI795924.1, AW009918.1, AW167186.1, AI278004.1, N49863.1, AW083882.1, AI283007.1, AI833063.1, AI478170.1, AI078346.1, AA707693.1, AI770160.1, AI126207.1, AW513624.1, N59383.1, H11342.1, AI679546.1, D60203.1, AW102995.1, AA047406.1, N67748.1, AI373915.1, 30 AA937689.1, AA535637.1, AW770695.1, AA088722.1, AI278065.1, AW470297.1, AI984753.1, AI281086.1, AI088753.1, N50512.1, N78439.1, AI089934.1, N50443.1, R75994.1, AI418032.1, AW069428.1, H28047.1, AA722233.1, AA934810.1, AW194761.1, AI679985.1, N70890.1, R82859.1, AW576214.1, R82647.1, R60689.1, AI383079.1, AW603760.1, R40078.1, H92752.1, H39632.1, AW388643.1, R44445.1, AA320578.1, R92461.1, AW118280.1, D55592.1, AA857398.1, AA579529.1, R82696.1, D52213.1, AA152134.1, C14917.1, N47394.1, AA369996.1, N47395.1, AA150127.1, 35 AI863820.1, AL079976.2, AA047526.1, AW545304.1, AW213944.1, AI844034.1, AI225307.1, AA175289.1, AW741826.1, AW324264.1, AW228128.1, AI849427.1, AI265537.1, AA175781.1, AI600081.1, AI111343.1, AV331675.1, AW254554.1, AW253791.1, AI714131.1, AI029154.1, AI171980.1, AV115523.1, AV340409.1, AV227184.1, AW914053.1, AC015462.5, AC023782.2, AC044821.2, AC013713.4, AC021761.3, AC021241.3, AL355341.3, AL157875.4, AL049756.16, AC025190.4, AC016797.4, AC024935.8, AC008595.4, AC025060.3, 40 AC023784.3, AC010907.3, AC022253.2, AC017109.2, AC018889.1, AL355378.1, AL118557.1,

SEQ ID NO.298

NGO-St-133

YS1783/T3 5'

- 45 NM\_014820.1, AB018262.1, Z19158.1, AP000007.1, AF102137.1, AE001690.1, Z80789.1, AB030817.1, AB025414.1, AE003713.1, AC004606.1, AL009175.1, AL139077.2, AL031012.1, AC007359.2, AC016752.2, AC003040.2, AF248484.1, AE003801.1, AE003616.1, AC007505.4, AE002280.1, AF127577.2, AF208226.1, AC007682.2, AC008175.2, AC015450.3, AC006481.3, AC012394.3, AC008040.7, AF166527.1, AC006463.3, AC006949.8, AC006578.5, AC006596.2, U00670.1, AC004293.1, AC005261.1, AC004473.1, AE001065.1, AL035536.1, Z82266.1, Z78065.1, 50 AL078611.1, AL163255.2, AL163243.2, AL163207.2, S38096.1, AL138657.1, AL132957.1, AL021069.1, Z71182.1, U07798.1, AP001710.1, AP001698.1, AP001601.1, Z79997.1, AP000208.1, AP000247.1, X71802.1, AP000130.1, M95516.1, AW468485.1, W76094.1, AA449405.1, AW230655.1, AA313460.1, AI325788.1, AI892481.1, AA076346.1, AA116789.1, AA373986.1, AV145606.1, AW227769.1, AW320879.1, AI535287.1, Z19251.1, AA155457.1, AW765531.1, AW281101.1, AI430671.1, AA985348.1, W33868.1, AW656932.1, AW481973.1, AW410280.1, AW356980.1, 55 AW336895.1, AW200321.1, AW050865.1, AL048825.1, AI478830.1, AA345311.1, AA278482.1, AA203592.1, W44281.1, R10075.1, T99341.1, T81329.1,

SEQ ID NO.299

NGO-St-134 combined;

- 60 NM\_003611.1, Y16355.1, Y15164.1, AC003037.1, AC010682.2, AC006991.2, AC016707.2, AC008175.2, AC007379.2, AC009947.2, AF121351.1, AE003417.1, AC005039.1, AF117269.1, AF077408.1, U09819.1, AL161498.2, AF016655.1, AL050231.2, Z99121.1, X71360.1, AP002039.1, NC\_001144.1, AC009411.2, AC010498.4, AF140536.1, AE003805.1, AE003690.1, AE003542.1, NM\_002062.1, AC009514.2, AC006026.2, AC006065.3, AC005839.1, U44051.1, U85195.1, U01156.1, AC004289.1, AC005179.1, AC004475.1, U22383.1, AE000658.1, AL163244.2, AB016214.1, U51234.1,

- AL136501.2, AL035690.10, AL008732.1, AL021367.1, U62778.1, U10037.1, U01157.1, AP001699.1, AP001604.1, M24635.1, X75598.1, D16413.1, L23503.1, U01104.1, AA463600.1, Z46206.1, R93559.1, R18599.1, C03715.1, AA493510.1, AA610816.1, AI954758.1, Z24812.1, AV373707.1, AV274641.1, AV261266.1, AI482404.1, T63643.1, AW851555.1, AW782871.1, AW764717.1, AW199070.1, AW187754.1, AI867176.1, AI779970.1, AI778733.1, AI778732.1, AI777779.1, AV072748.1, AU052904.1, AI191468.1, AI061454.1, C25733.1, AA517468.1, AA491434.1, C07818.1, H30070.1, AC025449.3, AC068719.1, AC025246.5, AC017005.4, AC068601.3, AC024183.3, AC022848.3, AC069130.1, AC009235.2, AC007322.3, AC024236.3, AC008061.1, AC007965.2, AC007315.2, AC068541.3, AC053495.3, AC022486.3, AC010146.5, AL354667.1, AC058810.3, AC026605.3, AC069232.1, AC021756.11, AC024043.4, AC021311.4, AC018967.3, AC022602.1, AC020065.1, AL356234.2, AL354755.2,
- 10  
SEQ ID NO.300  
NGO-St-134  
YS1695/T3 5'  
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- 20  
SEQ ID NO.301  
NGO-St-134  
YS1695/T7 3'  
NM\_003611.1, Y16355.1, Y15164.1, AC003037.1, AC007379.2, AC016752.2, AC008175.2, NM\_007845.1, S77750.1, U12565.1, AC024823.1, AE003682.1, AE002142.1, AF165124.1, AC005220.1, AL021328.1, AE002140.1, NM\_010077.1, AF143381.1, AC003042.1, AL117375.12, Z99772.1, X55674.1, D67043.1, AC005310.2, AC009327.6, AC008125.9, U21319.1, AC005371.1, AC002090.1, AJ235271.1, AB026658.1, AI916605.1, AI867405.1, AI971431.1, AI867404.1, AI376969.1, AI769120.1, AI634116.1, AI245948.1, AW167287.1, AA399610.1, AA173950.1, AA778870.1, AW118555.1, AI627406.1, AI769378.1, AI804265.1, AI309530.1, AW296642.1, D52284.1, AI277389.1, AI304731.1, N57735.1, AI280957.1, AA504821.1, AI049632.1, C14646.1, AA780326.1, C14712.1, AA994778.1, R41679.1, AI916018.1, T16276.1, N57749.1, AA173595.1, AA824530.1, AA621466.1, AW009492.1, D53159.1, AI917863.1, H05597.1, AW885416.1, AI908207.1, D60992.1, AI908204.1, AI561264.1, AI277708.1, W35241.1, AI620904.1, Z41831.1, AI277709.1, D53722.1, AI277707.1, AA428032.1, AA514458.1, D60582.1, D80593.1, AW118344.1, AI824750.1, AI719888.1, AI908201.1, D60909.1, R93560.1, D80428.1, AW887698.1, AW450863.1, AI333241.1, AA707111.1, AA693788.1, AW072670.1, AI022424.1, C14580.1, AI471729.1, AA398975.1, AI719895.1, AW271458.1, W23787.1, AW416841.1, AW554784.1, AW542764.1, AI480837.1, AW785419.1, AW785418.1, AI554988.1, AA634447.1, AW485325.1, AW375050.1, AW297567.1, AA871518.1, AA869166.1, AV197217.1, R14712.1, AW563271.1, AW270811.1, AI507728.1, AA247528.1, AC025449.3, AC068541.3, AC022486.3, AC007322.3, AC007965.2, AC007315.2, AC018789.2, AC008061.1, AC022783.2, AC020972.1, AC063924.3, AC008611.4, AC026910.2, AC021619.3, AC006879.2, AC006796.1, AC068165.1, AC021471.2, AC010873.3, AC015517.2, AL137069.2, AL158045.2, AC013318.4, AC063960.2, AC034138.2, AC012686.3, AC018872.2, AL137125.2, AL136218.7, AL353607.2,
- 30  
SEQ ID NO.302  
NGO-St-134  
YS318/T3 5'  
NM\_003611.1, Y16355.1, Y15164.1, AC003037.1, AC010682.2, AC007379.2, AC006991.2, AC008175.2, AC009947.2, AE003417.1, AC005039.1, AF117269.1, U09819.1, AF016655.1, AL050231.2, Z99121.1, X71360.1, AP002039.1, NC\_001144.1, AC009411.2, AF140536.1, AE003690.1, NM\_002062.1, AC009514.2, AC006026.2, AC006065.3, AC005839.1, U44051.1, U85195.1, U01156.1, U22383.1, AE000658.1, AL163244.2, AB016214.1, U51234.1, AL035690.10, AL008732.1, U62778.1, U10037.1, U01157.1, AP001699.1, AP001604.1, M24635.1, X75598.1, D16413.1, L23503.1, U01104.1, R93559.1, AA463600.1, C03715.1, Z46206.1, R18599.1, AA493510.1, Z24812.1, AV373707.1, AV274641.1, AV261266.1, AI482404.1, AW851555.1, AW782871.1, AW764717.1,
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- AW199070.1, AW187754.1, AI867176.1, AI779970.1, AI778733.1, AI778732.1, AI777779.1, AU052904.1, C25733.1, AA517468.1, AA491434.1, C07818.1, H30070.1, AC025449.3, AC068719.1, AC025246.5, AC017005.4, AC068601.3, AC024183.3, AC022848.3, AC069130.1, AC009235.2, AC068541.3, AC022486.3, AC007322.3, AC024236.3, AC008061.1, AC007315.2, AC010146.5, AL354667.1, AC058810.3, AC026605.3, AC069232.1, AC024043.4, AC021311.4, AC022602.1, AC020065.1, AL356234.2, AC044879.3, AC009545.4, AC018905.4, AC026076.2, AC026925.2, AC022937.3, AC016803.2, AC019039.2, AC012507.3, AC020414.1, AC007645.3, AC005059.1, AL139147.3, AL133402.10, AL162739.4, AP001998.1, AP000723.1,
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- SEQ ID NO.303  
NGO-St-134  
YS318/T7 3'
- 10
- NM\_003611.1, Y16355.1, Y15164.1, AC003037.1, AC007379.2, AC016752.2, AC008175.2, AC024823.1, AE003682.1, AE002142.1, AC005046.3, AF165124.1, AC005220.1, AE002140.1, AF143381.1, AC005922.1, AC003042.1, AL121674.12, AL033378.12, AL117375.12, Z99772.1, AL031285.1, D67043.1, AC005310.2, AC006029.2, AC009327.6, AC005827.3, AC005371.1, AJ235271.1, AL137189.1, AL008729.1, AB026658.1, AI867405.1, AI916605.1, AI971431.1, AI376969.1, AI867404.1, AI769120.1, AI634116.1, AI245948.1, AA173950.1, AA399610.1, AA778870.1, AW167287.1, AW118555.1, AI769378.1, AI627406.1, AI804265.1, AI309530.1, AW296642.1, AI277389.1, AI304731.1, N57735.1, D52284.1, AI280957.1, AA504821.1, AI049632.1, AA780326.1, C14646.1, AA994778.1, R41679.1, AI916018.1, C14712.1, T16276.1, N57749.1, AW009492.1, AA824530.1, AA621466.1, AI917863.1, D53159.1, AA173595.1, H05597.1, AW885416.1, D60992.1, W35241.1, AI908207.1, AI620904.1, Z41831.1, AI908204.1, AA428032.1, AA514458.1, D53722.1, D60582.1, AI561264.1, D80593.1, AI277708.1, AI277709.1, AI824750.1, AI719888.1, AI277707.1, R93560.1, D60909.1, D80428.1, AW887698.1, AW118344.1, AI908201.1, C14580.1, AI471729.1, AI719895.1, AW450863.1, AW072670.1, W23787.1, AW271458.1, AI333241.1, AA398975.1, AI022424.1, AA707111.1, AA693788.1, AW416841.1, AW554784.1, AW542764.1, AI480837.1, AW785419.1, AW785418.1, AI554988.1, AW485325.1, AV197217.1, R14712.1, AW563271.1, AW270811.1, AW119241.1, AI507728.1, AA247528.1, AC025449.3, AC068541.3, AC022486.3, AC007322.3, AC007965.2, AC007315.2, AC018789.2, AC008061.1, AC024524.3, AC063924.3, AC008611.4, AC021619.3, AC006796.1, AL136367.2, AL158205.4, AC021471.2, AC023409.1, AC010873.3, AC012501.1, AL159970.8, AP001318.1, AC012543.3, AC053523.2, AC008890.3, AC008732.4, AC034138.2, AL137125.2, AL136218.7,
- 15
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- SEQ ID NO.304  
NGO-St-135 5'combined;
- 35
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- 45
- SEQ ID NO.305  
NGO-St-135  
YS374/T3 5'
- 50
- 55
- 60
- AL022285.6,
- NM\_014781.1, D86958.1, Z35085.1, X82318.1, NC\_001865.1, AB001684.1, Z72514.1, AC002302.1, AC007486.1, AL049755.2, X79489.1, Z35853.1, AC010151.3, AC009234.3, AF083915.1, AL139074.2, AL132862.1, AC013737.4, U36927.3, AE003692.1, AC006473.2, AF056336.1, AL136363.4, AW502603.1, AI632607.1, AI889925.1, R59196.1, Z40222.1, H28996.1, Z30060.1, AW663145.1, N36767.1, T32056.1, T39659.1, T40715.1, AA063364.1, AW271526.1, AA795138.1, AW771911.1, AA998419.1, AI466480.1, AA880393.1, AI482282.1, AI841402.1, W52752.1, AI786567.1, AV221321.1, BB006621.1, AV254733.1, AW865505.1, AV330249.1, AL044138.1, AI655038.1, AV316950.1, AV348716.1, AV274459.1, AV317688.1, AV280612.1, AV352758.1, AV349442.1, AV245740.1, AV318689.1, AV330001.1, AV328749.1, AI138828.1, AA047474.1, R17528.1, R13828.1, T38143.1, AW861328.1, AW426185.1, AI980387.1, AI959585.1, AI621380.1, Z29358.1, AW851165.1, AV440128.1, AW203956.1, AV347279.1, AI830629.1, AI488952.1, AI361260.1, AI281023.1, AI276138.1, AA828299.1, AA682840.1, AA449644.1, AA425466.1, AC018960.3, AC037464.2, AC018621.3, AC023756.2, AC024448.2, AC016201.5, AL161663.1, AC023777.3, AC006279.6,
- AL022285.6,
- NM\_014781.1, D86958.1, Z35085.1, X82318.1, AL049755.2, D87675.1, AP001442.1, AP000141.1, AP000089.1, AC010151.3, AC009234.3, AC005771.1, AC006761.1, AE003692.1, AF172282.1, AC006478.2, AE001577.1, AC006473.2, AC006222.1, AF100669.1, AF016420.1, AL050322.10, AL022166.1, AB009049.1, AI889925.1, AW663145.1, H28996.1, Z40222.1, N36767.1, T32056.1, R59196.1, T39659.1, T40715.1, AA063364.1, AW271526.1, AA795138.1, AW771911.1, AA998419.1, AI482282.1, AI841402.1, AV221321.1, BB006621.1, AV254733.1, Z30060.1, AW865505.1, AV330249.1, AI655038.1, AV316950.1, AV348716.1, AI786567.1, AV274459.1, AV317688.1, AV280612.1, AV352758.1, AV349442.1, AV245740.1, AV318689.1, AV330001.1, AV328749.1, AI138828.1, AA047474.1, R17528.1, R13828.1, R20722.1, AW861328.1, AI980387.1, Z29358.1, AW851165.1, AW16256.1, AW572236.1, AV391062.1, AW328120.1, AV347279.1, AV220950.1, AW140056.1, AI830629.1, AI281023.1, AI276138.1, AI042194.1, AA682840.1, AA411650.1, AA194887.1, AA189098.1, H85292.1, R55580.1, AC018960.3, AL138741.3, AC022235.2, AC022198.2, AC023756.2, AL161663.1, AC023777.3, AC022224.20, AC019223.2, AL109767.2, AC022148.4, AC009138.5, AC016516.3, AC026891.1, AC016272.3, AC013530.3, AL354668.1, AL162211.3, AL049185.4,

SEQ ID NO.306  
NGO-St-135

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YS382/T3 5'

NM\_014781.1, D86958.1, NC\_001865.1, AB001684.1, AC006443.1, Z72514.1, AC004401.2, AC002302.1, AC007486.1, X79489.1, U41015.1, Z35853.1, Z35852.1, AL050403.13, AB019235.1, AC013737.4, U36927.3, AF121898.1, AE001381.1, AC004171.1, AF056336.1, AL136363.4, AL109983.1, AW502603.1, AI632607.1, Z30060.1, R59196.1, 5 AI466480.1, AA880393.1, W52752.1, Z40222.1, H28996.1, AI786567.1, AL044138.1, T39659.1, T38143.1, AW426185.1, AI959585.1, AI621380.1, AV440128.1, AW614639.1, AJ396349.1, AW467130.1, AW251790.1, AW251721.1, AW203956.1, AV381555.1, AW139206.1, AV384482.1, AW047876.1, AI996020.1, AI849553.1, AI776841.1, AI774351.1, AU073206.1, AI712752.1, AI584023.1, AI488952.1, AI474049.1, AI373038.1, AI361260.1, AI175635.1, AI081464.1, C92808.1, AA828299.1, AA449644.1, AA425466.1, AA397984.1, AA192413.1, W80808.1, N34826.1, 10 R27823.1, AC018960.3, AC037464.2, AC024448.2, AC012389.10, AL356295.3, AL160257.3, AC037454.2, AC064864.1, AC013328.5, AC004153.5, AC010985.3, AC006903.1, AL354763.1,

SEQ ID NO.307

NGO-St-135

15 YS382/T7 3'

NM\_014781.1, Z35085.1, D86958.1, X82318.1, AE003435.1, AC007371.16, AC007489.3, AC024763.1, AE003558.1, U80446.1, AW771911.1, AW271526.1, AI138828.1, AI655038.1, AA047474.1, R13828.1, AI122747.1, AA047435.1, R23393.1, R55580.1, H10270.1, AA374617.1, W60007.1, R17528.1, C75251.1, R22753.1, F13181.1, F11154.1, AI889925.1, N36767.1, R20722.1, AA952920.1, T77023.1, AA206152.1, AI153537.1, AI841402.1, AA795138.1, 20 AA063364.1, AA692714.1, AV316950.1, AI785170.1, AA200762.1, AV330249.1, AA998419.1, AV274459.1, AA976511.1, AA823667.1, AV221321.1, AW130616.1, BB006621.1, R16741.1, AV254733.1, AV280612.1, AV317688.1, AV349335.1, AV348716.1, AA808066.1, AW551190.1, AI627011.1, AV318248.1, AI447566.1, AI302306.1, AA974918.1, T24196.1, AC018960.3, AC051613.3, AC014392.1, AC013253.6, AC013535.4, AC016130.13, AC010113.4, AC017388.1, AC010557.2, AC006714.2, AC006746.1, AL355924.1,

25 SEQ ID NO.308  
NGO-St-136

YS042/T3 5'

NM\_002707.1, AX002424.1, Y13936.1, U81159.1, NM\_008014.1, U42383.1, AX002422.1, AL049551.1, L31397.1, 30 AF249327.1, NM\_011577.1, AF105069.1, L42456.1, U41021.1, AJ009862.1, M57902.1, AB009874.1, AC006592.5, NM\_011668.1, NM\_010473.1, NM\_008272.1, AF114039.1, AC007130.2, AF158597.1, AF132218.1, AF082835.1, AL022070.1, U18428.1, U96636.1, U82122.1, AL138558.1, U61980.1, X55318.1, X07647.1, M35603.1, AC010285.4, AC003692.1, AC010556.4, AC005908.1, AC005943.1, Z66566.1, AL136039.2, AL109967.2, Z85987.13, AP001595.1, AI650583.1, AI992326.1, AW384902.1, AW239336.1, AI879664.1, AW249422.1, AA070392.1, AW577345.1, 35 AW659941.1, AW659925.1, AL042520.1, AW367060.1, AW361618.1, AI894150.1, AA211434.1, AW672699.1, AW161662.1, AI928871.1, AA320736.1, AW850023.1, AI878909.1, AW849906.1, AI879284.1, T06191.1, AW490146.1, AA383664.1, H32905.1, AW163699.1, D76591.1, AA115688.1, AW160907.1, AW082745.1, AI417405.1, AA834611.1, AA085449.1, AI878881.1, AI929038.1, AA074643.1, N88715.1, AW578051.1, AW382863.1, W39347.1, W34891.1, AW321752.1, AL045879.1, AA171301.1, W65536.1, AA383628.1, AI879435.1, AW062337.1, AW630504.1, 40 AW872109.1, AA510019.1, AW871903.1, AW782552.1, AW760420.1, AI940409.1, AI323364.1, AA646479.1, AA190384.1, AC009427.2, AC025903.1, AC007497.2, AC027499.3, AC025642.2, AC022174.2, AL356108.2, AL158171.3, AP001128.1, AC026954.3, AC008006.3, AC027299.6, AL158816.4, AL117187.2, AC064846.3, AC026413.2, AC016575.6, AC026833.2, AC025898.2, AC016837.3, AC015677.4, AC021697.4, AC023379.2, AC023804.7, AC008841.1, AC024264.1, AC012531.1, AF165178.1, AL035477.5, AP001099.1,

45 SEQ ID NO: 309  
NGO-St-136

YS042/T7

NM\_002707.1, Y13936.1, AX002424.1, NM\_008014.1, U42383.1, U81159.1, U83913.1, Z81114.1, Z78415.1, 50 AL163233.2, U28789.1, AP001688.1, AP000961.2, AF213465.1, AC004519.1, AC002428.1, AC004839.1, AC007237.3, AF147259.1, U23527.1, AC004503.1, AL161507.2, AL163254.2, AL135744.2, AL049539.21, Z71782.1, AP001709.1, X87579.1, AP000204.1, AP000244.1, AP000126.1, M20814.1, AI623188.1, AI949680.1, AI769584.1, AW003495.1, AI016791.1, AW514319.1, AI674866.1, AA708807.1, AI954672.1, AI690420.1, AW771608.1, AW129519.1, AI563921.1, AA418416.1, AL044111.1, AI432554.1, AI634705.1, AI570350.1, AW087864.1, AA938139.1, AI917417.1, AI802218.1, 55 AI432562.1, AW250025.1, AW675447.1, AI697620.1, AI686700.1, AI359192.1, AI634891.1, AI587529.1, AI290844.1, AI619769.1, AW163096.1, AI150541.1, N53494.1, AI933325.1, AA190579.1, AI687672.1, AI204201.1, AI435812.1, AI335028.1, AW079871.1, AI587523.1, AI885074.1, AA831968.1, AA292839.1, AI378193.1, AA418531.1, AA115707.1, AI983072.1, AI991100.1, AL046114.1, AA132539.1, AI057142.1, AI962687.1, AI825350.1, AI637949.1, AI754481.1, AA460426.1, N36716.1, AW516535.1, AI445408.1, AA126965.1, N26077.1, AA613447.1, AA133683.1, AA994318.1, 60 T30419.1, AI207138.1, AA470639.1, AW612812.1, AA151641.1, AA079391.1, AI683064.1, AI655486.1, W38314.1, AW806697.1, AW605433.1, AI018391.1, AA580007.1, AA398657.1, AW136714.1, AA465129.1, AA070393.1, AA465723.1, W38641.1, AI634337.1, C02081.1, AI675741.1, AI372924.1, AA621622.1, AI909888.1, AA587456.1, F22497.1, Z39444.1, AW361020.1, AI909859.1, AI690302.1, R53936.1, AI963691.1, AL160290.3, AC048362.2, AC027484.3, AC026473.3, AC009169.4, AC009664.4, AC022478.3, AC010735.3, AC015622.3, AL137066.5,



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AL009206.1, AC037452.2, AC068637.3, AC069218.1, AC024094.8, AC006337.3, AC019043.3, AC040940.1, AC020685.3, AC011849.3, AC009549.3, AC021114.3, AC021002.3, AC016989.4, AC018717.5, AC020892.3, AC009665.4, AC016746.3, AC012529.1, AC004624.6, AC007913.1, AC007438.6, AC006086.7, AC006087.12, AC004670.1, AC005141.1, AL162264.4, AL355531.1, AL354876.1, AP001562.1,,

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SEQ ID NO: 310

NGO-St-137

YS1671/T3

10 NM\_015873.1, D88154.1, AP000497.1, J03781.1, AC007630.3, AL049867.2, AC008989.6, NM\_009509.1, AF009332.1, X85787.1, Z94160.1, AL163292.2, AP001747.1, AP001625.1, M98454.1, D26083.1, AL040451.1, AW226642.1, AW344693.1, AA222407.1, AA272458.1, AA109911.1, AW049791.1, AI842717.1, AW336334.1, H31419.1, AI944648.1, AA871446.1, AJ003346.1, AC015624.2, AC055818.1, AC015627.1, AC009292.7, AC021133.3, AL109918.24, AC023547.3, AC025871.3, AC058789.9, AC064818.3, AC027567.2, AC021876.3, AC011132.4, AF235106.1, AC009837.2, AL136090.10, AL136966.6, AP001274.,

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SEQ ID NO: 311

NGO-St-137

YS1671/T7

20 NM\_015873.1, D88154.1, AP000497.1, AE003608.1, AC005750.1, AC005164.1, AC004453.1, AE002079.1, AC007870.3, L48729.2, AC006211.1, U50713.1, U52431.1, AP000003.1, AB004870.1, AI207789.1, AI828390.1, AI887514.1, AI991204.1, AW087315.1, AI004782.1, AI394648.1, AW627720.1, AI660044.1, AA088690.1, AI699257.1, AA088827.1, AI440449.1, T57294.1, AW197506.1, AA641469.1, AL040452.1, AA992660.1, W85454.1, AV270064.1, AV143508.1, AW701384.1, AW908944.1, AW701603.1, AI182951.1, AW911867.1, AW665415.1, AW629286.1, AW593227.1, AW575674.1, AW573162.1, AW573006.1, AW510703.1, AW340616.1, AW340493.1, AW274644.1, AW183086.1, AW104924.1, AW082305.1, AI927494.1, AI868632.1, AI829672.1, AI827875.1, AI810093.1, AI809958.1, AI808895.1, 25 AI805139.1, AI740990.1, AI685360.1, AI290316.1, AI276754.1, AI273268.1, AI247350.1, AI222006.1, AA919014.1, AA913475.1, AA411451.1, AC015624.2, AC015627.1, AC022034.3, AC020275.1, AC018448.8, AL139236.3, AC069272.3, AC016257.6, AC009466.7, AC024947.2, AC026456.2, AC032008.2, AC027694.2, AC023136.3, AC024720.3, AC023437.2, AC016168.3, AC020778.4, AC010833.3, AC018492.3, AC024158.1, AC021911.1, 30 AC004958.1, AL139342.4, AL133291.3, AP001031.2, AP001802.1, AP001500.1, AP000880.1,

SEQ ID NO: 312

NGO-St-138

YS171/T3

35 NM\_002310.2, X61615.1, NM\_013584.1, S73495.1, D26177.1, S73496.1, D17444.1, D86345.1, U97364.1, M95099.1, AC010140.3, AC006446.3, AE003824.1, AE003687.1, AE003458.1, AF077407.1, AC004829.2, AC005965.1, AC003688.1, U15422.1, AL132902.2, AL132950.1, AB005248.1, AE003742.1, AE003521.1, U89335.1, AC006193.3, AF086440.1, Z81565.1, Z47547.1, AL353871.1, AL138664.1, AL136538.1, AL049550.5, AL035423.4, U19467.1, U28735.1, AJ224683.1, Z11527.1, AB000565.1, T18495.1, AA207338.1, AI226136.1, W20740.1, AI894070.1, 40 AA023181.1, AI195387.1, AA245317.1, AW626804.1, AW529846.1, AW529284.1, AW527135.1, AJ397726.1, AW434719.1, AW355500.1, AW299470.1, AV334964.1, AV294188.1, AW083883.1, AI715801.1, AI575955.1, AA997228.1, AI415987.1, AI011427.1, AA534664.1, AA440412.1, AA193084.1, W81340.1, W81339.1, W79447.1, N42705.1, D69835.1, H59829.1, AC010457.5, AC016324.4, AC022850.3, AC023948.2, AC068662.1, AC025882.2, AC015938.3, AC024169.1, AL354889.4, AL355587.3, AL161660.6, AL162852.3, AC026954.3, AC010176.7, 45 AC010395.5, AC012610.4, AC008782.4, AC027785.2, AC021621.3, AC013642.3, AC019195.4, AC022040.2, AC025285.1, AC021883.2, AC020182.1, AC020286.1, AC013646.3, AC008232.3, AC018232.1, AC007770.4, AC007822.3, AL158053.2, AC020639.4, AC068892.1, AC010376.3, AC012316.4, AC068216.1, AC009627.3, AC026038.2, AC009833.3, AC019141.3, AC013466.2, AC011172.4, AC010003.5, AC009368.5, AC021801.1, AC019524.1, AC020018.1, AC008200.3, AC007910.1, AC006714.2, AL139190.4, AL139098.4, AL137780.2, 50 AL160263.3, AL353606.2,

SEQ ID NO: 313

NGO-St-138

YS171/T7

55 NM\_002310.2, U66563.1, AC018748.3, AF220294.1, AC020728.4, AC009526.4, AC004861.1, AC002457.1, U12386.1, AF064866.1, AE000722.1, AF043945.1, U23517.1, AC000103.1, AL355916.1, AL163283.2, U19289.1, U02537.1, AB017064.1, AC006991.2, AC007661.2, AE003735.1, AE003696.1, AE003562.1, AE003559.1, AC009947.2, AC004746.1, AC004081.1, AF077407.1, AF051985.1, NM\_000810.2, AC004453.1, AC004993.1, AC006044.2, U42580.2, AF039907.1, AC007159.4, AC006409.2, AC005965.1, U89714.1, AC005176.1, Z83105.1, AL022289.1, U73646.1, 60 U73642.1, AL163261.2, AL121787.22, U65744.1, AL161666.2, X70645.1, X96995.1, L08485.1, AP001716.1, AP000188.1, AP000044.1, AP000298.1, AP000112.1, AI915539.1, AI439137.1, N67017.1, AI140597.1, R38064.1, R38159.1, AW766681.1, AW760222.1, AW645026.1, AW644379.1, AW643145.1, AI769415.1, AA825445.1, AA601263.1, AW633848.1, AW384967.1, AV361643.1, AI856958.1, AI807646.1, AI787356.1, AA833639.1, AA631386.1, AA322964.1, AA176759.1, D68013.1, AC010457.5, AC040167.2, AC008074.2, AC021418.3, AC026685.1,

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AC018821.3, AC018829.3, AC007906.2, AC068278.2, AC026811.2, AC068398.1, AC018958.2, AC024235.2, AC040994.1, AC024454.2, AC019295.3, AC022600.1, AC004133.1, AL138931.2, AL157936.3, AL163540.3, AP001536.1, AP000609.2,

5 SEQ ID NO: 314

NGO-St-139

YS313/T3

NM\_004404.1, AF038404.1, D28540.1, D63878.1, NM\_010891.1, D49382.2, AC005104.1, L33246.1, X67202.1, NM\_004574.1, AF073312.1, U88870.1, U88829.1, AF035811.1, NM\_011129.1, X61452.1, AE003722.1, AF129756.1, 10 AJ012008.1, AP000504.1, AE003568.1, AF181897.1, AF113831.1, AE000578.1, AE001491.1, AF063866.1, AF017777.1, AL163002.1, AL162751.1, U97193.1, M65026.1, Z98547.1, X57924.1, AP001313.1, D64003.1, AB005240.1, D10774.1, NC\_001139.1, AE003801.1, AE003691.1, AC005067.2, AC007681.3, AC006949.8, AC006112.2, AC006602.1, AC006502.2, AF106564.1, U00067.1, AC004293.1, AF014008.1, Z72946.1, AL117193.1, AL137230.2, AL035685.21, AJ243530.1, AL021182.1, AL049569.13, AL022397.1, X85807.1, Z72944.1, X57185.1, AJ224373.1, X88845.1, 15 U19801.1, L17338.1, AL043232.2, AA503494.1, AI299913.1, AI557336.1, AA134778.1, AA908712.1, AA516460.1, AW804638.1, AA207185.1, AA346077.1, AA346067.1, AW517043.1, AW580618.1, T79554.1, AA703550.1, AW580614.1, AW175610.1, AW175626.1, AW901420.1, AA309749.1, AW196938.1, AW175616.1, R58037.1, H34478.1, H34850.1, AA063813.1, AA405068.1, AI362531.1, AI588750.1, AW918329.1, AI740549.1, AA278469.1, AA278468.1, L44311.1, AW362022.1, AA091277.1, AI191427.1, W07036.1, AW242840.1, AI801603.1, AW380702.1, AW364487.1, 20 AW379484.1, N85237.1, W39483.1, AW607052.1, AI557335.1, AU000539.1, AA067306.1, AJ394459.1, AW128456.1, R89377.1, AW911380.1, AI287193.1, AW298883.1, AJ392338.1, AA325361.1, AW903179.1, AI991202.1, AI765951.1, AI632238.1, AI459499.1, AA780116.1, AA325651.1, AA324802.1, AA055270.1, AA024634.1, W69297.1, AW209482.1, AI894076.1, AI877025.1, AI323320.1, AI181122.1, AA023716.1, AI140073.1, AW691387.1, AW637056.1, AI412920.1, AI411171.1, AI116225.1, AA097604.1, N57875.1, AW462213.1, AI881739.1, AI584411.1, C57917.1, AC019318.2, 25 AC022958.1, AC012304.2, AC011757.10, AC009395.5, AC018015.1, AL132713.5, AC068059.2, AC008547.4, AC009563.3, AC007131.3, AC055122.1, AC018574.3, AC024722.2, AC025834.1, AC013980.1, AF165425.1, AL1353738.7, AL161432.3, AC022278.9, AC023507.5, AC019070.2, AC069047.1, AC020594.2, AC062030.2, AC067961.3, AC025188.3, AC024579.3, AC020927.4, AC010477.6, AC010475.3, AC008933.4, AC008515.5, AC008485.3, AC010289.3, AC027023.2, AC027676.2, AC008068.3, AC016881.4, AC027042.2, AC053481.1, 30 AC037477.1, AC021842.3, AC018953.5, AC015810.3, AC018684.2, AC024518.2, AC021000.3, AC016841.2, AC007710.10, AC023958.2, AC007223.1, AC016760.3, AC012354.3, AC017587.1, AC014457.1, AC008358.3, AL355335.3, AL109931.15, AL356372.1, AL139812.5, AL034372.30, AL133271.15, AL121952.6, AL162332.1, AL133168.1, Z98855.1, AP001591.1,

35 SEQ ID NO:315

NGO-St-139

YS313/T7

NM\_004404.1, AC005104.1, AF038404.1, D63878.1, D28540.1, NM\_010891.1, D49382.2, AL031779.5, Z98754.1, AL163229.2, AP001684.1, AP000657.1, AP000561.1, NM\_015759.1, AF017369.1, AF038172.1, AE003820.1, 40 AC004615.1, AC008165.3, AC005078.1, AC006572.2, AC005184.1, AC005242.1, AL049557.19, AC000386.1, AL157991.1, AL121963.10, AL132846.1, Z68276.1, AP001306.1, M63453.1, AI753689.1, AI114531.1, AI754501.1, AI088934.1, AW152364.1, AI609395.1, AA639591.1, AI160331.1, AI951387.1, AI955165.1, AI573059.1, AW473653.1, AI956125.1, AI126301.1, N21100.1, AI089658.1, AI632807.1, AW273787.1, N35895.1, AW020474.1, AI094932.1, AW026345.1, N67318.1, AW339045.1, AW886537.1, AA234940.1, AI137035.1, AW514047.1, AI346269.1, 45 AA218642.1, N67464.1, AA516108.1, AI829564.1, AI683327.1, AI355722.1, AA516499.1, AW022200.1, AA234941.1, AA206067.1, AI564619.1, AW769271.1, AI357439.1, AW517058.1, AI635685.1, AI087118.1, AI273328.1, AI143819.1, AI051872.1, AW474968.1, AW167451.1, AI754942.1, AI708338.1, AA775507.1, AA565842.1, AI130699.1, AA809247.1, AA430153.1, T15553.1, AW023986.1, AW469297.1, AI039303.1, AI521676.1, AA971524.1, AA487437.1, AW302623.1, AI880684.1, AI143019.1, AA812690.1, AI081421.1, AA043265.1, AW771795.1, AA599961.1, AA181698.1, AA071074.1, 50 AI754299.1, AI355732.1, AI027964.1, AI338308.1, AA808182.1, AA209392.1, AW192277.1, AI858793.1, AI304415.1, AI225151.1, AI139335.1, AW337224.1, AI434203.1, AI565741.1, AI217047.1, AI190711.1, AW129449.1, N25544.1, N53355.1, AW771405.1, AI636810.1, AI096434.1, AA928349.1, AA599844.1, AI024553.1, AI830555.1, AC067872.1, AC012304.2, AC019318.2, AC013382.3, AC022958.1, AL137008.2, AC027057.3, AC024706.3, AC011210.3, AL121819.2, AC010600.3, AC008525.4, AC027182.1, AC009146.2, AL133383.6, AC058801.2, AC027523.2, 55 AC022912.3, AC025164.8, AC021662.8, AC018548.7, AC021873.7, AC012514.8, AC069223.1, AC068763.2, AC069025.1, AC069013.1, AC068070.2, AC068708.2, AC007511.2, AC011209.3, AC067953.2, AC027344.2, AC026410.2, AC010419.3, AC046162.2, AC027812.2, AC067899.1, AC026935.2, AC020684.4, AC020778.4, AC024053.2, AC022986.3, AC021111.3, AC025706.3, AC013303.3, AC011774.4, AC024503.2, AC022923.3, AC016515.3, AC013637.3, AC023560.2, AC022568.3, AC025489.1, AC008853.1, AC005472.14, AC007472.5, 60 AC022016.2, AC014851.1, AF166490.1, AC007702.1, U82207.1, AL157761.2, AL157402.2, AL356218.1, AL353136.3, AL132868.12, AL355373.1, AL354809.1, AL161933.3, AL353731.1, AL159980.3, AL136360.7, AL135818.2, AL035066.20, AL021573.1, AP001848.1, AP001487.1, AP001486.1, AP001018.1, AP000875.1, AP000789.1,

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YS2312/T3

- 5 NM\_004724.1, U54996.1, AJ250458.1, AE003557.1, AC003949.1, AJ012166.1, U39676.1, AL031785.1, AC006332.3, AF244289.1, AF244276.1, AF244264.1, AF244262.1, AF244261.1, AE003628.1, AC003060.1, AC004830.1, AC004887.2, AE001709.1, AC005454.1, AF081108.1, AC005293.1, Z81567.1, Z69386.1, AL133334.16, S70930.1, AL138655.1, M80829.1, AL049861.18, AL137961.1, AW107591.1, AA693260.1, AV046551.2, AV147645.1, AA692808.1, AJ396591.1, AJ395373.1, AW375854.1, AV362443.1, AW003698.1, AI887627.1, C77594.1, AA541074.1, Z92701.1, AA148712.1, AC036188.2, AC068190.1, AC036226.1, AC020808.2, AP001882.1, AP000913.2, AP000744.1, AC021176.3, AC006591.12, AC018042.1, AC008303.1, AC026900.3, AC027690.4, AC027341.2, AC010276.5, 10 AC024383.3, AC023774.3, AC025551.3, AC019145.5, AC013693.3, AC023632.1, AC022652.1, AC010885.3, AC018617.2, AL138884.3, AL138796.3, AL136086.3, AL096819.12, AC036166.3, AC027821.3, AC060778.2, AC009783.7, AC012040.9, AC068764.2, AC012526.20, AC019041.3, AC053479.2, AC036181.2, AC060829.2, AC021082.2, AC010631.4, AC026474.3, AC026464.3, AC018646.1, AC064794.1, AC019055.3, AC024067.3, AC053522.1, AC051661.1, AC026561.2, AC012130.2, AC019058.3, AC023881.2, AC021469.3, AC011562.4, 15 AC015523.3, AC011972.3, AC011277.4, AC023013.2, AC024630.1, AC020607.2, AC021317.2, AC015973.1, AC013268.1, AC009849.6, AC012796.1, AL355853.3, AL355005.2, AL356117.1, AL136118.3, AL135915.2, Z98876.1,

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YS2312/T7

- 20 NM\_004724.1, U54996.1, AF003951.1, AC008085.1, AC004520.1, AF011889.1, AE001131.1, Z99162.1, AL031275.1, AP002068.1, AE003825.1, AE003435.1, AC007636.19, AC018833.3, NM\_006389.1, AC005483.1, AC007395.3, AC011663.5, AC005966.1, AC006442.1, AF004556.1, U65785.1, AC004518.1, AF045265.1, AC004237.1, AL163002.1, Z75552.1, AL096712.20, AL022397.1, J02027.1, V01170.1, Z73477.1, AB005240.1, AB005531.1, D86408.1, 25 AW235646.1, AA599145.1, AW575031.1, AW851090.1, AW057979.1, AI290602.1, AA076428.1, AI937662.1, AI025335.1, AI680594.1, AI810264.1, AA416982.1, AA252056.1, R38913.1, AW170221.1, Z41148.1, AA251899.1, R01885.1, T90448.1, AA812446.1, AW851089.1, T82954.1, AI684285.1, C21581.1, AI230413.1, AA940442.1, AA163727.1, AI060892.1, AV428214.1, AW644211.1, AW087475.1, AW045499.1, AI976733.1, AV048357.1, U21463.1, AA574864.1, AA365430.1, AA298325.1, AA175204.1, C17935.1, W30805.1, H86313.1, H85644.1, H06905.1, R13668.1, T74922.1, AC036188.2, AC068190.1, AC022429.3, AL121796.4, AC021596.1, AC026129.3, AC009518.6, AC016934.4, 30 AC026863.3, AC068174.1, AC023845.2, AC020874.2, AL356464.2, AC044882.3, AC026004.3, AC069274.1, AC069259.1, AC061981.2, AC034288.2, AC022101.3, AC022096.3, AC016602.5, AC010398.6, AC008842.4, AC008950.3, AC008687.3, AC068557.1, AC068310.1, AC009440.2, AC009309.2, AC009471.3, AC019043.3, AC011711.2, AC048354.1, AC026667.2, AC025706.3, AC015999.3, AC026819.1, AC026206.1, AC024518.2, 35 AC016750.4, AC021121.3, AC022773.2, AC022011.2, AC018835.3, AC007578.4, AC016394.3, AC022381.1, AC010165.2, AC019815.1, AC018014.1, AC006910.2, AL121928.11, AL157364.2, AL139000.3, AL135842.5, AL355335.3, AL139347.3, AL356461.1, AL356373.1, AL139424.3, AL157386.3, AL354956.1, AL353646.1, AP001983.1, AP001182.1, AP001098.2, AP000909.1, AP000877.1, AP000854.1, AP000833.1, AP000710.1,

40 SEQ ID NO: 318

NGO-St-141

YS1653/T3

- 45 AF220152.2, AF176646.1, AF095791.1, AB041546.1, AC009145.4, AF110520.1, U48455.1, AC007686.5, AC004000.1, AC006365.3, AC005820.1, AF135125.1, AC005519.2, AC006957.1, AL049734.11, Z84466.1, X60322.1, AA307658.1, AW295050.1, AW381667.1, AW654821.1, AW762888.1, AW062585.1, AW820659.1, AI450529.1, W40612.1, AW295045.1, AF150311.1, AI019873.1, U49254.1, AW451671.1, AL044797.1, C93889.1, AA215860.1, AW870886.1, AW870865.1, AW286314.1, AI711921.1, AI695573.1, AI450513.1, AI415393.1, T46771.1, AA381620.1, AA381302.1, AA224113.1, AA036086.1, AA008214.1, AA007765.1, W41129.1, AL135793.5, AC006180.1, AC040174.2, AC027279.2, AC009451.6, AC025959.3, AC055713.2, AC048331.5, AC046170.2, AC009449.2, AC025963.2, AC016438.3, 50 AC026894.1, AC024530.3, AC011061.4, AC010844.5, AC011318.8, AC068982.2, AC069010.1, AC025987.3, AC006534.3, AC068877.1, AC068837.1, AC068519.1, AC027824.2, AC068364.1, AC012272.2, AC025697.2, AC026378.4, AC055858.1, AC027031.2, AC040998.1, AC032017.1, AC023034.2, AC025368.1, AC013786.2, AC019340.2, AC021315.1, AC015706.2, AL355366.2, AL139109.2, AL138749.7,

55 SEQ ID NO: 319

NGO-St-141

YS1653/T7

- 60 AF220152.2, AF176646.1, AF095791.1, T54480.1, AA197191.1, AW103791.1, AW131855.1, AW379901.1, AW856286.1, AW856267.1, AW856115.1, AW856067.1, AW815565.1, AW815555.1, AW815535.1, AW815392.1, AW815391.1, AW582306.1, AW582296.1, AW582282.1, AW391319.1, AW380346.1, AW362647.1, AI525534.1, AW815543.1, AW605996.1, AW605995.1, AW605994.1, AW605992.1, AW605991.1, AW605988.1, AW582313.1, AW582268.1, AW380347.1, AW380331.1, AW380323.1, T29399.1, W25677.1, N57107.1, AW861030.1, AW861031.1, AW753790.1, AA133029.1, AW238260.1, AL135793.5, AL353777.6,

## SEQ ID NO.320

NGO-St-142

YS1703/T3 5'

- 5 NM\_003920.1, AF098162.1, AB015597.1, AK000721.1, NM\_011589.1, AF098161.1, AF071506.1, AB019001.2, AB015598.1, AF126480.1, AB019576.1, AC007043.3, AP000354.1, AC000105.41, AC011456.2, AE003430.1, NM\_006118.1, AC007655.1, AC007541.9, AC004032.7, U20824.1, U82696.1, AL132975.1, AL132954.1, U68566.1, AL035693.19, AL022330.4, AL034552.22, AJ248285.1, NC\_001136.2, AC020912.4, AC016662.5, AC012679.3, NM\_007682.1, NM\_001717.1, AC005035.1, AC007784.7, AF135787.1, AF135397.1, AF135395.1, AC007787.1, AF091398.1, AC006380.2, AC005069.2, AC006062.4, L34162.1, L19443.1, AF022365.1, U59694.1, AL049569.13, Z85996.1, Z74369.1, Z74368.1, Z26875.1, Z46796.1, Z95210.1, X55038.1, M26440.1, M15410.1, X68757.1, M19540.1, L03427.1, X82086.1, AW839959.1, W87879.1, AW672754.1, AW379444.1, AW840009.1, AW277013.1, AA853284.1, AW326647.1, AW658376.1, AW802270.1, AW614491.1, AW407158.1, AW343382.1, AW161333.1, AW055155.1, AI640251.1, AI494066.1, AI028107.1, AI017338.1, AA987779.1, AA550998.1, AA476555.1, AA378527.1, AA373491.1, AA348092.1, AA324524.1, AA324379.1, AA321961.1, AA216551.1, AA213579.1, W82846.1, C04452.1, C03261.1, W07180.1, W04378.1, W03539.1, W02741.1, N99738.1, N40129.1, N35204.1, N28312.1, H91970.1, R91592.1, AW485342.1, AW435759.1, AW426330.1, AW163683.1, AW013483.1, AV003759.1, AI618639.1, AI416196.1, AI201312.1, AA561002.1, D81215.1, R25330.1, AC025574.6, AC024884.6, AC009289.5, AC009056.3, AC012534.2, AC007424.20, AC024096.7, AC022438.3, AC032035.2, AC023767.3, AC020703.3, AC024418.2, AC025107.1, AC010532.2, AC010113.4, AC014387.1, AL354980.1, AL080246.13, AL121812.1, AP001652.1, AP001636.1, AP000576.2, AC018995.4, AC023130.3, AC034245.2, AC027309.2, AC010503.5, AC010862.5, AC010533.3, AC009139.5, AC023572.3, AC022217.3, AC016168.3, AC025100.2, AC009577.3, AC021762.3, AC017022.3, AC023341.3, AC015473.3, AC024019.2, AC023579.2, AC016018.7, AC023321.1, AF200455.1, AC011694.2, AL121901.18, AL136114.2, AL079336.13, AL353140.3, AL139274.6, AL160258.3, AL354822.1, AL353779.2, AL158845.2, AL157699.2, AL121715.2, AL132640.1, AC000382.1, AL139247.1,
- 25

## SEQ ID NO.321

NGO-St-142

YS1703/T7 3'

- 30 NM\_003920.1, AF098162.1, AK000721.1, AL022149.2, NM\_003599.1, AC009294.8, AF064804.1, AF069734.1, AF073930.1, AC004508.1, AL163285.2, AL163912.1, AL080243.21, M62354.1, AW136364.1, AI333322.1, AA809127.1, AW512259.1, AW167047.1, AW675811.1, AW418601.1, AI802251.1, AI283089.1, AI885862.1, AW769136.1, AW181883.1, AI969152.1, AI825472.1, AI494276.1, AW189438.1, AI278255.1, AA115381.1, AW731809.1, AW275265.1, AI559688.1, AI283087.1, AA679712.1, AW089758.1, AI002252.1, AW058036.1, AI696514.1, AA853283.1, T16124.1, AI446312.1, AI468188.1, AI417732.1, AA115380.1, AW134955.1, AW386251.1, AW372691.1, AW372725.1, AW386250.1, AW386246.1, AW386230.1, AW384593.1, AW373076.1, AW386279.1, AW386226.1, AW372712.1, AW151342.1, AW749244.1, AW372690.1, AW384617.1, AW373100.1, AW372711.1, AW386261.1, AI913828.1, AI887884.1, AW372727.1, AW386248.1, AW386266.1, AA564588.1, AC025574.6, AC024884.6, AC012647.15, AP000938.2, AP000894.2, AC068984.3, AC025188.3, AC020927.4, AC010621.3, AC008529.3, AC022553.2, AC037440.1, AC019231.3, AC025807.2, AC011035.3, AC023917.2, AC011898.2, AC017021.2, AC022999.1, AC011134.2, AL355873.2, AL161905.4, AJ011929.1,
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## SEQ ID NO.322

NGO-St-143 combined

- 45 AL137757.1, NM\_003683.1, U79775.1, AL163297.2, AP001752.1, AP001053.1, NM\_010925.1, U79773.1, U79774.1, AF227000.1, AF102850.1, AF032922.1, AF039698.1, AF103726.1, U48696.1, AF045432.1, AF027174.1, AF033097.1, AJ243486.1, S78798.1, AJ249625.1, U66300.1, U39066.1, AJ004935.1, U37573.1, Z97178.1, AJ010903.1, Y17148.1, U30169.1, Z49980.1, D61704.1, AF030515.1, AF061786.1, AJ277276.1, AJ277275.1, AJ001103.1, U34048.1, AJ243655.2, U35663.1, Y15421.1, AJ277097.1, AJ243250.1, X99051.1, AF033565.1, AJ237664.2, S83098.1, U65376.1, U52868.1, AJ242994.1, AF079586.1, AF033096.1, AF013238.1, AL163972.1, X99055.1, X65215.1, AC007193.1, Z92546.2, AC010793.3, AF155911.1, AC005049.2, AL163299.2, AP001754.1, AB023046.1, M22135.1, AI634547.1, AI905810.1, AI167158.1, AI860822.1, AI362799.1, AA879460.1, AW193286.1, AA621964.1, AA113148.1, AA085786.1, AA477106.1, AA814978.1, AI905802.1, AI160620.1, AI905797.1, AA425939.1, AI368572.1, AA135482.1, T07989.1, L25241.1, AI905807.1, AI762088.1, AI905803.1, AI905804.1, AI905811.1, AI905805.1, AI905808.1, AI905809.1, AA931669.1, AI905800.1, F36453.1, AA135818.1, H35525.1, AW743985.1, AL022772.1, AW230615.1, AA967213.1, AA240651.1, AA120481.1, AA072658.1, AI905822.1, AW416555.1, AA755933.1, AA870102.1, AV297071.1, AI292030.1, AA867502.1, AV267338.1, AW356977.1, AV280340.1, W58771.1, AA674077.1, N55721.1, AW587463.1, AA095435.1, N88018.1, AW587505.1, AV326909.1, AI816677.1, AI816676.1, AI816670.1, AI816665.1, AI816636.1, AI816635.1, AI816630.1, AI816629.1, AI816623.1, AI816621.1, AI816617.1, AI816615.1, AI816614.1, AI816613.1, AI816612.1, AI816606.1, AI816605.1, AI815377.1, AI815338.1, AI815337.1, AI815336.1, AA247964.1, AA249353.1, AA247827.1, AA096046.1, AA095641.1, AA093577.1, AA092086.1, N89520.1, N83168.1, N88601.1, N84855.1, N84830.1, N84781.1, N84718.1, N84712.1, N84048.1, N83993.1, N83992.1, N88518.1, AI816682.1, AI272402.1, AC003656.1, AC025913.2, AC015890.2, AC010832.3, AC011550.3, AC011512.5, AC008738.5, AC005038.2, AC023421.2, AF216667.1, AC010884.4, AC015871.1, AC019337.1, AC015860.2, AL137076.5, AC018714.3, AC022255.3, AC026513.2, AC016883.3, AC026232.1, AC021730.3, AC024123.1, AL157896.2, AC023494.5,
- 60

AC023883.4, AC026803.2, AC025224.3, AC022327.6, AC061963.1,

SEQ ID NO.323

NGO-St-143

5 YS1621/T3 5'

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SEQ ID NO.324

35 NGO-St-143

YS1621/T7 3'

AL137757.1, AL163297.2, AP001752.1, AP001053.1, NM\_003683.1, U79775.1, NM\_003830.1, AC007633.3, AF170484.1, U71383.1, AL109953.24, AL161831.1, AL161586.2, AL161515.2, AL079347.1, U32186.1, AC006920.10, AC005560.2, AE003552.1, AE003551.1, AE003542.1, AC005774.1, AF170972.1, AC009895.2, AC005049.2, 40 AF017257.1, AL163277.2, AL049795.20, AL031588.1, AL031848.11, L34771.1, U46669.1, AP001732.1, AP001040.1, AB023046.1, AI634547.1, AI167158.1, AI860822.1, AI362799.1, AA879460.1, AW193286.1, AA621964.1, AA113148.1, AA085786.1, AA477106.1, AA814978.1, AI160620.1, AI368572.1, AA135482.1, T07989.1, L25241.1, AI762088.1, AA425939.1, AA931669.1, F36453.1, AA135818.1, AI155506.1, AA386906.1, Z81226.1, W89417.1, AA049595.1, AW819008.1, AW812918.1, AW812808.1, AW651237.1, AW651235.1, AW182071.1, AV367551.1, AW118908.1, 45 AL121132.1, AI760754.1, AU050523.1, AU069491.1, AI538204.1, AI301191.1, AI204164.1, AI192033.1, AI188040.1, AI005113.1, AI004282.1, AI001990.1, AA829448.1, AA808355.1, AA805773.1, AA805770.1, AA805757.1, AA578718.1, AA461396.1, W49126.1, N42521.1, H77382.1, H69418.1, R83544.1, AC003656.1, AC010832.3, AC069214.1, AC011121.4, AC022255.3, AC019225.2, AC025865.2, AL160006.2, AC021886.4, AC025224.3, AC044866.1, AC018755.2, AC024514.2, AC006433.14, AC008764.6, AC020907.3, AC020553.3, AC023169.3, AC026279.3, 50 AC016207.4, AC010958.3, AC026392.2, AC026226.1, AC010751.3, AC010698.4, AC010043.4, AC015977.3, AC020578.3, AC014376.1, AC014962.1, AC020215.1, AC010107.5, AC010566.2, AL121991.4, AL354000.2, AL137077.4, AL158217.3, AL035362.1, Z96802.1, AP001522.1,

SEQ ID NO.325

55 NGO-St-144

YS273/T3 5'

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- AA179371.1, AA145014.1, W63826.1, AL139040.4, AC013751.3, AC068591.1, AC018720.3, AC015940.2, AC025843.2, AC015931.4, AC015801.3, AC009558.3, AC010959.3, AC008088.2, AC018665.2, AC018521.1, AL161638.2, AC063954.2, AC036174.2, AC068728.3, AC022420.3, AC010484.3, AC008439.3, AC032019.2, AC018644.3, AC009220.7, AC011443.4, AC031998.2, AC022285.5, AC062029.1, AC026591.2, AC022227.6, AC025707.3, AC040955.1, AC026154.3, AC025931.2, AC013345.3, AC013328.5, AC015670.4, AC015988.3, AC025590.2, AC026471.1, AC020560.2, AC020706.3, AC011165.3, AC011798.3, AC023022.1, AC012489.3, AF214634.1, AC020183.1, AC020509.1, AC009849.6, AC005124.2, AL356464.1, AL122034.8, AL353092.3, AL162255.5, AL121747.21, AL355314.1, AL354714.2, AL158217.3, AP001491.1,
- 10 SEQ ID NO.326  
NGO-St-144  
YS273/T7 3'
- AF134726.1, AP000502.1, AC003037.1, AC002040.1, AC006449.19, AC002044.1, AC004129.1, AC006441.13, AC002351.1, AF030876.1, AC005757.1, AC005620.1, AC004583.1, AF031078.1, AF223391.1, U96629.1, AC009516.19, AC005921.3, AP001052.1, AP000553.1, L48038.2, AC002059.3, AC000026.3, AF121781.1, AL163279.2, AC002326.1, AL009031.1, AC007956.5, AC006387.3, AC004098.1, AL133355.12, AC002456.1, AC005015.2, AC005519.2, AP000184.1, AP000040.1, AP000282.1, AP000108.1, U91321.1, AC003959.1, AL163215.2, AL135749.2, AD000864.1, L78810.1, Z93023.1, AL009172.1, AP001670.1, AC004668.1, AC003086.1, AC004465.1, AC004132.1, AC003684.1, AL121749.13, AC005067.2, AL035045.2, AC005057.2, AC004687.1, U62293.1, AF196971.1, AC006544.19, AC004382.1, AC006254.10, AL050307.13, Z86064.1, Z97054.1, AL031276.1, AL109798.19, AP000283.1, AC002126.1, AC003010.1, AL031848.11, Y07848.1, AC006111.2, U82828.1, AL023584.1, AF038458.1, U93037.1, AL031311.1, AC011455.6, AC005295.1, AC005104.1, AC004253.1, AL121809.4, AC006930.1, AL136418.2, AL139054.1, AL078644.10, AL022237.1, AA284189.1, AW338381.1, AA568535.1, AA579064.1, AA281850.1, AA994641.1, AW794982.1, AA857326.1, AL036622.1, N89207.1, AW591633.1, AW166629.1, AW088364.1, AI076062.1, AA748058.1, AA704850.1, AA570496.1, AA371011.1, AA044796.1, AA044741.1, M77904.1, AW081071.1, AI631359.1, AI580045.1, AI471805.1, AI469586.1, AI282705.1, AA854983.1, AA644545.1, AA503615.1, AA486925.1, AW875776.1, AW794828.1, AW193880.1, AI242847.1, AI085078.1, AI032984.1, AA812987.1, AA745404.1, AA482685.1, AA460896.1, AA377927.1, AA174138.1, AA059338.1, W01949.1, N21111.1, AW409692.1, AI051697.1, AA974475.1, AA579437.1, AA580000.1, AA564343.1, AA465689.1, AA338281.1, AW518364.1, AW373785.1, AW135699.1, AI798136.1, AI696117.1, AI475231.1, AI339498.1, AI168274.1, AI025850.1, AI017159.1, AA657377.1, AA614340.1, AA557393.1, AA525157.1, AA504723.1, N31583.1, N21688.1, T52837.1, AA507035.1, AA317869.1, AI223321.1, AA742637.1, H73550.1, T90362.1, H60462.1, H50970.1, AI679747.1, AI332671.1, AI014798.1, AW855113.1, AW086361.1, AI862231.1, AI792627.1, AI792525.1, AI349662.1, AI348722.1, AI254439.1, AI053903.1, AI053450.1, AA594091.1, AI469598.1, AW105737.1, AA830169.1, AW316747.1, AW836527.1, AA826285.1, AL139040.4, AL356352.2, AC067952.3, AL096887.7, AL160175.4, AC015904.3, AC016636.4, AC011461.2, AC009019.4, AC008732.4, AC024156.2, AC022037.1, AP000921.2, AP000571.1, AC008267.3, AC018506.3, AC016289.3, AL353653.5, AL354681.1, AC015551.9, AC023121.3, AC023970.2, AC027272.2, AC011152.4, AC011134.2, AC016703.3, AP000761.1, AP000685.1, AC008731.4, AC019207.3, AC017093.2, AL354656.1, AP001381.1, AC055815.2, AC026419.2, AC011495.3, AL162415.2, AC021836.3, AC018500.2, AL353712.2, AL158169.1, AL138798.2, AC021590.3, AC013691.3, AC012364.3, AC021565.1, AC008922.5, AC016916.4, AC021194.2, AC046135.4, AL159989.3, AL161672.2, AL138788.1, AC025164.7, AC064826.2, AC016675.4, AC009362.5, AC011477.3, AC009073.5, AC027372.2, AC023959.2, AC012182.3, AL139226.14, AC046176.2, AC016736.3, AL136360.7, AC010742.3, AC013797.2, AL109743.3, AC011484.2, AC026170.1, AC012433.5, AC026022.2, AC011499.2, AC032015.2, AC026300.2, AC026634.2, AC009335.2, AC022951.2, AL355001.3, AL137849.2, AC044819.2, AC020757.2, AL121926.16, AL354693.1, AC025918.3, AC012659.3, AC011785.3, AL160009.3, AL139022.1, AC007939.2, AL354745.3, AL139132.4, AL354808.3, AJ132411.1, AC044817.2, AC025090.2, AC013275.4, AP000668.1, AC009110.5, Z83844.5, AL031672.12, AL033376.17, AC002045.1, AC005377.2, AC006509.15, AC005071.2, AC005940.3, AC007029.3, AL050350.14, AC004506.1, Z82206.1,
- 50 SEQ ID NO.327  
NGO-St-145  
YS1411/T3 5'
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SEQ ID NO.328

-158-

NGO-St-145

YS1411/T7 3'

- 5 AL133161.1, AK001729.1, AF087969.1, AF177478.1, AL159179.2, AL049835.3, AL096851.1, AC007252.2, AF081241.1, AC008125.9, AF135183.1, AC004704.2, AC005937.1, AC003024.1, U71587.1, AE000904.1, AJ271161.1, U43282.1, U41530.1, AB042823.1, AP000511.1, AB023048.1, AJ007958.1, AL043584.1, AI131161.1, AL047721.1, AI074999.1, AI369743.1, AI191659.1, AI752102.1, AI804688.1, H70039.1, W63623.1, AA412273.1, AA345937.1, AA461564.1, AA346011.1, W39608.1, AA046569.1, AL045395.1, AA412608.1, H70038.1, AW263032.1, AA534737.1, AI854609.1, AU024381.1, AI235913.1, AW556867.1, AI464166.1, AI862154.1, AW195190.1, AW532431.1, AW134839.1, AI632675.1, AI333447.1, AW070552.1, AA776248.1, AI033598.1, AI492046.1, AI560827.1, AI990263.1, AI090658.1, 10 AW131196.1, AI337152.1, AA962117.1, AA216415.1, AI377836.1, AI032741.1, AI381470.1, AW182779.1, AA137689.1, AA865536.1, AA632347.1, W61524.1, AI307523.1, W88673.1, AI278969.1, H30866.1, AA460639.1, AW336387.1, R94150.1, AW499467.1, AA294458.1, AI401456.1, AA432615.1, AV390623.1, AW580849.1, AW580825.1, AW336569.1, AW336391.1, AW257455.1, AW217194.1, AV264232.1, AI439888.1, N53539.1, AL353736.1, AC010736.4, AC023254.3, AC061993.2, AC024232.2, AC025734.2, AL139125.3, AL158046.1,

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SEQ ID NO.329

NGO-St-145

YS144/T3 5'

- 20 AL133161.1, AK001729.1, AC005343.1, Z50797.1, NC\_001142.1, AE003727.1, AE003462.1, AF223391.1, AC004662.1, AC004254.1, AC006820.1, AC024205.1, NM\_007046.1, NM\_006521.1, AF162780.1, NM\_008448.1, AF207550.1, AF196779.1, AF088916.1, AC005275.1, AF049895.1, AE000113.1, AF068862.1, AC003694.1, AF070717.1, AF069716.1, AC004642.1, L43549.1, AL163239.2, AL133332.12, AL161985.1, AL161496.2, U86090.1, AL050138.1, Z70273.1, U29523.1, Z49452.1, D87675.1, AP001694.1, X97162.1, X96717.1, X51330.1, AP001443.1, AP000140.1, AB011100.2, AP000088.1, X54945.1, D10483.1, L27153.1, AL045394.1, AL047720.2, AW815677.1, AW447609.1, AW418275.1, 25 AI426794.1, AW668623.1, AA087606.1, AI380050.1, AA914152.1, AW774428.1, AW736393.1, AW649599.1, AW586591.1, AI138309.1, AI892798.1, AI739806.1, AA711482.1, AA692780.1, AA692302.1, AA671345.1, AA655714.1, AA415524.1, AA119710.1, AA097087.1, AA087538.1, AA087381.1, H33004.1, R50279.1, AL353736.1, AC012445.3, AC011030.4, AC009564.4, AC051613.3, AL132672.7, AP000478.2,

30

SEQ ID NO.330

NGO-St-145

YS144/T7 3'

- 35 AL133161.1, AK001729.1, AF087969.1, AF177478.1, AL159179.2, AL049835.3, AC006222.1, AC007252.2, AF081241.1, AC008125.9, AF135183.1, AC004704.2, AC005937.1, AC005180.1, U71587.1, AE000904.1, AJ271161.1, U43282.1, U41530.1, AB042823.1, AP000511.1, AB023048.1, AL043584.1, AI131161.1, AL047721.1, AI074999.1, AI369743.1, AI191659.1, AI752102.1, AI804688.1, W63623.1, H70039.1, AA412273.1, AA345937.1, AA461564.1, W39608.1, AA346011.1, AA046569.1, AL045395.1, AA412608.1, H70038.1, AW263032.1, AA534737.1, AI854609.1, AU024381.1, AI235913.1, AI464166.1, AW556867.1, AI862154.1, AW195190.1, AW532431.1, AW134839.1, AI632675.1, AI333447.1, AW070552.1, AA776248.1, AI033598.1, AI492046.1, AI560827.1, AI307523.1, AI990263.1, 40 AI090658.1, AW131196.1, AI337152.1, AA962117.1, AA216415.1, AI377836.1, AI032741.1, AI381470.1, AW182779.1, AA865536.1, AA137689.1, AA632347.1, W61524.1, AA460639.1, W88673.1, AI278969.1, H30866.1, AW336387.1, R94150.1, AA432615.1, AW499467.1, AA294458.1, AV390623.1, AI598316.1, AI401456.1, AW706903.1, AW580849.1, AW580825.1, AW257455.1, AW217194.1, AV264232.1, AI950381.1, W28723.1, N53539.1, H60201.1, H60196.1, R45124.1, R19599.1, R19570.1, AL353736.1, AC010736.4, AC023254.3, AC061993.2, AC021751.11, AC011448.2, 45 AC025792.2, AC025734.2, AC023932.2, AL139125.3, AL158046.1, AP001127.1,

SEQ ID NO.331

NGO-St-145

YS278/T3 5'

- 50 AL133161.1, AK001729.1, NM\_008958.1, AB028866.1, AB010833.1, NM\_014726.1, AF217796.1, AC002432.1, AC002303.1, AF077302.2, AC007298.17, AC005520.2, AF112866.1, U60822.1, AC004233.1, AL135752.2, AJ131018.1, AL096699.11, U10895.1, AK001621.1, AB018318.1, AW500657.1, AW673603.1, AW868998.1, AW869117.1, AI608224.1, AA387916.1, AW288019.2, AW654284.1, AW493485.1, AW487305.1, AW487276.1, AW461989.1, AW437659.1, AW403475.1, AW319454.1, AW239228.1, AW239051.1, AV217284.1, AV215050.1, AV205793.1, 55 AV155082.1, AV166903.1, AV152358.1, AV137501.1, AV123651.1, AV120391.1, AV117483.1, AV101080.1, AV098121.1, AV091752.1, AV084455.1, AV083583.1, AI763878.1, AV061031.1, AV060485.1, AV058197.1, AV057140.1, AV056958.1, AV055574.1, AI713124.1, AV006753.1, AI575485.1, AI527477.1, AI012556.1, AI179780.1, AI175786.1, AI119288.1, AI112286.1, AI111977.1, AI111490.1, AI072849.1, AI071746.1, AA874227.1, AA810909.1, AA797102.1, AA616728.1, AA445862.1, AA278495.1, AA182075.1, AA145911.1, AA072792.1, AA059888.1, 60 AA047908.1, AA041963.1, AA032369.1, AA003397.1, H61508.1, AL353736.1, AC012683.3, AC023955.2, AC018698.4, AC047322.1, AC049120.1, AC025999.3, AC019264.3, AC025655.2, AC010754.2, AL160235.1, AP001202.1, AC021048.8, AC024727.4, AC068810.1, AC025643.3, AC068488.1, AC019093.3, AC022842.4, AC023593.3, AC010268.3, AC019129.3, AC018673.3, AC025424.3, AC027044.2, AC021421.2, AC024731.5, AC013543.4, AC036147.1, AC024883.3, AC027777.1, AC021323.2, AC025133.2, AC020994.5, AC023658.1, AC016777.3,



AF202962.1, AC013679.1, AC005054.1, AL162714.4, AL121845.18, AL121880.15, AP001556.1, AP001368.1, AP000834.1, AP000757.1, AP000683.1,

## SEQ ID NO.332

5 NGO-St-145

YS278/T7 3'

- AF087969.1, AL133161.1, AK001729.1, AF177478.1, AL159179.2, AL049835.3, U40830.1, Z97055.1, AJ238394.1, X61677.1, M90087.1, AC004981.1, AF081241.1, AF135183.1, AC004704.2, AF064857.1, AL163281.2, AJ271161.1, Z82077.1, U43282.1, U41530.1, X89886.1, AB042823.1, AL045395.1, AW263032.1, AA534737.1, AI862154.1, 10 AW195190.1, AI333447.1, AW070552.1, AI632675.1, AI492046.1, AI033598.1, AA776248.1, AI560827.1, AI090658.1, AI990263.1, AI337152.1, AW131196.1, AI377836.1, AI381470.1, AI032741.1, AA216415.1, AW182779.1, AA046569.1, W63623.1, AA632347.1, AI278969.1, AA865536.1, AI401456.1, AI439888.1, W88673.1, AW028469.1, AA810290.1, AL047721.1, AA725456.1, AI074999.1, AI752102.1, AI191659.1, AI131161.1, AA412273.1, AI369743.1, AI699071.1, AI804688.1, AA461564.1, AW611821.1, AW083337.1, AL043584.1, AA620499.1, H70039.1, H27907.1, AI991681.1, W15240.1, AI684348.1, AI424392.1, AA229511.1, AA345937.1, AA046704.1, AA346011.1, AI608926.1, AI492935.1, 15 AA447104.1, AI235913.1, AU024381.1, AI854609.1, AI464166.1, AW556867.1, AW532431.1, AW134839.1, AW747938.1, AA962117.1, AA557671.1, AA137689.1, W61524.1, AA972005.1, W39608.1, H30866.1, H70038.1, AW336387.1, R94150.1, AW499467.1, AA294458.1, BB000336.1, AW580849.1, AW580825.1, AW257455.1, AW217194.1, AV315168.1, AV274485.1, AV264232.1, AW152551.1, AV046353.2, AI503741.1, C99210.1, AA795526.1, 20 C79929.1, AA607081.1, AA508474.1, AA248433.1, N53539.1, R29422.1, AL353736.1, AC010736.4, AL356241.2, AC061993.2, AC032025.2, AC027704.2, AC013712.3, AC022868.4, AC025734.2, AL139231.4, AL139125.3, AL158046.1, AC015551.9, AC062004.2, AC024895.5, AC023757.4, AC068652.1, AC044787.3, AC016567.4, AC009220.7, AC021091.2, AC009061.8, AC032021.2, AC068066.1, AC023041.2, AC009994.4, AC027480.2, AC009551.4, AC062039.1, AC027682.2, AC019243.3, AC024974.2, AC019214.2, AC012429.4, AC023264.2, 25 AC018689.2, AC012594.3, AC011138.2, AC012050.1, AL356242.2, AL356100.1, AL157905.2, AL022597.5, AP001910.1, AP001260.1, AP001093.2, AP000743.1, Z92865.1,

## SEQ ID NO.333

30 NGO-St-146

YS358/T3 5'

- AC006038.2, NM\_004434.1, U97018.1, AC002094.1, NM\_013589.1, AC018632.1, AC005881.3, AC007887.8, AF128394.1, AC006121.1, AL163203.2, AF004874.1, AL139078.2, AL050302.2, AL049911.2, U14611.1, AB019224.1, AB026642.1, X15122.1, Y00398.1, X02806.1, D00216.1, K02646.1, AE003844.1, AC004901.1, AF125520.1, AF017299.1, Z54281.1, Z68217.1, AL035562.14, U40426.1, AK000952.1, Z81167.1, AW851191.1, AW851190.1, 35 AW342912.1, AW306072.1, AL041588.1, AW683786.1, AW483175.1, AW471804.1, AW471754.1, AW433049.1, AW397869.1, AW397864.1, AW397818.1, AW397808.1, AW397328.1, AW397299.1, AW397225.1, AW397183.1, AW397082.1, AW396931.1, AW396867.1, AW395710.1, AW395684.1, AW395670.1, AW318300.1, AW318207.1, AW318175.1, AW318001.1, AW317912.1, AW317798.1, AW317683.1, AI941128.1, AI941087.1, AI940932.1, AI940896.1, AI795036.1, AI748210.1, AI735897.1, AI735879.1, AI735805.1, AI735804.1, AI736030.1, AI629905.1, 40 AU024702.1, AU024209.1, AA766572.1, AA760753.1, AA501257.1, AA501255.1, T08982.1, AC013322.5, AL133368.1, AC025644.2, AC021799.1, AC013567.2, AL138963.4, AL138693.6, AC027399.2, AC007445.2, AC016201.5, AC022035.2, AC017091.3, AF215845.1, AP001402.1, AC036149.2, AC025524.2, AC021486.3, AC019188.3, AL355301.3, AL158201.7, AL158031.4,

45 SEQ ID NO.334

NGO-St-146

YS358/T7 3'

- AC006038.2, AF131753.1, Z82268.1, Z94721.1, AC002074.1, AC006377.3, AL161532.2, AL049500.1, AF114156.1, AE003579.1, AC004111.1, AC006040.2, AC005075.2, AF125448.1, AC005149.1, AC002416.1, AF006762.1, 50 AL117694.3, AC005826.1, AC006956.15, AC004668.1, AC015445.3, AC004862.1, AC006379.2, AL163232.2, U56964.1, AL035634.7, U40410.1, AB022157.1, AP001687.1, AP001253.1, X83624.1, AC007590.1, AF070718.1, AL161536.2, AL110482.1, J04485.1, AL080250.11, AL031677.5, AL031599.1, AL049487.1, AL049656.1, U41545.1, AW173156.1, AW419091.1, AI240374.1, AI806503.1, AW152350.1, AW276130.1, AA449115.1, AW516027.1, AI290977.1, AI803121.1, AI192373.1, AI193573.1, AA587244.1, AI288196.1, AA977076.1, AI367149.1, AA421771.1, AI910966.1, 55 AI343706.1, AI499018.1, AA927517.1, AW445056.1, AI130998.1, AW771159.1, AW592377.1, AI097006.1, AI864290.1, AI097567.1, AI884377.1, N94895.1, AW511972.1, AI305161.1, AI304601.1, AW079658.1, AW044403.1, AW768529.1, AW151869.1, AA193343.1, AI341554.1, AI290345.1, AA193461.1, AA861909.1, AA527518.1, N29071.1, AI277874.1, AI027217.1, AA459958.1, AA716610.1, AI051389.1, AA836942.1, AA679242.1, AA553698.1, AA082407.1, AI873933.1, R38955.1, AW272553.1, AA865858.1, AA832468.1, AA417893.1, N27375.1, D11610.1, AI867049.1, AA917795.1, 60 AA256313.1, AA034164.1, N48340.1, H10359.1, AW119101.1, AA256438.1, N23618.1, AI240601.1, AA514495.1, AI290297.1, AI061272.1, AA443213.1, AA789034.1, H08100.1, R40145.1, D12463.1, AA482526.1, AI240093.1, AA493130.1, AA122021.1, AA994372.1, AW514004.1, AI523990.1, R84780.1, AA227683.1, H06663.1, X91713.1, AA062803.1, AA585119.1, AA890144.1, AI283724.1, AA056271.1, AI634524.1, AI644019.1, AW556280.1, AW142557.1, AW550088.1, AC013322.5, AL355365.2, AL354880.3, AP000621.1, AC027141.1, AL133458.12, Z93243.1,

Z83124.1, AC012022.5, AC068296.4, AC066601.1, AC007481.2, AC016775.4, AC015473.3, AC019993.1, AL157955.1, AC067723.2, AC025164.7, AC027301.3, AC007683.3, AC026087.3, AC015625.3, AL355542.2, AL136301.4, AP001965.1, AC016255.8, AC055821.2, AC058803.1, AC026233.2, AC024181.2, AC022087.3, AC022796.3, AC006280.6, AC018594.3, AC016255.7, AL138823.3, AL096784.2,

## SEQ ID NO.335

NGO-St-146

YS112/T3 5'

- 10 AC006038.2, NM\_012155.1, AF103939.1, AL096717.1, NM\_004434.1, U97018.1, AE003673.1, AE001573.1, AC001655.1, NM\_008519.1, NM\_006007.1, AF077673.1, AF062072.1, AF110104.1, AC006121.1, AF044030.1, AF062347.1, AF062346.1, AC003029.1, AC004226.1, U14611.1, D84515.1, AE003596.1, AC005191.1, AC007077.2, AF017299.1, Z96811.2, AL035562.14, U40455.1, AA983842.1, Z81167.1, AA681706.1, AI596558.1, AA465739.1, AA850758.1, AW593841.1, AW516768.1, AW475067.1, AW303490.1, AW188604.1, AI807190.1, AI767422.1, AI740707.1, AI739199.1, AI582285.1, AI473581.1, AI458952.1, AI376302.1, AI312515.1, AA775264.1, AA743080.1, AA428244.1, AA352385.1, AA043549.1, AW637997.1, AW631275.1, AW630845.1, AW483175.1, AW361213.1, 15 AL134742.1, AA410201.1, AA298178.1, AA298197.1, AA233347.1, AA228021.1, AA165101.1, AA035737.1, AA002175.1, W73050.1, N28928.1, D56390.1, D58486.1, H04632.1, R56367.1, R33003.1, R24775.1, F05590.1, T30904.1, Z42327.1, AW608299.1, AI903729.1, AV135789.1, AI629905.1, AU024209.1, AA648943.1, AA532311.1, T50574.1, AC013322.5, AC011480.2, AL049868.12, AL133368.1, AC022275.9, AC020282.1, AC063945.3, AC068051.2, 20 AC068642.2, AC062020.2, AC067870.1, AC024948.2, AC007445.2, AC020684.4, AC022986.3, AC021885.3, AC018864.4, AC022451.1, AF215845.1, AL160266.6, AL135924.10, AC068130.2, AC069220.1, AC046133.3, AC068545.2, AC055837.2, AC036149.2, AC026720.3, AC010477.6, AC008384.4, AC008562.3, AC064860.2, AC027581.2, AC012213.3, AC016881.4, AC006400.6, AC009609.5, AC036233.1, AC025370.2, AC025090.2, AC021463.2, AC022247.2, AC016169.3, AC016690.4, AC021877.4, AC013638.3, AC010940.3, AC015567.3, 25 AC019239.3, AC007873.4, AC008086.2, AC019047.2, AC024171.1, AC011997.3, AC013885.1, AC013401.1, AC015691.1, AC012116.1, AC000016.1, AL121952.6, AL355498.2, AL158210.6, AL158043.4, AL136992.18, AP001554.1, AP001484.1, AP001375.1, AP000834.1, AP000757.1,

## SEQ ID NO.336

30 NGO-St-146

YS112/T7 3'

- AC006038.2, AF131753.1, Z82268.1, AL161532.2, AL049500.1, AF114156.1, AE003579.1, AC004111.1, AC006040.2, AC005075.2, AF125448.1, AC005149.1, AC002416.1, AF006762.1, AC005826.1, AC006956.15, AC004668.1, AC002074.1, AC015445.3, AC005344.1, AL163232.2, U56964.1, Z68296.1, AL035634.7, U40410.1, AB022157.1, 35 AP001687.1, AP001253.1, X83624.1, AC004554.1, AL110482.1, AL133279.2, AL122021.3, AC000118.1, AL031677.5, AL009047.1, AL049487.1, AW173156.1, AW276130.1, AW419091.1, AI806503.1, AW152350.1, AA449115.1, AI240374.1, AW516027.1, AI290977.1, AI193573.1, AI803121.1, AI192373.1, AA587244.1, AI288196.1, AI367149.1, AA977076.1, AI910966.1, AI499018.1, AA421771.1, AW445056.1, AI343706.1, AA927517.1, AI130998.1, N29071.1, AI097567.1, AW592377.1, AW771159.1, AW079658.1, AI864290.1, AI304601.1, AI097006.1, AW044403.1, AI305161.1, 40 AW511972.1, AI884377.1, N94895.1, AW768529.1, AW151869.1, AA193343.1, AA193461.1, AI290345.1, AI341554.1, AA527518.1, AI277874.1, AA861909.1, AI027217.1, AI051389.1, AA459958.1, AA716610.1, AA836942.1, AA082407.1, AA679242.1, R38955.1, AA865858.1, AA553698.1, AA256438.1, AI873933.1, AW272553.1, AA832468.1, AA417893.1, AI867049.1, AA482526.1, AA256313.1, AA034164.1, N27375.1, D11610.1, AA917795.1, AW119101.1, N48340.1, H10359.1, AI240601.1, AI290297.1, AA514495.1, N23618.1, AA789034.1, H08100.1, AI061272.1, AA443213.1, 45 R40145.1, D12463.1, AI240093.1, AA493130.1, AA227683.1, AA122021.1, AW514004.1, AA994372.1, AI523990.1, R84780.1, AI634524.1, H06663.1, X91713.1, AA062803.1, AA585119.1, AI283724.1, AA890144.1, AA056271.1, AI644019.1, AW556280.1, AW142557.1, AW550088.1, AC013322.5, AL355365.2, AL354880.3, AP000621.1, Z93243.1, Z83124.1, AC027141.1, AC012022.5, AC068296.4, AC007481.2, AC015473.3, AC019993.1, AC006876.1, AC067723.2, AC025164.7, AC027301.3, AC007683.3, AP001965.1, AC016255.8, AC055821.2, AC025920.8, AC024162.2, 50 AC058803.1, AC026233.2, AC018555.3, AC021381.3, AC024181.2, AC022087.3, AC022796.3, AC006280.6, AC019111.3, AC016255.7, AC012410.2, AC012105.1, AL049184.5, AL096784.2,

## SEQ ID NO.337

NGO-St-146

55 YS266/T3 5'

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NGO-St-149

YS184/T7 3'

35 AC004952.2, AB002316.1, AC005171.2, AE003697.1, AC005233.2, AC008078.11, U73509.1, AC004600.2, AC004259.1, AC008498.3, AC007171.4, AC024864.1, AC024206.1, AC009248.6, AF133300.1, AC007157.6, AL353814.1, Z81081.1, AI041842.1, AA535122.1, AA858272.1, AW173550.1, AI075241.1, AI949683.1, AI459566.1, AW662874.1, AW016852.1, AI393789.1, W38376.1, AI660675.1, AW374022.1, AI092706.1, AA614653.1, N22273.1, AI374912.1, N81171.1, AI307141.1, AW316689.1, AA702628.1, N50149.1, AA665756.1, AA908261.1, AA906275.1, AA122792.1, 40 AI228214.1, R81288.1, AA789088.1, AI149042.1, AW544305.1, AA016222.1, AA781542.1, AA907460.1, AI787663.1, H95911.1, AI747696.1, AI408499.1, H69908.1, AA185425.1, AA493271.1, D82413.1, AI449623.1, AW020583.1, AA399746.1, AA165348.1, AI549947.1, AA458167.1, AA690581.1, C86225.1, C85754.1, AV296844.1, AA476396.1, AJ394925.1, AI227433.1, AA901298.1, AV314025.1, AV366383.1, AV304720.1, AV298962.1, AJ395178.1, AW803080.1, AV295103.1, AV304045.1, AV295412.1, AW365959.1, AW356172.1, AI457971.1, AJ392175.1, 45 AW805830.1, AI922173.1, AW010332.1, AA620178.1, AI974964.1, AW863569.1, AW285356.1, AW017227.1, AI976687.1, AI976615.1, AI975238.1, AV159280.1, AI803639.1, AV089896.1, AI471454.1, C99130.1, AA508293.1, AA508283.1, AA508275.1, AA233975.1, AA185761.1, AA185758.1, AA185813.1, AA185829.1, AA133583.1, Z45321.1, AL159974.3, AC025368.1, AC017000.2, AC024737.5, AC063941.4, AC063926.3, AC025837.2, AC023555.3, AC021587.1, AL356320.1, AL355606.2, AC068498.1, AC027320.2, AC026425.2, AC016099.3, AC022608.2, 50 AC021603.2, AC006095.1, AL355532.4,

SEQ ID NO.346

NGO-St-150

YS255/T3 5'

55 AL137786.2, AE001106.1, AL109657.8, AE003536.1, AL032649.1, AC000095.3, AC010283.5, AC007370.7, U02206.1, U39718.1, AC005319.1, AL163237.2, U59177.1, U59176.1, AL031729.16, Z70754.1, Z98885.1, L41917.1, L41886.1, X05181.1, X04572.1, AP001692.1, AP000147.1, AP000233.1, Z99105.1, Z99104.1, D14465.1, AB006424.1, D81907.1, AA186486.1, AI752319.1, AW515316.1, AI633878.1, AA724174.1, N98699.1, AW088411.1, AI818209.1, AA360504.1, AW207435.1, R77568.1, D78858.1, AW083012.1, AI927938.1, AI669659.1, AA902264.1, AW105148.1, H83314.1, 60 AA300827.1, AW410334.1, AA431514.1, AI420205.1, AI752320.1, AI283114.1, D78824.1, AI743602.1, AI417561.1, W00707.1, N66098.1, N90043.1, AA573278.1, AA043792.1, C00128.1, AW796219.1, AI819645.1, AA329088.1, AW796258.1, AA043666.1, AI434568.1, AA973972.1, AI631297.1, AI638738.1, AI440413.1, AI048750.1, AI702887.1, AA431188.1, AA653570.1, AA348799.1, AI749472.1, AA210446.1, AW275782.1, AW275777.1, AA105091.1, AA137746.1, AA704575.1, AA561636.1, AA096434.1, AI753861.1, AJ396210.1, AJ394687.1, AI962149.1, AA809488.1,

- AI440138.1, AL135399.1, AI058992.1, D62361.1, AW089455.1, AW322669.1, AA114807.1, AI925346.1, AA120374.1, AA153007.1, AW342822.1, AI982313.1, AA174177.1, AI981814.1, AU017382.1, AA561870.1, AW363585.1, AI576378.1, AW734057.1, AW333950.1, AW332559.1, AW257529.1, W31991.1, AC027672.3, AC013243.4, AL133461.2, AC023317.2, AL161659.10, AC010031.5, AC013267.2, AC017582.1, AL008876.1, AC016927.5, AC024903.5, AC068921.2, AC009463.6, AC008368.18, AC010448.4, AC009162.5, AC010727.3, AC021484.3, AC017044.2, AC022372.3, AC010901.3, AC019010.1, AC009624.2, AL353145.2, AL161451.4, AL138878.3, AL133543.2, AL031744.7,
- 5
- SEQ ID NO.347
- 10 NGO-St-150  
YS255/T7 3'
- AE003626.1, AC005890.1, AL034556.3, AL008971.1, AC008873.4, AE003736.1, AE003708.1, AC005242.1, AF034902.1, AL163225.2, AL132796.2, AL031905.7, AL035530.11, AJ131836.1, AL035532.1, AC008865.3, AC007047.6, AE003545.1, AE002786.1, AC004547.1, AC005251.1, AC012680.3, AC005489.1, AF121782.1, AC006421.1, AE001428.1, AE001413.1, AF078780.1, AF064857.1, AL163281.2, AL133299.2, Z99773.1, AL096770.14, U39847.1, Z99281.1, Z68215.1, Z97055.1, Z97209.1, U32078.1, U50071.1, Z31356.1, U21731.1, AJ235270.1, AB015469.1, Y11842.1, X94355.1, AW771521.1, AA126445.1, AW514659.1, AW182807.1, AW771502.1, AA938728.1, AI090291.1, AI493810.1, AW675411.1, AA427532.1, AA349431.1, N62707.1, AW512566.1, AA058340.1, AA345941.1, AA588743.1, AW189042.1, AA187281.1, AW089555.1, AI678159.1, AI366801.1, AA829470.1, C02522.1, AI332895.1, T40865.1, AA970774.1, D79887.1, AA456027.1, AW149169.1, AI220712.1, AA310489.1, T40872.1, AI932606.1, AI587187.1, AA054496.1, D61745.1, AA126569.1, AA455387.1, AA292619.1, AA767314.1, T39804.1, T39783.1, AA766576.1, AA292620.1, AW315966.1, AW312359.1, AI551720.1, AA445754.1, AI157081.1, AA879725.1, AW347573.1, AI527455.1, H64492.1, AI341051.1, AI082974.1, AW863369.1, AW637708.1, AW618562.1, AW618323.1, AW610946.1, AW533222.1, AW528171.1, AW514564.1, AW399714.1, AW399655.1, AW349594.1, AW293159.1, AW276976.1, AI843747.1, AI663436.1, AI392688.1, AI288400.1, AA805183.1, AA561027.1, AA537476.1, AA455793.1, AA447110.1, AA434507.1, AA282194.1, AA101103.1, R81554.1, AC013243.4, AL133461.2, AC027672.3, AC018864.4, AF215845.1, AC069162.1, AL355312.3, AC020324.1, AC007291.23, AL356254.1, AC011970.1, AC009613.2, AL163537.4, AL157957.1, AC068957.1, AC067779.1, AC011562.4, AC019950.1, AL121928.10, AL157396.3,
- 15
- 20
- 25
- 30 SEQ ID NO.348  
NGO-St-151  
YS1652/T3 5'
- AC003682.1, X15544.1, X16618.1, AK000267.1, M29411.1, NM\_007673.1, AF104031.1, Z81009.1, S74520.1, U00454.1, AC011749.2, AE003587.1, NM\_005231.1, NM\_006030.1, AC004793.2, U34879.1, AF040709.1, U37521.1, AF054997.1, AF042793.1, AF042792.1, AJ251368.1, AJ251367.1, Z84492.2, AJ251914.1, AL121757.7, Z92845.1, L31886.1, AB040919.1, Z35691.1, M98343.1, AB011130.1, AA160768.1, AA454976.1, AA524918.1, AA160767.1, AW177242.1, AA524934.1, AW603587.1, AI909371.1, AW754009.1, AW604563.1, AW843725.1, AA236418.1, AA327082.1, T64077.1, AI981337.1, AI795303.1, AI639685.1, W78194.1, AW761561.1, AW326881.1, AW326538.1, AI327188.1, AI323297.1, AI273360.1, AI272717.1, AA876719.1, AA016882.1, W63915.1, N39838.1, AW699234.1, AW677045.1, AW658137.1, AW578415.1, AW392015.1, AW370009.1, AL134942.1, AW034847.1, AI527711.1, AA543942.1, AA378725.1, AA315097.1, W14378.1, W07354.1, U18015.1, T49796.1, AC068266.1, AC011089.4, AC006330.3, AC061995.1, AC024115.7, AC021247.4, AC027349.1, AC022585.1, AC011166.2, AL133331.12, AL158834.4, AL353680.3, AL158065.3, AP001374.1, AP001339.1, AC010299.4, AC009143.4, AC009123.5, AC009041.5, AC017067.3, AC010131.2, AC025353.2, AC046157.1, AC023825.3, AC026070.2, AC035886.1, AC035885.1, AC028189.1, AC019231.3, AC022608.2, AC016716.2, AC011035.3, AC017033.2, AC024117.1, AC012004.3, AC021764.1, AC015049.1, AC008228.2, AL356241.2, AL355483.2, AL356116.1, AL356007.1, AP001554.1,
- 35
- 40
- 45
- SEQ ID NO.349
- 50 NGO-St-152  
YS1704/T3 5'
- AB033096.1, AF031242.1, M84990.1, L06863.1, U82671.2, AC003991.1, AF134576.1, AF070552.1, AC004040.1, U82696.1, AC001231.1, AL135745.2, AL121774.3, AC001477.1, AL133220.1, Z69655.1, Z33874.1, AW847517.1, AW762077.1, AW437401.1, AW463000.1, AI005887.1, AA133529.1, AI959464.1, AI650192.1, AA578951.1, R15953.1, M75813.1, AC026573.3, AL353588.2, AL353672.2, AC010195.7, AC009520.7, AC010274.3, AC010464.4, AC046150.2, AC025353.2, AC010864.2, AL139090.3, AL022344.1, AC011966.3, AC024727.4, AC009362.5, AC009180.7, AC011967.3, AC009621.4, AC007846.2, AC023959.2, AC023850.2, AC007608.2, AC007728.1, AC021596.1, AL136171.6, AL162741.3, AL162731.2, AL161933.3, AL139405.2, AP001591.1,
- 55
- 60 SEQ ID NO.350  
NGO-St-152  
YS1704/T7 3'
- AB033096.1, AC004812.1, AL133249.1, AC000052.16, AC004019.20, U62317.2, AL163285.2, AC002091.1, AL050307.13, AC000134.14, AC007051.3, AL031289.1, AC005412.5, AC006273.1, Z98884.11, AL034350.2, AL033392.5, AC005755.1, AF001549.1, AL160237.2, AL110502.1, AF053356.1, AC010328.4, AC008518.3,

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AC007917.15, AC007066.4, AL117352.12, U75285.1, Z83823.1, AC000159.6, AC020663.1, AC005288.1, AC004821.2, AC005324.1, AL121601.13, AL035411.27, AP000555.1, AC006344.2, AC006480.3, AC005856.1, AC005215.1, AC004057.1, AC008079.23, AC016025.12, AC008101.15, AC006138.1, AL023882.2, AL031224.1, Z95152.1, AF064862.1, AC004087.1, AC005231.2, AL096700.14, AC009516.19, AC005747.1, Z97630.11, AC005500.2, AC004982.1, AF037338.1, AC005785.1, AL133353.6, AL121964.16, AL096712.20, AP000188.1, AP000044.1, AP000112.1, AC007312.1, AC007097.4, AC005486.2, AC005013.1, AC008168.3, AC010170.3, AC005037.2, AP000193.1, AC007956.5, AC007055.3, AC006207.5, AC004210.1, AL049780.2, AC008925.3, AC006046.1, AP000191.1, AP000115.1, AC007655.1, AC005089.2, AC005740.1, AL033525.10, AC005018.2, AL022727.1, AP001412.1, AP000152.1, AC006582.13, AC000081.2, AC003006.1, AC007057.3, AP000692.1, AC007565.1, AP001331.1, AC011465.4, AC007766.1, W79504.1, AF150152.1, AI246796.1, AW303196.1, AW274349.1, AA441788.1, N54902.1, AI284640.1, AW872676.1, AW473467.1, AW301350.1, AA557686.1, AL135724.1, AI684097.1, AL041706.1, AW473163.1, AW168342.1, AW022379.1, AI633168.1, AI334435.1, T41242.1, AW338508.1, AI471481.1, AA381147.1, AL079645.1, AI732186.1, F36273.1, AI635818.1, AI569086.1, AI281881.1, AI160117.1, AI079910.1, AA598586.1, AA502155.1, AA491814.1, AA147750.1, AW057877.1, AI873916.1, AI537955.1, AA649642.1, AA487277.1, AW301809.1, AI439210.1, AA604607.1, AA179944.1, AW873290.1, AI499181.1, AI446464.1, AI432270.1, AI064864.1, AI061313.1, AA713891.1, AA482681.1, AL042856.3, AW088049.1, AA580808.1, AI561255.1, AA207129.1, AA171473.1, AA223206.1, AI085719.1, AA448858.1, AW615709.1, AW576503.1, AL138396.1, AI921061.1, AI754336.1, AI358812.1, AI079389.1, AI076766.1, AA634196.1, AA071393.1, C06339.1, AW081941.1, AW304805.1, AW152057.1, AW020992.1, AI920876.1, AI654247.1, AI571562.1, AI567712.1, AI358813.1, AI351698.1, AI289447.1, AI087133.1, AA533060.1, AI125107.1, AA765170.1, AA634272.1, AA633582.1, AA598425.1, AA551409.1, AA485930.1, AA151690.1, AA115165.1, AA082854.1, AA053128.1, W49595.1, N64547.1, AA443390.1, AL353672.2, AC026573.3, AL353588.2, AC009444.2, AC004795.2, AL137222.3, AC026413.2, AC017099.3, AC024088.3, AC008610.4, AC011442.3, AC011938.3, AC021455.3, AC018821.3, AC025287.2, AC020954.5, AC024438.2, AC013371.4, AC051660.3, AC019280.3, AL353729.2, AC017057.5, AC025341.2, AL136300.9, AL158830.5, AC023156.3, AC010607.4, AC034121.2, AC010130.4, AL117259.2, AC010395.5, AC009191.4, AC026397.2, AC013805.4, AC022181.3, AC023583.2, AC022460.2, AL161731.4, AL136311.3, AP001528.1, AC007780.2, AC026587.2, AC017083.4, AC023359.6, AC067749.2, AC026964.2, AC018989.3, AC011845.3, AC026294.1, AC022911.2, AC055890.2, AC024934.8, AC055791.2, AC025683.2, AL139109.2, AL138901.2, AC017100.3, AC009268.2, AC018862.3, AC024005.2, AC011092.1, AC025559.2, AC011443.4, AC007491.3, AC025145.2, AC027497.2, AL121971.2, AP001076.1, Y12335.1, AC026546.2, AC034181.1, AC022286.4, AC021024.2, AC021933.1, AC010455.3, AC024990.2, AC019206.3, AC021671.1, AL354986.1, AC022169.2, AC022966.2, AL355348.3, AF228728.1, AC025354.2, AC015726.3, AP001098.2, AC026050.3, AC025963.2, AC012128.3, AL160393.6, AC063960.2, AC022261.3, AC019291.4, AL356292.1, AC040922.2, AC012411.3, AC027546.1, AL353749.1, AC055767.1, AC011638.3,

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SEQ ID NO.351

NGO-St-153

YS1754/T3 5'

AC004498.1, AC007956.5, AE003532.1, AF050157.1, Z37979.1, AC003028.2, AE003794.1, AE003615.1, AC006530.4, AC007977.11, AC006120.1, AE000679.1, AL133073.1, Z69662.1, U11039.1, Z99113.1, Z99112.1, AI005288.1, AI750442.1, R44564.1, F01704.1, AW614231.1, AW058657.1, AI808100.1, AI743405.1, AI726212.1, AI692280.1, AI675621.1, AI343951.1, AI342528.1, AA400627.1, AA400382.1, H00353.1, R56558.1, AW530608.1, AW530607.1, AI941583.1, AV185720.1, AI229512.1, C42486.1, C42424.1, AA470046.1, AA446177.1, AA398518.1, AA393260.1, AA090525.1, D75049.1, AL138764.3, AL355355.1, AC008528.5, AC011350.4, AC008591.4, AC011325.8, AC013337.5, AC024018.1, AL118511.22, AC024400.2, AC025205.2, AC022816.9, AC022059.2, AC019274.3, AC013814.3, AC023206.2, AC012359.3, AF215849.1, AC019852.1, AP001564.1, AC068133.2, AC026029.3, AC023332.3, AC064814.3, AC009452.9, AC068727.1, AC010398.6, AC009440.2, AC013570.3, AC011116.3, AC019264.3, AC018606.3, AC025827.2, AC011278.4, AC020571.2, AC010858.3, AC022955.3, AC022937.3, AC007838.10, AC024032.2, AC012287.2, AC020967.1, AC019998.1, AC012229.2, AC018325.1, AC008345.2, AL158837.4, AL160235.1,

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SEQ ID NO.352

NGO-St-153

YS1754/T7 3'

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## 5 Splicing Factor Sip 1 SC35-interacting protein 1 (SRR129)

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## ZH062/T3

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## ZH062/T7

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## ZH085/T3

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AC000015.2, U28371.1, AP001047.1, AC006101.3, AC009223.2, AL132979.2, AL031586.2, U29376.1, AB017066.1, AC002337.2, AC008173.2, AC008124.8, AC005826.1, AL032657.1, U40938.1, AP000233.1, AB020878.1, AW003511.1, 25 AA921845.1, AI652147.1, AI693426.1, AI829962.1, AI434429.1, AA573137.1, AI332526.1, AI183429.1, AI435449.1, AI189561.1, AI378034.1, AI221962.1, N47325.1, AW118897.1, N41605.1, N48812.1, AW665247.1, AW340077.1, N29605.1, AA478519.1, AW190293.1, AA463875.1, AI292305.1, AA971089.1, AA463379.1, AA884954.1, AI858260.1, AI382934.1, AA931835.1, AI125820.1, AI125702.1, AI358631.1, AI080245.1, AI027833.1, AW021929.1, AI399648.1, AA769041.1, AW372265.1, AA738261.1, N67374.1, AI014533.1, N69081.1, AA459715.1, AA347851.1, AW439905.1, D12465.1, AI768667.1, H88007.1, AA948472.1, D56771.1, AI819214.1, H22651.1, AA293133.1, H21980.1, H42880.1, 30 H22650.1, AI186725.1, AA889214.1, H88179.1, AI492769.1, D56772.1, H87354.1, D56691.1, H22043.1, H87486.1, AW628965.1, AA600109.1, AA574243.1, AI453007.1, AI222635.1, H16217.1, AW241802.1, AW083302.1, H25165.1, AA095911.1, H44052.1, AI376308.1, H42946.1, AW429971.1, AV346363.1, R34052.1, AW271826.1, AV366809.1, AV354759.1, AV344488.1, AV298108.1, AV116868.1, R33250.1, AV355258.1, AV235683.1, AC010172.10, 35 AC007511.2, AC013660.4, AC020193.1, AC011141.2, AC018353.10, AC068723.1, AC027044.2, AC025863.2, AC021531.3, AC013748.3, AL161932.4, AC022217.3, AC019116.3, AC021362.4, AC021644.3, AC021159.2, AC017103.3, AC021986.1, AC010935.2, AC009741.4,

SEQ ID NO: 366

40 ZH1244/T3

NM\_004719.1, AF147405.1, AC000015.2, AF030234.1, Y11251.1, U16782.1, AL136419.2, AL111164.1, AE003490.1, AF045341.1, AL121841.5, NC\_001143.1, AC010283.5, AE003681.1, AF090924.1, AC006389.2, AC003950.1, AC004099.1, U16855.1, AL122013.3, Z69712.2, X76174.1, Z28239.1, L11172.1, AB013190.1, D83502.1, AB000162.1, AW152460.1, AI969507.1, AW084759.1, AI986247.1, AI811466.1, AI590951.1, AI984932.1, AI457465.1, T34545.1, 45 AA903034.1, AI915886.1, AA938734.1, AA812235.1, AW083255.1, T68840.1, M79122.1, AI934225.1, AA376018.1, F13709.1, AI475277.1, T68912.1, AA767811.1, T40900.1, AA103126.1, H30589.1, AW824184.1, AW556003.1, AW228186.1, AW414066.1, AI098240.1, AV252704.1, AV321035.1, AI790543.1, AV319958.1, AW227799.1, AV356664.1, AA407099.1, AA871902.1, AA616747.1, AI108941.1, AA140172.1, AW611398.1, AA836742.1, AA019444.1, AA012812.1, AC010172.10, AC021642.11, AC068273.2, AC061958.4, AC015669.4, AC022310.2, 50 AC021978.4, AC016866.3, AC012445.3, AC020072.1, AP000799.1, AP000641.1, AC025652.2, AC069063.1, AC016919.4, AC068892.1, AC010448.4, AC066310.1, AC027233.2, AC021484.3, AC012246.3, AC022714.2, AC023929.2, AC022895.2, AC006583.17, AC011966.2, AC013753.2, AC014256.1, AL137795.2, AP000941.2, AP000869.1, AP000846.1, AP000831.1,

55 SEQ ID NO: 367

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ZH1406/T3

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SEQ ID NO: 373

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- 10 SEQ ID NO: 374  
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ZH168/T3  
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- SEQ ID NO: 376  
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- 55
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- 5 NM\_013285.1, L05425.1, U69600.1, AL034379.8, AB015478.1, X99436.1, AC024751.1, AC006920.10, AC004805.1, Z68325.1, AP000067.1, AC007380.3, AF013149.1, AF016485.1, AL137230.2, AL163241.2, Z50028.1, Z97055.1, Z82204.1, S75106.1, AP001696.1, AP001596.1, AK000019.1, AW245855.1, AW409934.1, AW161434.1, AW163245.1, AA858436.1, AA316055.1, AA171883.1, AA690847.1, AA308223.1, AW362598.1, AI112354.1, AI573674.1, AA373618.1, AW326870.1, AA352159.1, AA989948.1, AA684606.1, AU077157.1, AW250083.1, H35016.1, AA686046.1, AL024316.1, AV125438.1, AW319272.1, AW245857.1, AW765532.1, H35824.1, AI853194.1, AA126101.1, AV125326.1, AV442312.1, AI994797.1, N38238.1, T80141.1, AW736578.1, AW412154.1, AW377648.1, AW377646.1, 10 AA930842.1, AA866918.1, AA717513.1, AA671873.1, AA272186.1, AA239193.1, AA210106.1, AA116767.1, AA068274.1, AA060411.1, AA020022.1, AW174228.1, AI908898.1, AI657589.1, AI657580.1, R23322.1, AW738493.1, AV107331.1, AI661426.1, AI482631.1, AC023077.3, AC027731.2, AL355880.2, AC006721.1, AC040963.2, AC024442.3, AC053546.3, AC064107.1, AC067611.1, AC056245.1, AC033416.1, AC027813.1, AC024380.2, AL353692.3, AL138799.2, AL138841.1, AC013475.4, AC027298.5, AC044833.2, AC025258.4, AC023151.3, AC018669.3, 15 AC022164.4, AC009026.5, AC023374.2, AC026277.3, AC026276.2, AC009768.4, AC027006.2, AC026951.2, AC025065.2, AC024191.3, AC023448.2, AC024531.2, AC011012.3, AC011693.4, AC018862.3, AC022052.2, AC011860.3, AC016666.2, AC023958.2, AC021716.2, AC010734.3, AC013675.1, AC016064.1, AL354855.3, AL136537.3, Z93240.1

20 SEQ ID NO: 378

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- 25 NM\_013285.1, L05425.1, AL034379.8, U69600.1, AE003547.1, D49682.1, AC007211.5, AC007020.4, AC006200.2, AF085279.1, AL031635.1, AF235098.1, AE003829.1, AF125444.1, AL121748.6, AF016684.1, AL078468.1, Z72514.1, AB021155.1, AF176688.1, AE003738.1, AC002454.1, AL049710.18, AL110509.2, AW157242.1, AA902387.1, AI628921.1, AI925558.1, AA401208.1, AW070650.1, AW162279.1, AW409935.1, AA722289.1, AA126418.1, AW172793.1, AA857353.1, AA780182.1, AW156969.1, AI376281.1, AW183614.1, AI826742.1, AA582490.1, AI474094.1, AA446557.1, AA483614.1, AW246802.1, AA846248.1, AI253092.1, AA934590.1, AA888018.1, AW804193.1, AI699045.1, AI867001.1, AA171554.1, AI954511.1, AI760439.1, AI763044.1, AI825244.1, AA126000.1, AW768894.1, AI671605.1, AW804232.1, AI702310.1, W81287.1, AA493881.1, AA863491.1, AW804255.1, AA766044.1, 30 AA635139.1, AW804270.1, AA831455.1, AW118384.1, AA659293.1, AA196109.1, AI244063.1, AA659297.1, AI470650.1, AI798554.1, N32569.1, AA515590.1, AI245761.1, AW002316.1, AI909114.1, AW250835.1, AW362969.1, AA524198.1, T27737.1, AI345764.1, AW301566.1, AI310849.1, AI310651.1, AW268086.1, AI589981.1, AW268169.1, AA056760.1, AW607751.1, AA614309.1, AW529039.1, AI112872.1, AI060050.1, AA546717.1, AW532741.1, AW557260.1, AV220510.1, AI646349.1, AI536459.1, AI853259.1, AV090573.1, AI058723.1, AV310274.1, AW653179.1, 35 AV236721.1, AV236719.1, AV167761.1, AV328006.1, AW111676.1, AV153940.1, AA290477.1, AV311465.1, AV296078.1, AV225966.1, AV136397.1, AV232948.1, AV121458.1, AC027731.2, AL355880.2, AC023077.3, AC010058.5, AC013019.1, AC067926.1, AC068683.1, AC026348.2, AC022553.2, AC018707.5, AC023000.2, Z98865.1, AC022165.3, AC022388.2, AC019056.4, AC016690.4, AC010732.3, AC015232.1, AC010859.2, AP001150.1, AP000679.2, AC025097.8, AC062025.1, AC021296.2, AC024248.3, AF235096.1, AC009472.2, AC024127.1, 40 AC016670.3, AC019749.1, AC009454.1, AL136116.2, AL136090.9

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ZHI371/T3

- 45 NM\_013285.1, L05425.1, U69600.1, AL034379.8, NC\_001146.1, Z71668.1, AF124045.1, AF124739.1, AF124737.1, AC010150.3, AL355632.1, AP000386.1, D89267.1, AC006200.2, AC011664.8, AC009755.5, AF012277.1, U56240.1, U40940.1, M32885.1, AA126544.1, AL135350.1, AA303227.1, AA403201.1, AA446682.1, W79685.1, AW246249.1, AW577783.1, AA692026.1, AA475404.1, AA451012.1, AA126101.1, AI907635.1, AA058438.1, AA821350.1, AI035443.1, AA581348.1, AW427911.1, AV138378.1, AW377646.1, AA271955.1, AW377648.1, W08841.1, AI763044.1, AA794525.1, AA320025.1, AI943334.1, AL024316.1, AV399123.1, AI974265.1, AI157210.1, AA120514.1, AW755414.1, 50 AI166916.1, AW179912.1, AI181476.1, AV409400.1, AW649268.1, AW362969.1, AW093091.1, AI488290.1, AW002316.1, AI781856.1, AA373618.1, H35824.1, AW747374.1, AW146627.1, AW067567.1, AW054133.1, AW017515.1, AI944299.1, AI184724.1, AA824259.1, AA399670.1, AC023077.3, AC027731.2, AL355880.2, AC018362.3, AL354981.1, AC024581.2, AC022120.4, AC016650.4, AC013658.3, AC012448.3, AL161648.5, AL139123.2, AC009780.4, AC067844.1, AC027070.2, AC040168.1, AC019089.3, AC021109.2, AC024063.1, 55 AC007495.3, AC023605.1, AL136959.2, AL138823.3, AL136104.3

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ZH205/T3

- 60 NM\_013285.1, L05425.1, U69600.1, AL034379.8, AB015478.1, X99436.1, AC024751.1, AC006920.10, AC004805.1, AC007380.3, AF013149.1, AF016485.1, AL137230.2, AL163241.2, Z50028.1, S75106.1, AP001696.1, AP001596.1, AW245855.1, AW409934.1, AW161434.1, AW163245.1, AA858436.1, AA316055.1, AA171883.1, AW362598.1, AA308223.1, AI112354.1, AA690847.1, AI573674.1, AW326870.1, AA373618.1, AA352159.1, AU077157.1, AA989948.1, AA684606.1, AW250083.1, H35016.1, AA686046.1, AW245857.1, AW319272.1, AW765532.1, AL024316.1, AV125438.1, H35824.1, AV442312.1, AI994797.1, N38238.1, T80141.1, AW736578.1, AA068274.1,

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SEQ ID NO: 381

10 Ubiquitin-Specific protease (UBP)

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SEQ ID NO: 382

25 ZH053/T3

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- 5 NM\_003368.1, AF117386.1, AL117575.1, AB014458.1, AE003523.1, AF069441.1, AL161500.2, AL032655.1, AL133421.1, Z85995.1, Z94721.1, AC006708.1, AE002611.1, AC008148.2, L29074.1, AC006060.1, AL133238.2, AL133372.2, AL121985.13, AL050322.10, AI478913.1, AW340312.1, AW340211.1, AW771501.1, AA832380.1, AA749334.1, AA743294.1, AI911716.1, AI656969.1, AA723943.1, AA099033.1, T09031.1, AA921156.1, AI050545.1, AA684326.1, AW663812.1, AA445060.1, AA016112.1, AW749359.1, AA010709.1, AW601534.1, AI764163.1, T34154.1, AA389075.1, AA110253.1, N50647.1, AW123867.1, AW121935.1, AI006640.1, AI006507.1, AI815490.1, AV074783.1, 10 C96400.1, AW605305.1, AW605290.1, AW485355.1, AV334525.1, AV316977.1, AV271577.1, AV271011.1, AI925190.1, AI880405.1, AV089080.1, AU053253.1, AI601868.1, AI577543.1, AI568768.1, AI416338.1, AI354858.1, AI132532.1, AA797782.1, AA789662.1, AA418927.1, AA242816.1, AA007209.1, N75527.1, N26669.1, H44548.1, T50640.1, AC025396.2, AL355389.1, AC011171.3, AP001167.1, AP000942.2, AC027757.2, AC025742.4, AC010054.4, AC009375.5, AC014849.1, AC022172.4, AC026984.1, AC006839.13, AL136322.2, AC026084.2, AC010594.4, 15 AC008504.4, AC027800.2, AC027392.2, AC021514.3, AC025821.2, AC009578.3, AC021258.3, AC018491.7, AC012545.1, AL136442.10, AL139406.2

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- 20 NM\_016520.1, AF218421.1, AF151054.1, AL137549.1, AL008726.1, AL163249.2, AC010620.4, AC008044.4, AC002377.1, AC004921.1, AC004383.1, AL163212.2, AL096801.18, Z96074.4, Z84483.1, AP001667.1, AP000962.2, AC006055.1, AL163262.2, Z98036.1, AP001717.1, AP000191.1, AP000047.1, AP000115.1, AC006511.5, AC005089.2, AC005145.1, AL022316.2, AC006344.2, AF001550.1, AL078463.11, AP000348.1, AC004024.1, AC004076.1, AL135998.2, AL133448.3, AJ003147.1, AC004000.1, AC004491.1, AC007308.13, AC006251.3, AL023553.5, 25 AP000509.1, AC010491.3, AC005086.2, AF139813.1, AC004228.2, AC005755.1, AL163953.2, U50871.1, AL121580.8, AL033521.2, AC005231.2, AC004913.2, AC007360.2, AC007435.12, AF035396.1, AL121751.12, Z82215.1, AP000049.1, AP000311.1, AC006464.3, AC006349.3, AC004850.2, AC006317.3, AC004997.2, AC007229.1, AC006958.1, AC005562.1, AC005220.1, AL109627.18, AJ251973.1, AL008582.11, AL021453.1, Z92542.2, AL031311.1, AC018769.2, AC004999.1, AC009405.3, AC002554.1, AC002558.1, AL161670.2, AL031296.1, AC008969.5, U96629.1, AL157915.2, AC004150.8, AC005808.1, AL021393.1, Z82206.1, AP000555.1, AL132986.2, Z97630.11, AL096776.12, AP000212.1, 30 AP000134.1, AC004531.1, D83253.1, AP000009.2, AL031767.13, AI141544.1, AI651600.1, AI376077.1, AA503812.1, AA516476.1, AI458346.1, AI052479.1, AI146331.1, AI695736.1, AI812016.1, AI863150.1, AI214622.1, AI002868.1, AA639060.1, AI057130.1, AI913816.1, AI686336.1, AI685712.1, AI686315.1, AA503513.1, AA311466.1, AI765330.1, AI917006.1, AA934021.1, AW589928.1, AI763234.1, AW023167.1, AA761722.1, W80591.1, AA470915.1, AW088965.1, AA579082.1, AA522864.1, AA156183.1, AA155817.1, W69639.1, N99245.1, AI459879.1, AW608403.1, AW162762.1, F00937.1, AW392038.1, AA132445.1, AW795901.1, D44871.1, W78986.1, AI242236.1, AI520984.1, AW388476.1, H89643.1, AW078646.1, AW072963.1, AI444575.1, AI344906.1, AI318548.1, AA505108.1, R87193.1, AW504667.1, AI917132.1, AI523356.1, AA947352.1, AA489939.1, AI699746.1, AA015948.1, W60000.1, W03800.1, AW247866.1, AI003391.1, AA663579.1, AL138226.1, AL044701.1, AW779609.1, AW131394.1, AW105463.1, AI918350.1, 40 AI754257.1, F35684.1, AI631299.1, AI277617.1, AA664963.1, AA633804.1, AA595370.1, AA576672.1, T99365.1, T52366.1, T40388.1, AW419288.1, AI702018.1, AA573335.1, AA526529.1, N72195.1, T71936.1, AI791664.1, AI654336.1, AA348890.1, AI809776.1, AA287363.1, AA569648.1, AA230203.1, AA419403.1, AC027008.2, AL158207.3, AC016109.3, AL138963.4, AC011638.3, AC021211.2, AC021055.6, AC012014.4, AC021026.3, AC018356.7, AC011448.2, AC020561.2, AC023268.2, AP000761.1, AL109932.2, AC044812.2, AC011501.5, AC011495.3, 45 AC021420.3, AC019162.3, AC024944.2, AC026192.1, AC010130.4, AL353653.5, AL133230.19, AC022145.4, AC017008.4, AL136135.2, AC023271.3, AC004085.1, AL354935.3, AC010247.6, AC021971.3, AC009008.2, AL139398.2, AL139109.1, AC068707.2, AC035146.2, AC027342.2, AC008784.5, AC020931.3, AC025163.7, AC008551.3, AC025370.2, AC021469.3, AC009996.3, AC023201.2, AL161787.4, AC008053.2, AC009863.2, AC013421.5, AC009027.4, AC007256.2, AC055774.1, AC007912.4, AC024583.3, AC027474.2, AC024051.3, 50 AC022021.2, AC016124.2, AL138810.6, AL136097.10, AC013446.3, AC024582.3, AC025162.7, AC011498.4, AC011480.2, AC024045.3, AC015945.3, AL161736.5, AL356140.1, AL355978.1, AL110504.2, AP000597.1, AC020558.3, AC021187.4, AC008032.12, AC019131.3, AL158156.3, AL136233.3, AL031711.23, AC027178.3, AC010264.4, AC067910.1, AC027250.2, AC062024.1, AC016385.3, AC005995.2, AL159993.3, AL160171.2, AP001084.2, AC022766.2, AC011511.4, AC011486.5, AC009127.5, AL121914.20, AL161778.2, AP001075.2, 55 AC007616.2, AC068603.1

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Carboxyterminus HSP70 (CHIP)

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- 25 AL137392.1, NM\_016195.1, AL117496.1, U93121.1, AL132715.2, AF123535.1, AF025309.2, AF049111.1, AF074609.1, AF074608.1, AF074607.1, AF025308.1, AJ277139.1, M64795.1, X82669.1, NC\_001134.1, AC010582.6, U34732.1, U56248.1, Z35775.1, L33863.1, X77199.1, AE003812.1, AE003781.1, AC005359.1, Z36753.1, AA206237.1, AA402625.1, AI640101.1, AA166435.1, AI449051.1, AW641069.1, AV229003.1, AW637360.1, AW636913.1, AW104978.1, AI873411.1, AI744621.1, C82336.1, AI493892.1, AI468801.1, AA944214.1, AA814955.1, AA742281.1, AA477401.1, AA479561.1, AA437337.1, H61147.1, H18470.1, T90042.1, AL157389.3, AC031975.3, AC027641.1, AC022008.2, AC016018.7, AC019190.2, AC010975.3, AC069156.1, AC068918.2, AC026074.4, AC022269.3, AL355997.1
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- 35 AF161348.1, AC006568.7, AE000692.1, AE003650.1, AE003415.1, AL078603.4, NC\_001137.2, AC006020.2, AC005940.3, AC006924.3, AC006258.1, AF054502.1, AF051344.1, U18779.1, AD000092.1, AL031289.1, AL034426.4, AL021917.1, M69188.1, AI948670.1, AI478382.1, AW160598.1, AW658028.1, AW793862.1, AA421360.1, AW326431.1, AA774426.1, AW165025.1, AI959670.1, AI496955.1, AW777910.1, AW281091.1, AV224187.1, AI167050.1, AA741176.1, AA148784.1, T98755.1, AL355978.1, AC024509.2, AC019070.2, AC067740.2, AC055809.2, AC024705.4, AC063848.1, AC021360.3, AC021038.3, AC009965.4, AC017767.1, AC011049.3, AC026633.3, AC053511.2, AC020934.6, AC024190.2, AC027759.2, AC026561.2, AC023862.2, AC011189.4, AC011058.3, AC009792.4, AC020642.3, AC024480.2, AC011566.3, AC025598.1, AC021535.2, AC023917.2, AC023847.2, AC013374.4, AC022888.2, AC012106.2, AC009483.2, AF178220.1, AL121936.9, AL354812.5, AL161720.3, AL133338.3, AL356122.1, AL355983.1, AL157413.6, AL355379.1, AL354914.1, AL031669.27, AL353614.1, AL157775.3, AL139353.1
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SEQ ID NO: 396

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- 50 AF039690.1, U79271.1, AL117525.1, AF136378.1, AL031650.21, AC006919.5, AC006607.1, AE003496.1, NM\_012776.1, AC008056.6, NM\_001619.2, AC007538.5, S81843.1, S48813.1, U08438.1, Z22173.1, Z68282.1, AL121757.7, AL049544.4, AL031681.13, U39674.1, L23127.1, M34073.1, M80776.1, X61157.1, M74822.1, M87854.1, X53421.1, AI735499.1, AW028371.1, AI445418.1, AI266387.1, AI288955.1, AW193663.1, AI298467.1, AI168222.1, AI148323.1, AI140814.1, AI089322.1, AA879456.1, AA843811.1, AA829894.1, AA102109.1, AA029201.1, W72147.1, N51485.1, AI808317.1, AI033069.1, AA161465.1, AA812519.1, N64528.1, H99906.1, AA886109.1, R71679.1, AI970343.1, AA744290.1, AW021346.1, AA099913.1, AW195719.1, AI267979.1, AA083859.1, AI038590.1, N51277.1, AA883684.1, R07471.1, H98684.1, R36854.1, R39448.1, F25334.1, AA083954.1, R54092.1, H09074.1, AA346369.1, AA910762.1, N21975.1, D59844.1, AW195087.1, H11525.1, AA971254.1, W77907.1, AW057648.1, AL041060.1, AI659852.1, AA878973.1, AW392482.1, AI057361.1, AA715235.1, F35739.1, W29097.1, AW022199.1, AA860455.1, AI963422.1, AA026096.1, AW427844.1, AI481147.1, T26899.1, AW413553.1, AW046739.1, AI529534.1, AI661769.1, AA269966.1, N71178.1, AI614472.1, AI713205.1, AI575014.1, AI112396.1, AI073194.1, AA026516.1, AI651890.1, AI575171.1, AA466212.1, AV162955.1, AW495689.1, AI397450.1, AW547034.1, AW502609.1, AW479264.1, AI685864.1, AI652378.1, AA985290.1, AA161236.1, AC022960.2, AP001333.1, AC018648.2, AC068004.1, AC013699.2, AC021912.3, AC018685.5, AC016418.4, AF202962.1, AL139349.15, AL132661.15, AL117190.2, AC036143.2, AC010798.6, AC026746.3, AC016645.3, AC034117.2, AC018640.1, AC009244.20, AC068501.1, AC009444.2,
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SEQ ID NO: 397

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SEQ ID NO: 398

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SEQ ID NO: 430

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10 NM\_015642.1, AL050276.1, AF194030.1, AF185576.1, AC008843.5, NM\_001166.1, U37547.1, L49431.1, AC011738.4, NM\_006585.1, AC006972.2, AC006384.2, AC004828.2, AC007052.4, AF077215.1, AC005144.1, AL163249.2, AL163243.2, AL109752.13, AL031283.26, AJ251713.1, AJ251712.1, AL035415.22, Z68332.1, AL035073.4, AL110503.1, D42052.1, AP001698.1, AP001601.1, D13627.1, AA578163.1, AA069836.1, AW237166.1, H85064.1, AW502748.1, AW611145.1, AW106649.1, AI828036.1, AI221632.1, AA464297.1, AI151799.1, AW729812.1, AW372984.1, 15 AW372983.1, AW235267.1, AI032501.1, AA702174.1, AA354613.1, AA281621.1, AA034048.1, W80497.1, W17275.1, T73134.1, AW731100.1, AW730874.1, AW730644.1, AW730370.1, AW728863.1, AW728739.1, AW728717.1, AW727809.1, AW673083.1, AW618417.1, AW247278.1, AW213355.1, AI648841.1, AA984168.1, AA385412.1, AA347604.1, H88667.1, AC069063.1, AC026560.4, AC027493.2, AC055739.2, AC020896.4, AC063979.1, AC025358.3, AC036131.2, AC041009.1, AC034154.1, AC027790.1, AC012056.3, AC024606.2, AC021712.3, AC022736.2, 20 AL161444.2, AP001959.1, AC046138.4, AC022293.9, AC032022.2, AC068656.1, AC025763.2, AC022894.2, AC025897.2, AC019309.3, AC021754.3, AC011330.5, AC011171.3, AC016135.1, AL136990.14, AP001830.1, AP001167.1, AP000942.2, AC061973.2, AC064862.2, AC040957.2, AC025767.3, AC020930.4, AC008839.4, AC036127.2, AC037456.4, AC022218.4, AC019176.3, AC034167.2, AC026542.2, AC015992.3, AC021506.3, AC021005.2, AC025891.2, AC011853.3, AC011848.5, AC012571.3, AC025009.2, AC009899.5, AC020565.4, 25 AC011642.5, AC025346.1, AC021141.2, AC015950.2, AC017056.3, AC021047.2, AC019648.1, AC007432.7, AC009437.1, AF129075.1, AL356137.2, AL356322.1, AL162716.4, AL109751.18, AL160265.4, AL137144.4, AL355386.1, AL354778.1, AL137074.4, AL157365.3, AP002083.1, AP002013.1, AP001841.1, AP001569.1, AP001365.1, AP001356.1,

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NM\_001278.1, AF080157.1, AF009225.1, AF012890.1, U22512.1, NM\_007700.1, U12473.1, AC012147.7, AE003769.1, AF227841.1, AC009888.1, AL132641.2, AL049775.2, AL132986.2, AF127936.2, AC010685.3, AC006730.1, 50 AE003493.1, AC009464.7, AC007377.3, AF130351.1, AC007785.1, AL355094.2, AL163257.2, AL163207.2, AL132853.1, AL121808.2, AL135745.2, AL121774.3, AL031768.9, AL096710.8, AL078473.2, U29521.1, U29450.1, AP001712.1, AP000213.1, AP000031.1, AP000255.1, AP000135.1, AW611010.1, AW822592.1, AA512576.1, AW159773.1, AW159313.1, AA721189.1, AV400040.1, AI553167.1, AU004118.1, AA518188.1, AA109551.1, R03450.1, 55 AW769650.1, AW497368.1, AW496881.1, AW485684.1, AW344422.1, AT001962.1, AI241905.1, AI200843.1, AI037034.1, AA704752.1, AA660505.1, AC018783.3, AL138921.6, AC026883.2, AL158168.5, AC018351.8, AC015797.2, AC027704.2, AC027438.2, AC024130.3, AC012204.3, AL050344.25, AL355517.2, AP001963.1, AP001816.1, AC041002.1, AC011259.3, AC021846.3, AC012202.2, AC002489.1, AL133313.1, AC016962.8, AC061978.2, AC026270.2, AC068854.1, AC068368.1, AC024134.2, AC025661.2, AC010941.3, AC013497.4, 60 AC021403.4, AC011755.3, AC022238.1, AC010129.2, AC013189.1, AC004071.1, AL353645.2, AL139216.4, AL136362.2, AL356094.1, AL353764.1, AL139020.1,

SEQ ID NO: 433

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SEQ ID NO:434

ZHI214/T3

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SEQ ID NO:435

ZHI214/T7

40 X92474.1, D43948.1, AJ251130.1, AF061744.1, AF001863.1, AF102850.1, U48696.1, AF045432.1, AJ243486.1, Y16849.1, AJ243656.1, U39066.1, U37573.1, Y16299.1, X99058.1, X99060.1, X99051.1, X99057.1, X99056.1, X99052.1, Z97178.1, Y16851.1, AF033096.1, U48697.1, AF011573.1, X99055.1, AJ270223.1, X99054.1, X99053.1, AF128444.1, Y17148.1, Y07542.1, AF224771.1, AF184239.1, U23715.1, AL161559.2, AL031326.1, AC000095.3, AC002522.2, AC004461.3, L77570.1, AL031430.1, AL109939.13, AC000121.1, AF146603.1, AE003700.1, AC000092.1, AC004099.1, AC004231.1, U82964.1, AL031277.1, U30368.1, X73502.1, X73501.1, AW374979.1, R14180.1, 45 AW407477.1, AW176568.1, AW239387.1, W27586.1, AA805103.1, AA767900.1, Z20910.1, AA094395.1, AA568734.1, AA299590.1, Z19789.1, AJ396976.1, AW409741.1, AI857031.1, AI857046.1, AI816693.1, AI816668.1, AI816651.1, AI815345.1, AI816702.1, AI816701.1, AI816700.1, AI816699.1, AI816697.1, AI816696.1, AI816695.1, AI816694.1, AI816692.1, AI816690.1, AI816689.1, AI816688.1, AI816667.1, AI816664.1, AI816663.1, AI816662.1, AI816661.1, AI816660.1, AI816659.1, AI816658.1, AI816657.1, AI816656.1, AI816655.1, AI816654.1, AI816653.1, AI816652.1, 50 AI816650.1, AI816649.1, AI816648.1, AI816647.1, AI816646.1, AI816645.1, AI816644.1, AI816643.1, AI816641.1, AI816640.1, AI816639.1, AI816638.1, AI815377.1, AI815376.1, AI815375.1, AI815374.1, AI815373.1, AI815371.1, AI815370.1, AI815369.1, AI815368.1, AI815367.1, AI815366.1, AI815365.1, AI815363.1, AI815362.1, AI815361.1, AI815360.1, AI815347.1, AI815344.1, AI815343.1, AI657485.1, AA933356.1, AA933350.1, AA933216.1, AA933125.1, AA933095.1, AA933094.1, AA660699.1, N83963.1, AI815364.1, AI816698.1, AI816642.1, AI446849.1, AI353568.1, 55 AA933275.1, AA933111.1, AA933353.1, AA933184.1, AW455598.1, AI617314.1, AI354018.1, AI353756.1, AC012054.1, AC018448.8, AC041023.2, AC068800.3, AC009452.9, AC026031.3, AC024663.3, AC068617.1, AC026659.3, AC027191.2, AC027065.2, AC025309.2, AC026522.1, AC024628.2, AC010187.6, AC023800.3, AC017028.5, AC068493.3, AC037481.2, AC023859.2, AC022133.3, AC010218.4, AC008680.3, AC008665.3, AC011500.5, AC027735.2, AC009786.2, AC026990.2, AC025484.2, AC022357.3, AC022705.3, AC011226.3, AC011795.4, 60 AC017007.5, AC020586.2, AC015529.3, AC021694.2, AC013786.2, AC016820.2, AC022281.1, AC014336.1, AC016381.1, AL137003.2, AL159970.7, AL138890.3, AL139004.3, AL355839.1, AL355497.1, AL161447.4, AL138795.1, AP001947.1, AP000812.1, AP000665.1,

SEQ ID NO:436



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## ZH1217/T7

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## SEQ ID NO: 438

- ZH1222/T3  
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AL157786.2, AL136302.6

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- 5 Z99129.1, NM\_004506.2, M65217.1, NM\_008297.1, AF045627.1, X61754.1, AF172640.1, AL163912.1, Z68160.1, L41499.1, U40424.1, D17366.1, AC011809.2, AC008126.9, AC000104.1, AL133216.10, Z92844.1, AC002329.2, AE003811.1, AE003525.1, AE003517.1, AE003486.1, AE002786.1, AC018748.3, AF102707.1, Z83318.1, AI923911.1, AI990935.1, AI203377.1, AI056677.1, AW269952.1, AI989487.1, AI472020.1, AI524322.1, AI700694.1, AI561266.1, AI979106.1, AW008963.1, AW468756.1, AW183922.1, AI688920.1, AA905319.1, AI690727.1, AA707596.1, AI499774.1, AA551748.1, AA551757.1, AI536850.1, AA969316.1, AI480249.1, AA253434.1, AA832045.1, AI270358.1, AI810705.1, AI433107.1, AA651949.1, AA969392.1, N39221.1, AA868883.1, AI142644.1, AL035757.1, AA136344.1, AI453040.1, AA860985.1, AA913304.1, AA913486.1, AW468554.1, R39144.1, AA815117.1, AI473089.1, H24055.1, AI539466.1, AA971072.1, T53314.1, H72024.1, R46149.1, D53854.1, D52415.1, AW028964.1, H72025.1, AA250730.1, D52616.1, D52419.1, H14792.1, F04785.1, T29491.1, N46665.1, C20787.1, T53313.1, AW142847.1, AI740594.1, AI230246.1, AI167251.1, AA944812.1, AI661205.1, AA268498.1, AV259149.1, AA832774.1, AI962803.1, AI556468.1, AA818911.1, AI170959.1, AI010919.1, AI102092.1, AL121954.4, AL109916.3, AC027000.2, AC068022.1, AC027082.2, AC024345.2, AL049180.3, AC011602.6, AC027648.6, AC025854.2, AC027355.1, AC022387.2, AC022480.4, AC025302.2, AC009754.3, AC009816.5, AC024260.1, AC011683.3, AC010660.4, AL121954.4, AL109916.3, AC027000.2, AC068022.1, AC027082.2, AC024345.2, AL049180.3, AC011602.6, AC027648.6, AC025854.2, AC027355.1, AC022387.2, AC022480.4, AC025302.2, AC009754.3, AC009816.5, AC024260.1, AC011683.3, AC010660.4

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ZHI233/T3

- 25 AB006198.1, Y14314.1, AB014722.1, AB014721.1, AF129931.1, AF147725.1, AC007915.3, AF028338.1, L20095.1, L20680.1, NM\_015933.1, AC011462.4, AE003765.1, AC000029.17, AF161448.1, AF077202.1, U39402.1, AC004196.1, U67478.1, AL163816.1, Z97832.11, AL049853.1, AL112418.1, AL021930.1, L09190.1, AK001152.1, AB023212.1, M15100.1, AB017022.1, W27222.1, AW402760.1, AL047890.1, AI594593.1, AW820827.1, AA607769.1, AI120962.1, AI509410.1, AI908693.1, AW393484.1, AW652595.1, AI964608.1, AA979854.1, AA979772.1, AI661459.1, AI642054.1, AJ228935.1, AA751847.1, AW758324.1, AI827037.1, AV417239.1, AW674436.1, AW615491.1, AW245981.1, AW074946.1, AW006944.1, AI924762.1, AI880663.1, AI880658.1, AI709253.1, AI708293.1, AI708235.1, F33596.1, F30411.1, F28809.1, F28190.1, F27897.1, AI666115.1, AI570650.1, AI459983.1, AI418553.1, AI370584.1, AI364309.1, AI339191.1, AI333234.1, AI290693.1, AI090805.1, AA910393.1, AA563619.1, AA364686.1, AA321138.1, AA280277.1, AA279851.1, AA229404.1, AA151350.1, AA149268.1, AA134303.1, AA082333.1, AA046848.1, AA026455.1, W95678.1, W76586.1, W51757.1, W04465.1, N84053.1, N80509.1, N78206.1, N76058.1, R07233.1, T91349.1, T80989.1, AP001201.4, AP000592.2, AP001191.1, AP000586.2, AC008683.4, AC018996.3, AC046141.3, AC068951.1, AC022120.4, AC008405.3, AC008658.2, AC011069.6, AC013189.1, AC055744.2, AC068667.3, AC027309.2, AC027307.3, AC022091.3, AC010377.4, AC008453.4, AC008450.3, AC064317.1, AC064056.1, AC052499.1, AC044355.1, AC045178.1, AC041917.1, AC040463.1, AC034640.1, AC028038.1, AC021328.3, AC021286.3, AC007903.2, AC026184.1, AC019127.4, AC018734.2, AC011233.2, AC023950.2, AC010899.3, AC015903.1, AC014411.1, AC018045.1, AC006579.3, AL136136.2, AL136119.3, AL109955.13, AL135939.9, AL133282.13, AL133284.12, AL032818.2

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- 45 AJ236885.1, L04282.1, AF039019.1, U30381.1, NM\_011749.1, X98096.1, AJ001165.1, U80078.1, AL133244.1, AL121656.2, AC008125.9, AL049648.6, AC007444.1, AE003754.1, AC005552.1, AJ006687.1, AL038916.1, AI158501.1, AA967471.1, AW261045.1, AW425025.1, AI093969.1, AW667700.1, AW619431.1, AW619430.1, AW359900.1, AA911993.1, D86150.1, AC019289.3, AC032043.1, AC026618.1, AC020598.3, AC019180.4, AC009770.4, AC023077.3, AC040911.1, AC034145.1, AC023199.2, AC027362.1, AC026243.2, AL139189.4, AL354939.3, AL354985.2, AC069141.1, AC020609.4, AC016965.6, AC019074.3, AC026116.7, AC026441.2, AC024588.2, AC022113.4, AC016648.4, AC010308.4, AC022554.2, AC023560.2, AC021219.2, AC020787.2, AC007825.5, AC012075.3, AC016484.1, AC016965.5, AC019694.1, AC010120.4, AC012550.1, AL353575.3, AP001972.1

55 SEQ ID NO: 442

ZHI235/T7

- 60 AF039019.1, AJ236885.1, U30381.1, NM\_011749.1, U80078.1, X98096.1, AJ001165.1, U96633.1, L04282.1, AE003673.1, AF214658.1, AE001574.1, AC005379.1, AC002512.1, AC005817.7, AC004005.2, AC003063.7, AF181967.1, U90222.1, AF113957.1, AC004189.1, U97191.1, Z81052.1, AJ245414.1, AJ012638.1, AJ012636.1, AP000517.1, AB023055.1, AB023054.1, AI263859.1, AA563588.1, AI056295.1, AA287619.1, AI743361.1, AW779476.1, AI384073.1, AI382374.1, AW051393.1, AA613057.1, AA943882.1, AI848462.1, AI323627.1, AW272463.1, AW772534.1, H12745.1, AW823563.1, AA110786.1, AI467973.1, AI283469.1, AI077636.1, AI003273.1, AA622568.1, AA552124.1, AA192099.1, AW732203.1, AI955302.1, AI955293.1, AI696880.1, AI283452.1, H70711.1, AA764105.1, AI393951.1, H12746.1, AI864852.1, AW214414.1, AI589987.1, AA631115.1, C06563.1, AI202723.1, AI030160.1,

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10 ZH1239/T3

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SEQ ID NO: 446

15 ZH1246/T7  
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40 ZH1252/T3  
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5      SEQ ID NO:449

**ZH1256/T3**

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SEQ ID NO: 450

20 ZH1256/T7

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55 ZH1268/T3

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5 ZHI275/T3  
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- 5 NM\_005271.1, X07769.1, X07674.1, M20867.1, M37154.1, X66312.1, J03248.1, AC006144.1, X66310.1, U08997.1, X67491.1, X66314.1, AF086070.1, NM\_012570.1, NM\_008133.1, X14223.1, X14044.1, X57024.1, AL021396.5, AC004944.1, AE003805.1, AC011198.2, AE001699.1, AC004335.1, X92729.1, AW008481.1, AW161914.1, AL121462.1, AI796326.1, AI767015.1, AI719871.1, AI688677.1, AI685203.1, AI683603.1, AI609634.1, AW152299.1, AW778779.1, AI936502.1, AI924085.1, AI870436.1, AI220414.1, AI017359.1, AI860803.1, AI818481.1, AI373143.1, AI476186.1,
- 10 AI432139.1, AI434555.1, AI052741.1, AW779007.1, AI453009.1, AA705949.1, AA612700.1, AA576729.1, AI346963.1, AA719691.1, AW440634.1, AW299819.1, AI953347.1, AI669386.1, AW316988.1, AA579763.1, AI479598.1, AI041934.1, AI865818.1, AA931220.1, AA639014.1, AW469758.1, AW105271.1, AI039164.1, AI628503.1, AI547078.1, AI580269.1, AW131820.1, AI955767.1, AI768285.1, N55432.1, AW662165.1, AI949911.1, AA968749.1, AI948510.1, H23769.1, AA205716.1, AA622009.1, AI766220.1, AI628736.1, AA961548.1, W32185.1, N58794.1, AA603980.1,
- 15 AI200249.1, AI433759.1, AI799717.1, AA227280.1, AW206141.1, AA507097.1, AI871324.1, AI220678.1, D19635.1, AA506817.1, AI023057.1, AI167726.1, AA984899.1, H22628.1, AL119832.1, AI590208.1, AA995612.1, T29318.1, H52944.1, AI220953.1, N62651.1, AI104010.1, AA932126.1, AW614089.1, AA352492.1, AI942453.1, H57922.1, AA541774.1, AI424426.1, R54424.1, W69491.1, AA934829.1, AW779733.1, AI932689.1, AI582068.1, AL136982.1, AL161935.5, AP001776.1, AL163534.3, AC021193.3, AC023150.2, AC007117.1, AL137063.5, AL160158.2,
- 20 AC025731.7, AC040988.2, AC063968.1, AC010902.3, AC022833.2, AC025924.2, AC021450.3, AC011791.3, AC016365.4, AC016802.5, AC021761.3, AC023482.2, AC016991.2, AC020959.1, AC020024.1, AC018408.1, AL160162.4, AL136088.2, AL133269.8, AL355140.2, AL354743.1

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- NM\_003011.1, U51924.1, X75091.1, M93651.1, D45198.1, AC005666.1, Z95126.1, AC007649.12, AC008865.3, S68987.1, S68589.1, AL121985.13, AB015613.1, AB022692.1, AB022691.1, AF027174.1, AJ243486.1, AF102850.1, AF032922.1, AF039698.1, AF103726.1, U48696.1, U34048.1, AF045432.1, AF033097.1, AJ243655.2, S78798.1, AJ249625.1, U66300.1, U39066.1, AJ004935.1, U37573.1, AJ001103.1, Z97178.1, AJ010903.1, Y17148.1, U35663.1,
- 30 U30169.1, Z49980.1, D61704.1, AC004106.1, AL118512.8, S64573.1, AC011809.2, AF030515.1, AF061786.1, AL121575.24, AC002091.1, AJ277276.1, AJ277275.1, AL109941.17, S64574.1, X99051.1, D13957.1, AW804718.1, AW297865.1, AI907472.1, AI348548.1, AW291539.1, AW819112.1, AW384700.1, AI656103.1, TI9570.1, AI348464.1, AW580047.1, AA738062.1, AW463846.1, AW390103.1, AW373693.1, AL022685.1, AI316314.1, AA611351.1, AA549598.1, AA414765.1, AA123463.1, AA796821.1, AA667063.1, AA118033.1, C79263.1, AA607821.1, AW373676.1,
- 35 AW681843.1, AJ398907.1, AA714153.1, AA206519.1, AW390843.1, AA069741.1, AW842631.1, AV097455.1, AI267315.1, AA329702.1, AA313621.1, AA233558.1, D54409.1, AA409879.1, H34224.1, AW375988.1, AW536757.1, AA099025.1, AU045232.1, AW537027.1, AW375987.1, AW239416.1, AI768142.1, AA377175.1, AA356749.1, AA318099.1, AA314914.1, AA296390.1, AA206939.1, AA074744.1, AA069861.1, AI981321.1, AW390108.1, AA461024.1, AA474415.1, AW682597.1, AW209981.1, AL118403.1, C89073.1, AA624202.1, AA474356.1, AA170936.1,
- 40 AA103478.1, D28721.1, D21513.1, AW629348.1, AI101820.1, AL024232.1, AI467387.1, AA341055.1, AA122619.1, AA793865.1, AW773136.1, AA179445.1, AW390844.1, AA606606.1, AW644081.1, AW638871.1, AW634071.1, AW158383.1, C89511.1, AA377176.1, U47704.1, AJ396687.1, AI815353.1, AW547461.1, AI815356.1, AA549660.1, AW682308.1, AW543995.1, AW537538.1, AI477163.1, AI477134.1, AC067721.3, AC024160.2, AC016607.5, AC008879.3, AC008818.4, AC023066.2, AL138838.2, AC036148.2, AC027472.2, AC068438.1, AC008905.5, AC018394.2, AI163195.2, AC017015.3, AC027082.2, AP000831.1, AP000713.1, AC025974.2, AC018915.3, AP001148.1, AC024503.2, AL161451.4, AC011076.2, AC068294.2, AC015767.1, AC027457.2, AC044882.2, AL159155.2, AC021505.1, AC025391.3, AC044900.2, AC058821.2, AC026506.2, AC021248.3, AL121938.4, AL136359.4, AL355150.3, AL162371.5, AL136312.1

50 SEQ ID NO:456

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- AW801878.1, AW078466.1, AW303316.1, AI092597.1, AA579413.1, AA668238.1, AA578980.1, AA564790.1, AA630703.1, AA482218.1, AA516095.1, AW674250.1, AA748113.1, AA737104.1, AI419588.1, AA352137.1, T94763.1, AA714153.1, AC011076.2, AC023066.2, AC015767.1, AC067721.3, AC024160.2, AC008905.5, AC008401.3, AC027457.2, AC027082.2, AC036148.2, AC027472.2, AC024503.2, AL163195.2, AC016607.5, AC008879.3, AC008818.4, AL138838.2, AC010951.4, AC018372.4, AC018394.2, AC017015.3, AP000831.1, AC021355.3, AP000713.1, AL161451.4, AL121594.2, AC016150.5, AC068294.2, AC021853.3, AC015936.3, AC025624.3, AC068198.6, AC023430.9, AC008558.4, AC008746.5, AC025802.2, AC005507.6, AC016711.3, AC013534.1, AC005504.3, AC004710.3, AL162271.2
- 10 SEQ ID NO: 457  
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- 25 SEQ ID NO: 458  
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- 40 SEQ ID NO: 459  
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- 5 AF040964.1, Z49250.1, Z83850.1, AE001145.1, AF191070.1, AC009248.6, AF016450.2, U49830.1, NM\_014386.1, AF182034.1, AC024869.1, AC020647.9, AF118125.1, AC007232.5, AF130342.1, AL035464.20, AL080238.9, AL034427.1, AP000561.1, AI808442.1, AA664012.1, AI628516.1, AA630380.1, AW043655.1, R69790.1, AW513701.1, H56500.1, R69789.1, H56688.1, Z21088.1, AA652148.1, AW610692.1, AW553895.1, AI451124.1, C80481.1, AI462312.1, C85371.1, AI591821.1, AI604189.1, AA177891.1, AI449315.1, AW554802.1, U83055.1, AV314215.1, H61855.1, AV207115.1, AV295151.1, AV368467.1, AV214236.1, AV295152.1, AV257539.1, AV295169.1, AV367514.1, D29398.1, AA183653.1, AW681938.1, AW046876.1, AV145607.1, AA210324.1, AA174896.1, AA332492.1, 10 AW414996.1, AW339249.1, AW335085.1, AW158276.1, AV385524.1, AL037685.2, AV183523.1, AV178057.1, AI807819.1, AI696097.1, AI626600.1, AI544578.1, AI477034.1, AA980276.1, AA928231.1, C65891.1, C61074.1, C53590.1, AA279783.1, C10643.1, AL158068.4, AC026977.2, AC019140.3, AC040892.1, AL133373.1, AC010302.3, AC009795.3, AC013807.3, AC027533.1, AC012056.3, AC006906.2, AL133326.8, Z82209.1, AP001257.1, AP001181.1, AP000726.2, AC036220.2, AC025435.3, AC010314.4, AC009436.2, AC034172.2, AC025660.2, AC012528.2, 15 AC009957.5, AL353739.2

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- 20 AL117590.1, AC007245.3, AC003683.1, AL355072.2, AE003652.1, AC005120.1, AC006214.1, AL161550.2, AL021687.1, AC007063.5, AC004535.1, AC013453.1, AC004752.1, AL049777.5, AL096862.18, AF000265.1, AL132764.1, Z70205.1, AP000139.1, AP000226.1, AP000087.1, D85389.1, AC005970.2, AC021640.5, AC006287.1, AE001368.1, AC004629.1, AL163232.2, AL049860.8, AL031177.1, AL031733.3, AL031600.4, Z82195.1, AL031653.5, AP001687.1, AA175375.1, AI740728.1, AA332493.1, AI074062.1, AI580915.1, AI087846.1, AI810796.1, AW874606.1, AI016838.1, AA470819.1, W85623.1, W85600.1, AI449083.1, AI549242.1, AI845400.1, AV015395.1, AV375672.1, 25 AV327111.1, AV354227.1, AI383006.1, AV300969.1, AV253424.1, AI604667.1, AA771574.1, AV376539.1, AW332467.1, AW642408.1, AW636829.1, AW635398.1, AW634742.1, AW634652.1, AI467036.1, AA285835.1, AL135649.1, AV377755.1, AI915385.1, AV064014.1, AV062554.1, AA808321.1, AA525659.1, AA458724.1, AA232022.1, AA118229.1, R12836.1, T37449.1, AC034212.3, AC022121.3, AC008522.4, AC008531.2, AC011129.3, AC025069.3, AC021824.2, AC023528.3, AC020916.4, AC023808.3, AC004689.5, AL354852.3, AC036175.2, 30 AC019106.2, AC019274.3, AC015595.3, AC006280.6, AC022947.2, AC023567.2, AC022977.1, AL137780.2, AL135926.4, AC048385.2, AC016650.4, AC032009.2, AC005077.2, AC027637.2, AC015497.3, AC021515.3, AC025385.2, AC019328.4, AC021562.3, AL354805.2, AL139284.3, AL355811.2, AL031749.7

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SEQ ID NO: 466

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-203-

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SEQ ID NO: 468

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SEQ ID NO: 469

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60 SEQ ID NO: 470

ZH13301/T7

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- 30 SEQ ID NO: 472  
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- 15 NM\_014633.1, D63875.1, NM\_009431.1, L49502.1, AC004796.2, NM\_003670.1, AC006989.3, U78027.1, AL034370.1, AL031007.1, AL035422.12, AB004066.1, AC025744.5, AC027377.2, AC024240.2, AC023374.2, AC010144.2, AC060757.2, AC019025.4, AC055119.2, AC009506.3, AC009315.3, AC017073.4, AC060823.1, AF235105.1, AC024192.2, AC021807.3, AC021192.3, AC025292.6, AC019229.4, AC015974.4, AC022184.2, AC023000.2, AC011303.4, AC010948.2, AC009907.2, AL138772.2, AL137783.4, AL133476.4, AI140348.1, AW575179.1, AA313178.1, AI302523.1, AI343468.1, H88182.1, AI924726.1, AI279164.1, AI675472.1, AI694570.1, C05893.1, AI935120.1, AW573224.1, AW070842.1, W27038.1, H49849.1, AW338994.1, AW173599.1, AW192729.1, AI935109.1, AA775398.1, AI418449.1, AA649176.1, AA977091.1, H99003.1, AI921383.1, AA111977.1, AW057891.1, N45992.1, AA903179.1, AA725733.1, AA769208.1, AI050019.1, AA972949.1, AA907605.1, AI650806.1, AI040043.1, AA976298.1, AA663521.1, AA599535.1, AI392652.1, W15276.1, N20975.1, AA382400.1, AI015136.1, AI830477.1, AI702518.1, AA448303.1, AA133685.1, D62244.1, H11922.1, Z21605.1, AA883364.1, AA120987.1, H71942.1, T18935.1, AW236770.1, H88183.1, AA970675.1, AA906369.1, AA778495.1, AA569907.1, AF074673.1, AI110766.1, T36008.1, H49850.1, AA448439.1, H13635.1, H14826.1, H72101.1, AI882558.1, AA990321.1, AI231369.1, AA794084.1, AW391124.1, AA126436.1, AI540567.1, AW338921.1, AW008252.1, AI983861.1, AI926982.1, AI811452.1, AI801550.1, AI697038.1, AI692253.1, AI680537.1, AU061411.1, AL047652.1, AI384049.1, AI274740.1, AI129012.1, AI050840.1, AA935903.1, AA502930.1, AA459382.1, W39236.1, H50006.1, H47024.1, T40923.1

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- 35 AB020660.1, AC004560.1, AC002335.2, AC011749.2, NM\_014119.1, NM\_001385.1, AC010135.3, AC004021.1, AF090901.1, AE001806.1, AE001523.1, AF003694.1, L44117.1, AB008681.1, AB004678.1, AP000500.1, D78011.1, NM\_000206.1, NM\_014892.1, AC022492.5, AC006264.3, AE003605.1, AE003528.1, AF225899.1, AC003093.1, NM\_007167.1, AC006007.1, AF191067.1, AF191066.1, AF191065.1, AF199490.1, AF055470.1, AF105999.1, AC005599.5, AC006524.1, AL163231.2, AL023496.1, AL035684.25, AL034552.22, AL035555.10, Z93928.1, AJ243221.1, U12968.1, AP001686.1, AP001116.1, D11086.1, M59706.1, AB013356.1, AB029039.1, M60729.1, M37157.1, AW301888.1, AI568547.1, AI583768.1, AI936629.1, W27274.1, M62235.1, AI480106.1, W25908.1, AI695267.1, AW877787.1, AW028690.1, N62788.1, AA055767.1, H35697.1, AI154653.1, AA684914.1, AI314818.1, AW304578.1, AW701243.1, AA730316.1, W27573.1, AA747507.1, AW701235.1, AU062105.1, AU054035.1, AU039346.1, AW779331.1, AW612623.1, AW612325.1, AW449054.1, AW300369.1, AW271596.1, AW257923.1, AW243196.1, AW242821.1, AW197670.1, AW028159.1, AW024860.1, AW024852.1, AI991537.1, AI936331.1, AI912813.1, AI831914.1, AI765642.1, AI672449.1, AI629008.1, AI478498.1, AI469047.1, AI291149.1, AI114808.1, AI033077.1, AA704840.1, AA704236.1, W03786.1, N98259.1, R91017.1, AW819289.1, AW819284.1, AW768498.1, AW768346.1, AW686186.1, AW504627.1, AW391566.1, AW211317.1, AW193466.1, AW183964.1, AV258097.1, AW081914.1, AL110372.1, AI864987.1, AI860562.1, AI684615.1, AI440025.1, AI370166.1, AI091610.1, AA988240.1, AA832000.1, AA807563.1, AA632170.1, AA447899.1, AA132727.1, AA100128.1, AA099559.1, AA054459.1, W61266.1, N54821.1, R91111.1, Z29120.1, AL157758.5, AC016693.4, AC008574.3, AC021709.2, AC022756.2, AC021050.4, AC055748.5, AC021818.3, AC012239.3, AC025400.2, AC024412.2, AC018987.3, AC012511.3, AC006184.1, AL139089.4, AC068889.4, AC023509.9, AC021865.7, AC036240.3, AC013487.3, AC021158.2, AC024557.1, AC015566.4, AC013262.3, AL353999.1, AP001011.1, AP000805.1, AC005973.4, AC034257.2, AC036184.2, AC068914.1, AC036131.2, AC013335.5, AC010297.3, AC008722.4, AC068464.1, AC009836.3, AC024603.2, AC026975.2, AC037428.1, AC022402.2, AC010066.5, AC014420.1, AC014889.1, AC015913.2, AC016400.1, AC016110.1, AL139349.16, AL096865.22

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- 60 AB020660.1, AC002336.2, NM\_014119.1, NM\_001385.1, AF090901.1, AC006365.3, AE001523.1, AB004678.1, D78011.1, AC011504.2, AC022492.5, AE003522.1, AE003419.1, U82695.2, AC005251.1, AC003093.1, AF191067.1, AF191066.1, AF191065.1, AC007535.3, AF007865.2, AL079352.3, AL049588.11, AL121806.2, AL034552.22, AL132769.1, U12968.1, M59706.1, J03498.1, AW301888.1, AI568547.1, AI583768.1, W27274.1, AI936629.1, M62235.1, AI480106.1, AI695267.1, AW877787.1, W25908.1, AW028690.1, N62788.1, AW304578.1, AA055767.1, AA730316.1,



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50 ZH057/T3  
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ZH057/T7

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ZH1276/T3

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45 SEQ ID NO: 493

ZH176/T3

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SEQ ID NO: 494

ZH176/T7

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15 SEQ ID NO:495

ZH183/T3  
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ZH1213/T3  
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Acidic 82 kDa

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ZH12110/T3

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SEQ ID NO: 513

ZH13410/T3

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SEQ ID NO:514

ZH141/T3

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SEQ ID NO: 515

ZH141/T7

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SEQ ID NO: 516

Progesterone Induced protein (DD5)/KIAA0896

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SEQ ID NO: 518

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SEQ ID NO: 524

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SEQ ID NO: 525

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- 20 SEQ ID NO: 531  
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- 30 SEQ ID NO: 532  
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- AC007312.1, AC007938.1, AF235098.1, AC003084.1, AF126403.2, AC005874.3, AF134471.1, AC005971.5, AC006600.4, AC005823.1, AF024496.1, AC002525.1, AL022162.1, X79283.1, AC007349.1, AF117341.1, AC008757.5, AF208389.1, AF205586.1, AC002044.1, AC002530.1, AC006364.3, AC005820.1, AC007488.15, AF118865.1, AF118859.1, AC007436.1, AF118864.1, AF118863.1, AF118861.1, AC006522.5, AC000015.2, AC004816.1, AC006256.1, AC005669.1, AL136452.7, AL023856.1, AL008721.1, Z99916.1, Z81479.1, AL034416.1, AL031733.3, AL022398.1, AL008634.1, AL030995.1, AL111626.1, U58755.1, AP000815.1, AW797580.1, AI473891.1, AA368397.1, AA306548.1, AC034129.2, AC040905.2, AC026033.3, AC013336.7, AP001813.1, AP001354.1, AC067739.3, AC023891.7, AC015970.4, AC044856.2, AC034233.3, AC026434.2, AC016599.3, AC008566.3, AC016173.2, AC067715.1, AC027098.2, AC026858.2, AC016250.3, AC016039.3, AC025683.2, AC025361.2, AC011686.3, AC016916.4, AC025207.2, AC012513.4, AC011245.3, AC015721.2, AC010936.2, AC016010.1, AC010733.1, AL355586.4, AL354820.3, AL136138.1, AP002010.1, AP001834.1, AP001501.1, AC012041.8, AC066613.2, AC009148.6, AC068045.1, AC067795.1, AC019140.3, AC010139.3, AC044789.1, AC026975.2, AC020779.3, AC021880.2, AC016721.4, AC020755.2, AC021708.2, AC024159.1, AC022612.1, AF188028.1, AL136124.8, AL135786.8, AL162452.3, AL139122.3, AL138708.2, AC048378.2, AC025178.3, AC022444.3, AC068557.1, AC067850.1, AC034149.2, AC037196.1, AC022778.3, AC024030.2, AC016441.4, AC023453.1, AL139231.4, AL356459.1, AL139248.3, AL138724.2, AL136106.2, AP001536.1

SEQ ID NO: 563

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SEQ ID NO: 564

Group ZH139

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SEQ ID NO: 565

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-237-

AC027699.1, AC009833.3, AC022264.2, AC013707.2, AC020617.2, AC012593.3, AC012410.2, AC012248.2, AC013152.1, AP001455.1, AC046133.3, AC046187.2, AC008885.3, AC060232.3, AC013361.4, AC004932.2, AC044804.1, AC011186.3, AC019207.3, AC016061.3, AC016916.4, AC023470.2, AC016500.3, AC023567.2, AC023399.2, AC016444.2, AC014380.1, AL356132.3, AL354884.2

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SEQ ID NO: 566

ZH1402/T3

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SEQ ID NO: 567

ZH1402/T7

AL050302.2, AL163203.2, AL049911.2, NM\_014915.1, AB028997.1, AB011137.2, AF090187.1, AC004499.1, AL009051.1, AL138654.1, AP000365.1, AP000548.1, AC011661.5, AP001302.1, AC004936.2, AC006157.2, AL161940.6, U40160.1, AC008912.4, AC004142.1, AC006996.2, AC009513.2, AC005358.1, AL161595.2, AL022605.3, X70810.1, AL035531.17, AW373574.1, AW170035.1, AA759177.1, AL046701.1, AV242491.1, AV228746.1, AI957948.1, C87958.1, AA837612.1, AA837592.1, AW469178.1, AW331138.1, AW320227.1, AW171900.1, AW087179.1, AW052899.1, AW042526.1, AI972424.1, AI950371.1, AI920706.1, AI784583.1, AU072482.1, AU071886.1, AI684965.1, AI460172.1, AI148480.1, AI093327.1, AI025802.1, AA990150.1, AA970354.1, AA708873.1, AA151117.1, AA150449.1, AA149652.1, AA136980.1, AA101607.1, AA071350.1, W73028.1, H97559.1, H96023.1, AL157387.1, AL162272.3, AC015940.2, AC022596.3, AC008088.2, AF228659.1, AC023067.3, AC016739.2, AC025384.2, AL354819.2, AL157695.2, AL138965.3, AL137219.1, AL049185.4, AC008690.1, AC026427.2, AC008390.6, AC026081.2, AC010785.3, AC016215.4, AC019042.3, AC021755.4, AC007342.2, AC012174.2, AC018792.2, AL356312.1, AL161912.3

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SEQ ID NO: 568

ZH154/T3

AP000025.1, AP000026.1, AL163203.2, AL050302.2, AL049911.2, NM\_014915.1, AK001137.1, AB028997.1, AC007617.10, AE003447.1, AJ223186.1, AC004739.1, AC006355.3, AC006045.2, U48386.1, AF044083.1, AL163224.2, Z70270.1, Z74696.1, U41993.1, D82813.1, AP001679.1, AP001506.1, AP000961.2, AC005522.2, AC007379.2, AE003459.1, AC006478.2, AC007099.3, AC005879.3, AC005650.1, AC005331.1, AC004045.1, AL163291.2, AL132766.13, AL096867.15, AL078644.10, Z22180.1, AL021406.1, AL022395.2, Z82193.1, Y18930.1, AJ238787.1, AJ238786.1, AP001746.1, AP001623.1, AI951118.1, AW000914.1, AI922499.1, AI871874.1, AA991162.1, W08579.1, AW030402.1, AA661357.1, C60377.1, AA471702.1, AA095151.1, AW611472.1, AW519678.1, AW449940.1, AW394816.1, AV282871.1, AI902224.1, AV121102.1, AV064061.1, AV051246.1, AV045752.2, AI311562.1, AU045123.1, AI137187.1, AU021965.1, AU021770.1, AI075925.1, C87414.1, C85160.1, AA828186.1, AA701829.1, AA667026.1, AA015732.1, AC067744.2, AL162272.3, AC007351.16, AC027141.1, AC024370.2, AC022175.1, AC014239.1, AC035145.2, AC068481.1, AC061987.1, AC027699.1, AC012410.2, AC012248.2, AC013152.1, AP001455.1, AC046187.2, AC026428.2, AC022418.3, AC010622.3, AC008885.3, AC027696.2, AC004932.2, AC023988.2, AC016444.2, AC011128.2, AF186999.1, AC005139.3

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SEQ ID NO: 569

ZH154/T7

AL163203.2, AL050302.2, AL049911.2, AP000542.1, AL163202.2, AP001464.1, NM\_014915.1, AB028997.1, AB011137.2, AF077534.1, AL009051.1, U32775.1, AL161957.1, AL110120.11, AL078614.2, U19872.1, AP001465.1, AK000712.1, AC008154.6, AC005670.1, AL133475.14, AL021633.2, AL096861.9, Z84482.1, AL080283.1, AW373574.1, AI951118.1, AW297642.1, AA579752.1, AI989660.1, AI825717.1, AI084496.1, AA331953.1, AW614036.1, AI236531.1, AI180434.1, AI180260.1, AI176501.1, AA892166.1, AI058351.1, AI044283.1, AA464382.1, AW656081.1, AW656019.1, AW564696.1, AI984814.1, AV127940.1, AI770175.1, AI446107.1, AA736439.1, AA219203.1, R62950.1, AW578955.1, AW541472.1, AW540560.1, AW363481.1, AV350817.1, AV346364.1, AV322534.1, AI955034.1, AI790539.1, AV131385.1, AI647944.1, AI631727.1, AI583901.1, AI368143.1, AI324262.1, AI193904.1, AI168669.1, AI133530.1, AI086364.1, AI065683.1, AI008640.1, AA910838.1, AA738088.1, AA623276.1, AA554531.1, AA533501.1, AA518668.1, AA423412.1, AA250678.1, AA222830.1, AA046147.1, AA046322.1, W54181.1, N72190.1, Z33598.1, AL157387.1,

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AC024252.3, AL353626.1, AC036170.2, AL162272.3, AC067744.2, AC015940.2, AC008088.2, AC026271.2, AC022596.3, AP000776.1, AL133290.3, AC011254.3, AL355499.5, AC024107.9, AC012435.6, AC011040.3, AC010959.3, AC015650.1, AL133322.3, AP000872.2, AP001133.1, AC048371.2, AC068183.1, AC027493.2, AC025485.2, AC021488.3, AC010994.9, AC011829.2, AL354771.1

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SEQ ID NO: 570

ZH185/T3

- AL163203.2, AL050302.2, AL049911.2, AP000026.1, AP000025.1, NM\_014915.1, AK001137.1, AB028997.1, AC007617.10, AE003447.1, AJ223186.1, AE003494.1, AC004739.1, AC006355.3, AC006045.2, U48386.1, AC005177.1, AF044083.1, AL163233.2, AL163224.2, Z70270.1, Z74696.1, U41993.1, D82813.1, AP001679.1, AP001688.1, AP001506.1, AP000961.2, AC005522.2, AC008430.3, AC007379.2, AE003675.1, U91327.1, AC006478.2, AC004996.1, AC007099.3, AC005100.2, AC007100.3, AC005879.3, AC006952.6, AC005331.1, AC004045.1, AL133465.30, AF016685.1, AL132766.13, AL109985.2, AL078644.10, AL030999.2, AL022395.2, Z82193.1, Y18930.1, AI951118.1, AW000914.1, AI922499.1, AI871874.1, AA991162.1, AA661357.1, C60377.1, AA471702.1, AA095151.1, AW819103.1, AW519678.1, AV282871.1, AI902224.1, AV045752.2, AI311562.1, AI075925.1, AA828186.1, AA701829.1, AC067744.2, AL162272.3, AC009401.2, AC027141.1, AC024370.2, AC014239.1, AC036209.2, AC012622.4, AC024184.1, AC061987.1, AC027699.1, AC013707.2, AC012410.2, AC019081.1, AC012248.2, AC013152.1, AL121993.6, AP001455.1, AL022284.1, AC062015.2, AC046187.2, AC022418.3, AC012631.3, AC008885.3, AC011734.4, AC025113.2, AC027696.2, AC004932.2, AC046156.1, AC026529.2, AC026035.2, AC011710.2, AC016916.4, AC012549.2, AC023988.2, AC023567.2, AC009972.4, AC016444.2, AC011296.1, AL356132.3, AL355351.2

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SEQ ID NO: 571

ZH185/T7

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SEQ ID NO: 572

Group ZH184

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55 SEQ ID NO: 573

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SEQ ID NO: 578

ZH1219/T3

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5 ZH1219/T7

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- 5 AK000577.1, NM\_016223.1, AF130979.1, NM\_011861.1, X85124.1, AF188630.1, NM\_011862.1, AF128535.1, AB037800.1, AE003840.1, AF139495.1, AF139494.1, AF139493.1, AF139492.1, NM\_007229.1, AF128536.1, AF104402.1, AL022476.2, AC007680.2, AF030876.1, AC004561.2, AC012467.9, AE003731.1, AE003480.1, L27063.1, AF031075.1, AF094828.1, AC007021.3, AF055895.1, U52112.1, X99335.1, AL009204.1, AB041584.1, D14068.1, AB020878.1, AW328241.1, AI415693.1, AI427270.1, W46097.1, AA171908.1, AW908012.1, W24724.1, AA499441.1, 10 AA289880.1, AA793579.1, W44248.1, W24725.1, AW408380.1, AW641932.1, AL119244.1, AW762532.1, AW471083.1, AW255104.1, AI627848.1, AI275465.1, H81644.1, AI275938.1, AW492862.1, AW098801.1, AW086524.1, AI881986.1, AI645579.1, AA994288.1, AA902835.1, AA844675.1, AA757670.1, AA620827.1, AA518826.1, AA140167.1, W57231.1, AC024045.3, AL157372.6, AC025634.1, AC014463.1, Z82199.1, AC012469.6, AL158217.3, AC013307.5, AC034099.2, AC012515.11, AC012264.8, AC011938.3, AC010787.3, AC022488.2, AC023204.1, AC007771.6, AC010988.3, 15 AC013305.4, AC017943.1, AC015396.1, AL138894.3, AL353773.1, AL353141.1, AP001459.1, AP000803.1

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40 SEQ ID NO: 584

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55 SEQ ID NO: 585

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- Z99281.1, U95974.1, AC005702.1, AL161533.2, AL078606.1, AB010074.1, AF145751.1, AE003429.1, AL021978.1, Z83237.1, AC001226.1, AL050391.1, AL022100.13, Z82185.1, Z68871.1, Z97200.1, AL035209.1, AB005229.1, D88363.1, AA040001.1, AI026945.1, Z43817.1, AW404545.1, N59030.1, AA024476.1, AI879131.1, AA028041.1, 60 AW326298.1, AA428948.1, AA655517.1, AW071642.1, AI967928.1, AI831898.1, AI262999.1, AI149361.1, AI535381.1, AW837103.1, AW575737.1, AW785553.1, AW352814.1, AA717582.1, AI156144.1, R15907.1, AI202924.1, AI605706.1, AA589995.1, AA546348.1, AA210197.1, AW123704.1, AA455901.1, AA415948.1, AW355025.1, AW610618.1, X94529.1, AI984945.1, AI800263.1, AI436690.1, AI344209.1, AI007144.1, AI007142.1, AI124576.1, W26293.1, AW680443.1, AW446558.1, W12131.1, AV373768.1, AV369884.1, AV351169.1, AI908470.1, AI822397.1, AA888988.1,



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40 AL137730.1, AK000015.1, AC009046.4, AC011745.3, AL161541.2, Z97338.2, U53729.1, AL114938.1, AC004669.2, AE003635.1, AC007321.2, AC005711.1, AC005922.1, AF068624.1, AL020991.1, Z82086.1, AL160236.2, AL132766.13, AL023694.1, Z83821.1, Z48432.1, Z74065.1, M12624.1, Z94847.1, AC007391.3, AF001549.1, AC004253.1, U67496.1, AL161584.2, AL031032.1, AL109838.11, AL096862.18, U39652.1, T78076.1, AI367972.1, AA815204.1, N52394.1, AW607992.1, T86971.1, AW303429.1, AW196107.1, H87717.1, AI703119.1, AV145264.1, AA872637.1, AI350255.1, AW371247.1, AW414549.1, AA932625.1, AW143059.1, AA679262.1, AI803182.1, AU034554.1, N76675.1, 45 AW812434.1, AW799395.1, AW799392.1, AW799279.1, AW799276.1, AW730023.1, AJ397496.1, AV251422.1, AW141778.1, AI862716.1, AV023111.1, AI137198.1, AA765214.1, C62559.1, AA094474.1, AA068788.1, N88898.1, H57885.1, AL353664.3, AC026292.2, AC023120.3, AC011672.3, AC011675.2, AC016390.3, AL354661.2, AC068286.2, AC069133.1, AC025734.2, AC007923.2, AC019342.4, AC022030.1, AC012197.2, AC006779.3, AL157765.2, AL356385.1, AL117380.27, AL050349.25, AL162872.1, AL049185.4

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60 AL049911.2, AL163203.2, AL050302.2, AP000542.1, AL163202.2, AP001464.1, AP000026.1, AP000025.1, NM\_014915.1, AK001137.1, AB028997.1, AE003447.1, AJ223186.1, AC015600.6, AE003494.1, AC004739.1,

- AC006355.3, AC006045.2, U48386.1, AF044083.1, AL161578.2, AL021633.2, Z70270.1, AL080283.1, AL163233.2, AL163224.2, Z74696.1, U41993.1, D82813.1, AP001679.1, AP001688.1, AP001506.1, AP000961.2, AC005522.2, AC008929.3, AC007379.2, AE003664.1, AE003509.1, AC012654.2, AC004079.1, AC006478.2, AC004996.1, AC005100.2, AC007100.3, AC005879.3, AC007617.10, AC007437.16, AC005331.1, AC004045.1, Y18930.1, Z99116.1, X95911.1, AL117195.1, X63956.1, AL032637.1, AL109925.11, AL133465.30, AL132639.2, AL132766.13, AL109985.2, AL078644.10, AL050322.10, AL022395.2, Z82193.1, Y15880.1, L09228.1, M84227.1, AI951118.1, AW373574.1, AA579752.1, AI989660.1, AI825717.1, AW000914.1, AI922499.1, AI871874.1, AA991162.1, AV127940.1, AA736439.1, C60377.1, AA219203.1, AA095151.1, AW578955.1, AW418577.1, AW363481.1, AW403036.1, AW262107.1, AV346364.1, AV322534.1, AV282871.1, AI935447.1, AI902224.1, AI754384.1, AV045752.2, AI671778.1, AI591085.1, AI583901.1, AI478844.1, AI360552.1, AI311562.1, AI168669.1, AI150310.1, AI086364.1, AA828186.1, AA746252.1, AA724030.1, AA701829.1, AA280548.1, AA151455.1, W16804.1, N72190.1, AC067744.2, AC036170.2, AL157387.2, AC024252.3, AL353626.1, AL162272.4, AP000776.1, AC017005.4, AC009401.2, AC011254.3, AC012582.3, AC012551.3, AC014239.1, AC062004.2, AC068739.2, AC036209.2, AC007131.3, AC061987.1, AC027699.1, AC012542.4, AC012248.2, AC013152.1, AP001133.1, AL022284.1
- 15 SEQ ID NO: 591  
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- 55 SEQ ID NO: 592  
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- AI585542.1, AA546260.1, AA263149.1, AI505847.1, AW106399.1, AA127538.1, AA285232.1, AW456026.1, AI588808.1, AI384994.1, AA981002.1, AW566712.1, AI787751.1, AW536727.1, AW413150.1, AV265194.1, AV219084.1, AI844907.1, AI842969.1, AV160844.1, AV165707.1, AV124038.1, AI779552.1, AV085555.1, AV047038.2, AV046630.2, AI325552.1, AU045190.1, AU018790.1, AU016981.1, AU016595.1, AU016513.1, AU015043.1, AU014858.1, AA252091.1, AA197255.1, AA108210.1, Z74637.1, FO1019.1, AW705280.1, AJ281093.1, AW398070.1, AW398039.1, AW397497.1, AW397370.1, AW397141.1, AW397013.1, AW396970.1, AW396868.1, AW395825.1, AW395703.1, AW395679.1, AW395606.1, AW395515.1, AW225544.1, AW186387.1, AI973567.1, AI960869.1, AI941243.1, AI941225.1, AI940836.1, AI883261.1, AL079496.1, AI795023.1, AI759696.1, AI748161.1, AI748087.1, AI736054.1, AI736025.1, AI736012.1, AI406060.1, AI109316.1, AI109205.1, AI063325.1, AA902197.1, AA784297.1, AA553106.1, AA497210.1, AA466795.1, AA462438.1, AA432643.1, AA313904.1, C13433.1, F12959.1, AV185121.1, C66585.1, AL138878.4, AL139095.5, AC010893.4, AL109933.21, AC025343.2, AC008760.4, AC024364.3, AC063933.3, AC025925.2, AC021185.2, AC023350.1, AC016546.4, AC034197.2, AC021814.2, AC026219.1, AC016723.4, AC007218.2, AC012373.13, AC022890.1, AC017288.1, AC018551.1, AC015313.1, AL139011.6, AP001075.2, AC025685.2, AC061978.2, AC008427.5, AC021869.6, AC027631.2, AC026233.2, AC013364.7, AC013350.6, AC026232.1, AC018740.2, AC023364.3, AC008050.3, AC024301.1, AC010003.5, AC009368.5, AC017158.1, AC008367.3, AC020124.1, AF215848.1, AC008236.3, AC017830.1, AC017944.1, AC012952.1, AL122026.2, AL049185.4, AC068808.4, AC037424.7, AC016634.4, AC008904.3, AC009550.3, AC021972.2, AC020804.2, AC021305.3, AC023103.3, AC020080.1, AC020324.1, AC012195.2, AL138711.3, AL160153.4, AL031745.7
- 20 SEQ ID NO: 593  
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**Table 2: Relation between nucleotide sequences and polypeptide sequences**

Nucleic acid SEQ ID NO	Polypeptide SEQ ID NO	Nucleic acid SEQ ID NO	Polypeptide SEQ ID NO	Nucleic acid SEQ ID NO	Polypeptide SEQ ID NO
1	665	199	818	397	1117
2	678	200	819, 820	398	—
3	679	201	821	399	1118
4	761, 762	202	822	400	1119
5	763, 764, 765	203	823, 824	401	1120
6	782	204	825, 826	402	—
7	783	205	827, 828, 829	403	1121
8	767	206	830, 831	404	1122
9	604	207	832	405	1123
10	—	208	833	406	1124
11	606	209	834, 835	407	—
12	624	210	836, 837	408	—
13	599	211	838	409	1125
14	776, 777, 778, 779	212	839, 840, 841	410	—

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15	780, 781	213	842, 843	411	1126
16	802	214	844, 845, 846	412	1127
17	803	215	847, 848	413	1128
18	607	216	849	414	--
19	594	217	850, 851, 852	415	1129
20	595, 596, 597	218	853, 854	416	1130, 1131, 1132
21	--	219	--	417	1133
22	598	220	--	418	1134
23		221	855, 856, 857	419	1135, 1136
24	600	222	858, 859, 860	420	1137, 1138
25		223	861, 862, 863	421	1139
26	601	224	864	422	--
27	--	225	865	423	1140
28	602	226	866, 867, 868	424	1141, 1142
29	603	227	869, 870	425	1143
30	605	228	871	426	1144, 1145
31	--	229	872	427	--
32	608	230	873	428	1146, 1147
33	609	231	874	429	1148, 1149, 1150
34	610	232	875, 876, 877	430	--
35	611, 612	233	878	431	1151
36	--	234	879, 880	432	1152
37	--	235	881, 882	433	--
38	613	236	883	434	1153
39	614	237	884, 885	435	1154
40	--	238	886	436	--
41	615	239	887, 888	437	1155
42	--	240	--	438	1156
43	616	241	889, 890	439	--
44	--	242	891, 892	440	1157
45	617, 618	243	893, 894	441	1158
46	619	244	895	442	1159
47	620	245	896	443	1160
48	621	246	897	444	1161
49	--	247	898	445	1162
50	622	248	899	446	--
51	623	249	900, 901	447	1163
52	625	250	902	448	--
53	--	251	903	449	1164
54	626	252	904	450	1165
55	627, 628	253	905	451	1166

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56	629	254	906	452	—
57	—	255	907, 908, 909	453	1167
58	630	256	910, 911	454	—
59	—	257	912, 913, 914	455	1168
60	631	258	915	456	—
61	632	259	916	457	1169
62	—	260	917, 918, 918	458	1170
63	633	261	920, 921	459	1171
64	634	262	922, 923	460	1172
65	635	263	924, 925, 926	461	1173, 1174, 1175
66	—	264	927, 928, 929	462	1176, 1177
67	636	265	930, 931	463	1178
68	—	266	932	464	1179
69	637	267	933, 934	465	1180
70	—	268	935	466	1181, 1182, 1183
71	—	269	936	467	1184
72	—	270	937, 938	468	1185
73	—	271	939	469	1186
74	—	272	940	470	1187
75	—	273	941, 942	471	1188
76	—	274	943, 944	472	—
77	638	275	945	473	1189
78	—	276	946, 947, 948	474	1190
79	—	277	949	475	—
80	—	278	950, 951, 952	476	1191, 1192
81	639	279	953, 954	477	1193
82	—	280	955, 956	478	1194
83	640	281	—	479	1195
84	641	282	957	480	1196
85	—	283	958	481	1197
86	642	284	959	482	1198
87	—	285	960, 961	483	1199
88	643	286	—	484	1200, 1201
89	—	287	962, 963, 964	485	1202
90	644	288	965	486	1203
91	—	289	966	487	1204
92	645	290	967, 968, 969, 970	488	1205
93	646	291	971, 972, 973, 974	489	1206
94	647	292	975, 976	490	1207
95	648	293	977, 978, 979,	491	1208

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			980		
96	649, 650	294	981, 982, 983	492	1209
97	651, 652	295	984, 985	493	1210
98	653	296	986, 987	494	--
99	654	297	988, 989	495	1211
100	655	298	990	496	1212
101	656	299	991	497	1213
102	657	300	992	498	--
103	658	301	993	499	1214
104	659, 660	302	994	500	--
105	661	303	995	501	1215
106	662, 663	304	996	502	1216
107	664	305	997	503	1217
108	666	306	998	504	1218
109	667	307	999	505	1219
110	--	308	1000, 1001	506	1220
111	668, 669, 670	309	1002, 1003	507	1221
112	671, 672, 673, 674, 675	310	1004, 1005	508	1222
113	676	311	1006, 1007, 1008	509	--
114	677	312	1009, 1010	510	1223
115	680	313	1011, 1012, 1013	511	1224
116	681	314	1014, 1015	512	1225
117	682, 683	315	1016, 1017	513	1226
118	684	316	1018, 1019	514	1227
119	685	317	1020	515	1228
120	686	318	1021	516	1229, 1230
121	687, 688	319	1022	517	1231
122	689, 690, 691	320	1023	518	--
123	692	321	1024, 1025, 1026	519	1232
124	693, 694	322	1027, 1028, 1029, 1030	520	1233
125	695	323	1031, 1032, 1033	521	1234
126	696	324	1034, 1035, 1036	522	1235
127	697	325	1037, 1038	523	--
128	698	326	1039, 1040	524	1236
129	699	327	1041, 1042, 1043, 1044	525	--
130	700, 701, 702	328	1045, 1046	526	1237
131	703, 704	329	1047	527	--
132	705	330	1048, 1049	528	1238
133	706, 707	331	1050	529	1239

134	708	332	1051, 1052	530	1240, 1241
135	709, 710	333	1053	531	1242, 1243, 1244
136	711	334	1054, 1055	532	1245
137	712	335	1056	533	1246, 1247
138	713	336	1057, 1058	534	—
139	714	337	1059	535	1248
140	715	338	1060, 1061	536	1249, 1250, 1251
141	716	339	1062	537	1252, 1253, 1254
142	717	340	1063	538	—
143	718	341	1064, 1065	539	1255
144	719	342	1066	540	1256
145	720	343	1067, 1068	541	1257
146	721	344	1069	542	1258
147	722	345	1070, 1071	543	1259, 1260
148	723, 724	346	1072	544	1261
149	725, 726	347	1073, 1074	545	1262
150	727	348	1075, 1076	546	1263
151	728, 729	349	1077, 1078, 1079	547	1264
152	730, 731	350	1080	548	1265, 1266
153	732, 733	351	1081	549	1267
154	734, 735, 736	352	1082, 1083	550	—
155	737	353	1084	551	1268
156	738	354	1085	552	1269, 1270
157	739, 740	355	—	553	1271, 1272
158	741	356	1086	554	1273, 1274
159	742, 743, 744	357	—	555	1275
160	745	358	1087	556	1276
161	746	359	1088	557	1277
162	747, 748	360	1089	558	1278
163	749	361	1090	559	1279
164	750	362	1091	560	1280
165	751, 752	363	—	561	1281
166	753	364	1092	562	1282, 1283
167	754, 755, 756	365	—	563	1284, 1285
168	757, 758, 759, 760	366	1093	564	1286, 1287
169	766	367	1094	565	1288, 1289, 1290
170	768	368	1095	566	1291, 1292
171	769	369	1096	567	1293, 1294
172	770	370	1097	568	1295
173	771	371	—	569	1296, 1297, 1298
174	772	372	—	570	1299



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175	773, 774, 775	373	1098	571	1300
176	784	374	1099	572	1301
177	785	375	--	573	1302, 1303
178	786, 787, 788	376	1100	574	1304
179	--	377	1101	575	--
180	789	378	1102	576	1305, 1306
181	790	379	1103	577	1307
182	791	380	1104	578	1308
183	792, 793	381	1105	579	1309
184	794	382	1106	580	1310
185	795, 796	383	1107	581	1311, 1312, 1313
186	797, 798, 799, 800	384	1108	582	1314, 1315, 1316
187	801	385	--	583	1317, 1318
188	804, 805	386	1109	584	1319
189	806	387	1110	585	1320, 1321
190	807	388	1111	586	1322
191	808, 809	389	--	587	1323, 1324
192	810	390	1112	588	1325
193	811	391	--	589	1326
194	812	392	1113	590	1327
195	813	393	1114	591	1328, 1329
196	814	394	1115	592	1330, 1331
197	815	395	--	593	1332
198	816, 817	396	1116		

### Example 2: Preparation of recombinant cancer associated antigens

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. Where gaps exist in the gene sequences represented by the clones disclosed herein, or where flanking sequences are desired, such nucleic acid sequences can be isolated according to standard procedures. For example, where 5' and 3' clones of a gene sequence are known, PCR primers can be designed for amplification of the nucleotide sequence between the clones. Flanking sequences can be isolated using procedures such as RACE PCR. Such sequences also can be isolated by standard hybridization cloning protocols.

In one method of preparing recombinant cancer associated antigens, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells.

Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

### **Example 3: Preparation of antibodies to cancer associated antigens**

The recombinant cancer associated antigens produced as in Example 2 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

### **Example 4: Expression of breast, gastric and prostate cancer associated antigens in cancers of similar and different origin.**

The expression of one or more of the breast, gastric and/or prostate cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic

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serotyping using a modified SEREX protocol (as described above).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used  
5 as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

10

**Example 5: HLA typing of patients positive for cancer associated antigen**

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the breast and/or gastric cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient  
15 and typed for HLA class I or class II, as well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

**20 Example 6: Characterization of cancer associated antigen peptides presented by MHC class I and class II molecules.**

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented  
25 by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast and/or gastric cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described above, the HLA types which  
30 present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For

example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (*see, e.g.*, Parker et al, *J. Immunol.* 152:163, 1994; D'Amato et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL <http://bimas.dcrt.nih.gov>. Methods for determining HLA class II peptides and making substitutions thereto are also known (*see, e.g.* International applications PCT/US96/03182 and PCT/US98/01373). Computer software for selecting HLA class II binding peptides is also available (TEPITOPE; Sturniolo et al., *Nature Biotechnol.* 17:555-561, 1999; Manici et al., *J. Exp. Med.* 189:871-876, 1999). Peptides which are thus selected can be for inducing specific CD4<sup>+</sup> lymphocytes and identification of peptides. Additional methods of selecting and testing peptides for HLA class II binding are well known in the art.

**Example 7: Identification of the portion of a cancer associated polypeptide encoding an antigen**

To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (*see, e.g.*, Knuth et al., *Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.* 24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230, 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by <sup>51</sup>Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by exonuclease III digestion or other standard molecular biology methods. Synthetic peptides

are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or  $^{51}\text{Cr}$  release as above.

Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by T cells. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

#### 15 **Example 8: Recognition of cancer antigens by cancer patient sera**

Several of the cancer antigen identified herein were tested for reactivity with sera from normal and breast cancer patients according to standard procedures (e.g., the SEREX procedure outlined above).

20 **Table 3: Serology of antigens**

SEQ ID NO	Gene/Clone	Breast Cancer Patient Sera	Normal Sera
1	Br-38/HSP105 (MK)	6/31	0/30
2,3	Br-39/HSP105 (MK)	3/31	0/30
4,5	RGS-GAIP interacting protein GIPC (MK)	3/31	0/30
6,7	NS1-binding protein/KIAA0850 (MK)	3/31	0/30
8	Opa-interacting protein OIP2 (MK)	3/31	0/30
9,10	Kinesin family protein 3B (KIF3B) (MT)	2/31	0/30
11	Endothelial-monocyte activating protein (EMAP2) (MT)	2/31	0/30
12	Unknown TOM1 protein (MT311)	2/31	0/30
13	Outer mitochondrial membrane protein 34kDa (MT)	1/31	0/30

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14,15	IPL (MK)	1/31	0/30
16,17	Mus ACF7 neural isoform (MK)	1/31	0/30
18	Cyclin D3 (MT)	1/31	0/30

The data show that proteins encoded by SEQ ID NO:1-12 were recognized by multiple breast cancer patients' sera, but not by control individuals' sera. Proteins encoded by SEQ ID NO:13-18 were recognized by only a single breast cancer patient's sera, but not by control individuals' sera. The

#### EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

All references disclosed herein are incorporated by reference in their entirety.

We claim:

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**Claims**

1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:  
contacting a biological sample isolated from a subject with an agent that specifically  
5 binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and  
determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.
- 10 2. The method of claim 1, wherein the agent is selected from the group consisting of  
(a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules or a fragment thereof,  
(b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules or a  
15 fragment thereof,  
(c) a nucleic acid molecule comprising NA group 5 nucleic acid molecules or a fragment thereof,  
(d) an antibody that binds to an expression product of NA group 1 nucleic acids,  
(e) an antibody that binds to an expression product of NA group 3 nucleic acids,  
20 (f) an antibody that binds to an expression product of NA group 5 nucleic acids,  
(g) an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,  
(h) an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 3 nucleic acid, and  
25 (i) an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 5 nucleic acid.
3. The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of  
30 agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.



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4. The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast cancer associated antigen precursor.
5. A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising
- monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of
- (i) the protein,
  - (ii) a peptide derived from the protein,
  - (iii) an antibody which selectively binds the protein or peptide, and
  - (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule,
- as a determination of regression, progression or onset of said condition.
6. The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.
7. The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of
- (a) an antibody which selectively binds the protein of (i), or the peptide of (ii),
  - (b) a protein or peptide which binds the antibody of (iii), and
  - (c) a cell which presents the complex of the peptide and MHC molecule of (iv).
8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.
9. The method of claim 5, comprising assaying the sample for the peptide.
10. The method of claim 5, wherein the nucleic acid molecule is a NA Group 3 molecule.
11. The method of claim 5, wherein the nucleic acid molecule is a NA Group 5 molecule.

12. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different one of the plurality of proteins, at least one of which is a cancer associated protein encoded by a NA Group 1 molecule.
13. A pharmaceutical preparation for a human subject comprising  
an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and  
a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule comprises a NA Group 1 molecule.
14. The pharmaceutical preparation of claim 13, wherein the agent comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen, wherein at least one of the human cancer associated antigens is encoded by a NA Group 1 molecule.
15. The pharmaceutical preparation of claim 14, wherein the plurality is at least two, at least three, at least four or at least 5 different such agents.
16. The pharmaceutical preparation of claim 13, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.
17. The pharmaceutical preparation of claim 13, wherein the agent is selected from the group consisting of  
(1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof,  
(2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof,  
(3) a host cell expressing the isolated polypeptide, or functional variant thereof, and  
(4) isolated complexes of the polypeptide, or functional variants thereof, and an HLA

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molecule.

18. The pharmaceutical preparation of claims 13-17, further comprising an adjuvant.
- 5 19. The pharmaceutical preparation of claim 13, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.
20. The pharmaceutical preparation of claim 13, wherein the agent is a cell expressing an  
10 isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.
21. The pharmaceutical preparation of claim 13, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human  
15 cancer associated antigen or functional variant thereof, wherein at least one of the human cancer associated antigens is encoded by a NA Group 1 molecule.
22. The pharmaceutical preparation of claim 13, wherein the agent is a PP Group 2 polypeptide.  
20
23. The pharmaceutical preparation of claim 13, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.
24. The pharmaceutical preparation of claim 20, wherein the cell expresses one or both of  
25 the polypeptide and HLA molecule recombinantly.
25. The pharmaceutical preparation of claim 20, wherein the cell is nonproliferative.
26. A composition comprising  
30 an isolated agent that binds selectively a PP Group 1 polypeptide.
27. The composition of matter of claim 26, wherein the agent binds selectively a PP Group

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2 polypeptide.

28. The composition of matter of claim 26, wherein the agent binds selectively a PP Group 3 polypeptide.

29. The composition of matter of claim 26, wherein the agent binds selectively a PP Group 4 polypeptide.

30. The composition of matter of claim 26, wherein the agent binds selectively a PP Group 5 polypeptide.

31. The composition of claims 26-30, wherein the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides.

32. The composition of claims 26-30, wherein the agent is an antibody.

33. The composition of claim 31, wherein the agent is an antibody.

34. A composition of matter comprising  
a conjugate of the agent of claims 26-30 and a therapeutic or diagnostic agent.

35. A composition of matter comprising  
a conjugate of the agent of claim 31 and a therapeutic or diagnostic agent.

36. The composition of matter of claim 34, wherein the conjugate is of the agent and a therapeutic or diagnostic that is a toxin.

37. A pharmaceutical composition comprising an isolated nucleic acid molecule selected from the group consisting of NA Group 1 molecules and NA Group 2 molecules, and a pharmaceutically acceptable carrier.

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38. The pharmaceutical composition of claim 37, wherein the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule.

39. The pharmaceutical composition of claim 37, wherein the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different human cancer associated antigen.

40. The pharmaceutical composition of claims 37-39 further comprising an expression vector with a promoter operably linked to the isolated nucleic acid molecule.

10

41. The pharmaceutical composition of claims 37-39 further comprising a host cell recombinantly expressing the isolated nucleic acid molecule.

42. A pharmaceutical composition comprising  
an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and  
a pharmaceutically acceptable carrier.

43. The pharmaceutical composition of claim 42, wherein the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

20

44. The pharmaceutical composition of claim 42, wherein the isolated polypeptide comprises at least two different polypeptides, each comprising a different human cancer associated antigen.

45. The pharmaceutical composition of claim 42, wherein the isolated polypeptides are breast cancer polypeptides or HLA binding fragments thereof.

46. The pharmaceutical composition of claim 42, wherein the isolated polypeptides are gastric cancer polypeptides or HLA binding fragments thereof.

30

47. The pharmaceutical composition of claims 42-46, further comprising an adjuvant.

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48. An isolated nucleic acid molecule comprising a NA Group 3 molecule.
49. An isolated nucleic acid molecule comprising a NA Group 4 molecule.
- 5 50. An isolated nucleic acid molecule selected from the group consisting of
- (a) a fragment of a nucleic acid molecule having a nucleotide sequence selected from the group consisting of nucleotide sequences set forth as SEQ ID NOs:1-593, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor,
- 10 (b) complements of (a),
- provided that the fragment includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of
- (1) sequences having the GenBank accession numbers of Table 1, and other publicly available sequences,
- 15 (2) complements of (1), and
- (3) fragments of (1) and (2).
51. The isolated nucleic acid molecule of claim 50, wherein the sequence of contiguous nucleotides is selected from the group consisting of:
- 20 (1) at least two contiguous nucleotides nonidentical to the sequence group,
- (2) at least three contiguous nucleotides nonidentical to the sequence group,
- (3) at least four contiguous nucleotides nonidentical to the sequence group,
- (4) at least five contiguous nucleotides nonidentical to the sequence group,
- (5) at least six contiguous nucleotides nonidentical to the sequence group,
- 25 (6) at least seven contiguous nucleotides nonidentical to the sequence group.
52. The isolated nucleic acid molecule of claim 50, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24
- 30 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

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53. The isolated nucleic acid molecule of claim 50, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.
- 5 54. An expression vector comprising an isolated nucleic acid molecule of any of claims 48-53 operably linked to a promoter.
55. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.
- 10 56. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.
57. A host cell transformed or transfected with an expression vector of claim 54.
- 15 58. A host cell transformed or transfected with an expression vector of claims 55 or 56.
59. A host cell transformed or transfected with an expression vector of claim 54 and further comprising a nucleic acid encoding HLA.
- 20 60. A host cell transformed or transfected with an expression vector of claim 55 and further comprising a nucleic acid encoding HLA.
61. An isolated polypeptide encoded by the isolated nucleic acid molecule of claim 48 or  
25 claim 49.
62. A fragment of the polypeptide of claim 61 which is immunogenic.
63. The fragment of claim 62, wherein the fragment, or a portion of the fragment, binds  
30 HLA or a human antibody.
64. An isolated fragment of a human cancer associated antigen precursor which, or portion



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of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

65. The fragment of claim 64, wherein the fragment is part of a complex with HLA.

5

66. The fragment of claim 65, wherein the fragment is between 8 and 12 amino acids in length.

67. An isolated polypeptide comprising a fragment of the polypeptide of claim 61 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

10

68. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising

15

a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of (a), wherein the contiguous segments are nonoverlapping.

20

69. The kit of claim 68, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

70. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising

25

administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

30

- (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules,
- (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

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(c) a nucleic acid molecule comprising NA group 5 nucleic acid molecules.

71. The method of claim 70, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of  
5 agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen, wherein at least one of the human cancer associated antigens is encoded by a NA Group 1 molecule.

72. The method of claim 71, wherein the plurality is at least 2, at least 3, at least 4, or at  
10 least 5 such agents.

73. The method of claims 70-72, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, and PP  
15 Group 5.

74. The method of claims 70-72, wherein the disorder is cancer.

75. The method of claims 73, wherein the disorder is cancer.

20 76. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

- (i) removing an immunoreactive cell containing sample from the subject,
- (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen  
25 which is a fragment of the precursor,
- (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the  
30 group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, and NA Group 5.

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77. The method of claim 76, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

78. The method of claim 76, wherein the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

79. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(i) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule;

(ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c);

(iii) culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

80. The method of claim 79, further comprising identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

81. The method of claim 79, wherein the immune response comprises a B-cell response or a T cell response.

82. The method of claim 81, wherein the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

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83. The method of claim 79, wherein the nucleic acid molecule is a NA Group 3 molecule.

84. The method of claims 79 or 80, further comprising treating the host cells to render  
5 them non-proliferative.

85. A method for treating or diagnosing or monitoring a subject having a condition  
characterized by expression of an abnormal amount of a protein encoded by a nucleic acid  
molecule that is a NA Group 1 molecule, comprising  
10 administering to the subject an antibody which specifically binds to the protein or a  
peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an  
amount effective to treat the condition.

86. The method of claim 85, wherein the antibody is a monoclonal antibody.  
15

87. The method of claim 86, wherein the monoclonal antibody is a chimeric antibody or a  
humanized antibody.

88. A method for treating a condition characterized by expression in a subject of abnormal  
20 amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid  
molecule, comprising  
administering to a subject a pharmaceutical composition of any one of claims 13-25  
and 37-47 in an amount effective to prevent, delay the onset of, or inhibit the condition in the  
subject.

25 89. The method of claim 88, wherein the condition is cancer.

90. The method of claim 88, further comprising first identifying that the subject expresses  
in a tissue abnormal amounts of the protein.

30 91. The method of claim 89, further comprising first identifying that the subject expresses  
in a tissue abnormal amounts of the protein.

92. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

- 5 (i) identifying cells from the subject which express abnormal amounts of the protein;  
(ii) isolating a sample of the cells;  
(iii) cultivating the cells, and  
(iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

10

93. The method of claim 92, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

94. A method for treating a pathological cell condition characterized by aberrant  
15 expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

- 20 95. The method of claim 94, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

96. The method of claim 94, wherein the agent is an antisense nucleic acid molecule  
25 which selectively binds to the nucleic acid molecule which encodes the protein.

97. The method of claim 94, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

- 30 98. A composition of matter useful in stimulating an immune response to a plurality of a proteins encoded by nucleic acid molecules that are NA Group 1 molecules, comprising a plurality of peptides derived from the amino acid sequences of the proteins, wherein

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the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

99. The composition of matter of claim 98, wherein at least a portion of the plurality of  
5 peptides bind to MHC molecules and elicit a cytolytic response thereto.

100. The composition of matter of claim 99, further comprising an adjuvant.

101. The composition of matter of claim 100, wherein said adjuvant is a saponin, GM-CSF,  
10 or an interleukin.

102. The composition of matter of claim 98, further comprising at least one peptide useful  
in stimulating an immune response to at least one protein which is not encoded by nucleic  
acid molecules that are NA Group 1 molecules, wherein the at least one peptide binds to one  
15 or more MHC molecules.

103. An isolated antibody which selectively binds to a complex of:  
(i) a peptide derived from a protein encoded by a nucleic acid molecule that is a  
NA Group 1 molecule and  
20 (ii) and an MHC molecule to which binds the peptide to form the complex,  
wherein the isolated antibody does not bind to (i) or (ii) alone.

104. The antibody of claim 103, wherein the antibody is a monoclonal antibody, a chimeric  
antibody, a humanized antibody, or a fragment thereof.

25

## SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research

5 <120> BREAST, GASTRIC, AND PROSTATE  
CANCER ASSOCIATED ANTIGENS AND USES THEREFOR

10 <130> L0461/7064WO

<150> US 60/136,526

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&lt;210&gt; 59

&lt;211&gt; 700

&lt;212&gt; DNA

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 59

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&lt;210&gt; 60

&lt;211&gt; 1889

&lt;212&gt; DNA

40 &lt;213&gt; Homo sapiens

&lt;400&gt; 60

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&lt;210&gt; 61

&lt;211&gt; 739

&lt;212&gt; DNA

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 61

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&lt;210&gt; 62

&lt;211&gt; 665

&lt;212&gt; DNA

35 &lt;213&gt; Homo sapiens

&lt;400&gt; 62

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50

&lt;210&gt; 63

&lt;211&gt; 1003

&lt;212&gt; DNA

55 &lt;213&gt; Homo sapiens

&lt;400&gt; 63

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&lt;210&gt; 64

&lt;211&gt; 765

&lt;212&gt; DNA

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 64

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&lt;210&gt; 65

&lt;211&gt; 566

&lt;212&gt; DNA

35 &lt;213&gt; Homo sapiens

&lt;400&gt; 65

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&lt;210&gt; 66

50 &lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

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<210> 67  
 <211> 976  
 <212> DNA  
 <213> Homo sapiens

5

&lt;400&gt; 67

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25

<210> 68  
 <211> 487  
 <212> DNA  
 <213> Homo sapiens

30

&lt;400&gt; 68

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40 tgcctag						487

40

<210> 69  
 <211> 826  
 <212> DNA  
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45

&lt;400&gt; 69

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<210> 70  
 <211> 1015

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

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&lt;210&gt; 71

&lt;211&gt; 1140

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

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&lt;213&gt; Homo sapiens

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15 &lt;213&gt; Homo sapiens

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35 &lt;213&gt; Homo sapiens

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&lt;211&gt; 2441

&lt;212&gt; DNA

55 &lt;213&gt; Homo sapiens

&lt;400&gt; 136

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&lt;211&gt; 1026

&lt;212&gt; DNA

40 &lt;213&gt; Homo sapiens

&lt;400&gt; 137

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

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&lt;400&gt; 204

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&lt;210&gt; 205

&lt;211&gt; 494

&lt;212&gt; DNA

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 205

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&lt;210&gt; 206

&lt;211&gt; 1315

&lt;212&gt; DNA

35 &lt;213&gt; Homo sapiens

&lt;400&gt; 206

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&lt;210&gt; 207

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

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&lt;210&gt; 208

&lt;211&gt; 979

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 208

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&lt;210&gt; 209

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 209

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&lt;210&gt; 210

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 210

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<210> 213  
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

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&lt;211&gt; 672

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 214

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&lt;210&gt; 215

&lt;211&gt; 779

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 215

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&lt;210&gt; 216

&lt;211&gt; 734

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 216

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&lt;211&gt; 759

15 &lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 295

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&lt;210&gt; 296

&lt;211&gt; 824

35 &lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 296

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&lt;210&gt; 297

&lt;211&gt; 834

55 &lt;212&gt; DNA

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&lt;400&gt; 297

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&lt;210&gt; 298

&lt;211&gt; 800

&lt;212&gt; DNA

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 298

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35 &lt;213&gt; Homo sapiens

&lt;400&gt; 299

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&lt;213&gt; Homo sapiens

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&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 349

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&lt;210&gt; 350

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 350

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;211&gt; 772

&lt;212&gt; DNA

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 352

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&lt;210&gt; 353

&lt;211&gt; 1102

&lt;212&gt; DNA

40 &lt;213&gt; Homo sapiens

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&lt;213&gt; Homo sapiens

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&lt;213&gt; Homo sapiens

&lt;400&gt; 387



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 20 20 25 30  
 Arg Arg Lys Arg Arg Arg Pro Cys Met Arg Arg Arg Trp Lys Gly Lys  
 35 40 45  
 Arg Ser Pro Arg Arg Arg Glu Asn Trp Gly Arg Thr Gln Thr Leu Thr  
 50 55 60  
 25 Gln Ala Ser Cys Leu Ile Glu Thr Val Arg Arg Arg Ile Gly Phe  
 65 70 75 80  
 Gly Lys Ser Cys Gly Arg Ser Gly Lys Pro Ser Arg Arg Arg Ser Arg  
 85 90 95  
 Val Arg Arg Ser Arg Ser Pro Ser Ala Thr Gly Met Ala Leu Gly Thr  
 100 105 110  
 30 Gly Arg Thr Val Lys Met Arg Lys Gly Asn Thr Met Xaa Gln Phe Cys  
 115 120 125  
 Xaa Xaa Arg Ser Arg Ser Phe Gly Lys Thr Phe Ser Glu Leu Arg Ser  
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 35 40 45  
 Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Thr Val Gly  
 50 55 60  
 Leu Val Thr Leu Asn Asp Met Lys Ala Lys Gln Glu Ala Leu Val Lys  
 55 65 70 75 80  
 Glu Arg Glu Lys Gln Leu Ala Lys Lys Glu Gln Ser Lys Glu Leu Gln  
 85 90 95  
 Met Lys Leu Glu Lys Leu Arg Glu Lys Glu Arg Lys Lys Glu Ala Lys  
 100 105 110  
 60 Arg Lys Ile Ser Ser Leu Ser Phe Thr Leu Glu Glu Glu Glu Glu Gly  
 115 120 125  
 Gly Glu Glu Glu Glu Ala Ala Met Tyr Glu Glu Glu Met Glu Arg  
 130 135 140

Glu Glu Ile Thr Thr Lys Lys Arg Lys Leu Gly Lys Asn Pro Asp Val  
 145 150 155 160  
 Asp Thr Ser Phe Leu Pro Asp Arg Asp Arg Glu Glu Glu Asn Arg  
 165 170 175  
 5 Leu Trp Glu Glu Leu Arg Gln Glu Trp Glu Ala Lys Gln Glu Lys Ile  
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 Lys Ser Glu Glu Ile Glu Ile Thr Phe Ser Tyr Trp Asp Gly Ser Gly  
 195 200 205  
 10 His Arg Pro Asp Ser Gln Asp Glu Lys Gly Gln His His Ala Xaa Val  
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 225 230 235  
  
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 Xaa Cys Met Val Leu Pro Phe Leu Ile Leu Thr Val Arg Pro Val Pro  
 25 35 40 45  
 Arg Ala Ile Pro Val Ala Glu Gly Asp Leu Asp Leu Thr Leu Asp  
 50 55 60  
 Leu Leu Leu Leu Gly Phe Pro Leu Leu Pro Gln Leu Phe Pro Lys Pro  
 65 70 75 80  
 30 Ile Leu Leu Leu Leu Thr Val Ser Ile Arg Gln Glu Ala Cys Val Asn  
 85 90 95  
 Val Trp Val Leu Pro Gln Phe Ser Leu Leu Arg Gly Asp Leu Phe Pro  
 100 105 110  
 Phe His Leu Leu Leu Ile His Gly Arg Leu Leu Phe Leu Leu Ala Ser  
 35 115 120 125  
 Leu Phe Phe Leu Leu Gln Gly Glu Gly Gln Ala Gly Asp Leu Pro Leu  
 130 135 140  
 Gly Phe Leu Leu Thr Leu Leu Leu Ser Lys Leu Leu Gln Leu His Leu  
 145 150 155 160  
 40 Gln Leu Leu Gly Leu Leu Leu Gly Gln Leu Leu Leu Pro Leu Leu  
 165 170 175  
 His Gln Ser Leu Leu Leu Gly Leu His Val Ile Gln Gly His Glu Thr  
 180 185 190  
 His Gly Ala Gly Leu Glu Leu Cys Leu His Arg Val Val Val Arg Arg  
 45 195 200 205  
 Glu Leu Leu Val Asn Val Gly Phe His Asp Val Leu Leu Arg Asp Ala  
 210 215 220  
 Leu Leu His Leu Leu His Leu Leu Ala Leu Leu Pro Leu Leu His  
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 245 250 255  
  
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 Arg Phe Ser Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser

[illegible]

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	Asp	Ser	Val	Glu 20	Glu	Leu	Arg	Ala	Ala 25	Gly	Asn	Glu	Ser	Phe 30	Arg	Asn	
	Gly	Gln	Tyr	Ala	Glu	Ala	Ser	Ala	Leu	Tyr	Gly	Arg	Ala 45	Leu	Arg	Val	
50	Leu	Gln	Ala	Gln	Gly	Ser	Ser	Asp	Pro	Glu	Glu	Glu	Ser	Val	Leu	Tyr	
	Ser	Asn	Arg	Ala	Ala	Cys 70	His	Trp	Lys	Asn 75	Gly	Asn	Cys	Arg	Asp	Cys 80	
55	Ile	Lys	Asp	Cys	Thr 85	Ser	Ala	Leu	Ala	Leu 90	Val	Pro	Phe	Ser	Ile	Lys	
	Pro	Leu	Leu	Arg	Arg	Ala	Ser	Ala	Tyr	Glu	Ala	Leu	Glu	Lys	Tyr	Pro	
	Met	Ala	Tyr	Val	Asp	Tyr	Lys	Thr	Val	Leu	Gln	Ile	Asp	Asp	Asn	Val	
60	Thr	Ser	Ala	Val	Glu	Gly	Ile	Asn	Arg	Met	Thr	Arg	Ala	Leu	Met	Asp	
	Ser	Leu	Gly	Pro	Glu	Trp	Arg	Leu	Lys	Leu	Pro	Ser	Phe	Pro	Leu	Val	

145                      150                      155                      160  
 Pro Val Ser Ala Gln Lys Arg Trp Asn Phe Leu Pro Ser Glu Asn His  
                                  165                      170                      175  
 5    Lys Glu Met Ala Lys Ser Lys Ser Lys Glu Thr Thr Ala Thr Lys Asn  
                                  180                      185                      190  
 Arg Val Pro Ser Ala Gly Asp Val Glu Lys Ala Arg Val Leu Lys Glu  
                                  195                      200                      205  
 Glu Gly Asn Glu Leu Val Lys Lys Gly Asn His Lys Lys Ala Ile Glu  
                                  210                      215                      220  
 10    Lys Tyr Ser Glu Ser Leu Leu Cys Ser Asn Leu Glu Ser Ala Thr Tyr  
                                  225                      230                      235                      240  
 Ser Asn Arg Ala Leu Cys Tyr Leu Val Leu Lys Gln Tyr Thr Glu Ala  
                                  245                      250                      255  
 Val Lys Asp Cys Thr Glu Ala Leu Lys Leu Asp Gly Lys Asn Val Lys  
                                  260                      265                      270  
 15    Ala Phe Tyr Arg Arg Ala Gln Ala His Lys Ala Leu Lys Asp Tyr Lys  
                                  275                      280                      285  
 Ser Ser Phe Ala Asp Ile Ser Asn Leu Leu Gln Ile Glu Pro Arg Asn  
                                  290                      295                      300  
 20    Gly Pro Ala Gln Lys Leu Arg Gln Glu Val Lys Gln Asn Leu His  
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 Phe Lys Ile Leu Val Ala Thr Asp Ile His Leu Gly Phe Met Glu Lys  
                                  20                      25                      30  
 Asp Ala Val Arg Gly Asn Asp Thr Phe Val Thr Leu Asp Glu Ile Leu  
                                  35                      40                      45  
 35    Arg Leu Ala Gln Glu Asn Glu Val Asp Phe Ile Leu Leu Gly Gly Asp  
                                  50                      55                      60  
 Leu Phe His Glu Asn Lys Pro Ser Arg Lys Thr Leu His Thr Cys Leu  
                                  65                      70                      75                      80  
 Glu Leu Leu Arg Lys Tyr Cys Met Gly Asp Arg Pro Val Gln Phe Glu  
                                  85                      90                      95  
 40    Ile Leu Ser Asp Gln Ser Val Asn Phe Gly Phe Ser Lys Phe Pro Trp  
                                  100                      105                      110  
 Val Asn Tyr Gln Asp Gly Asn Leu Asn Ile Ser Ile Pro Val Phe Ser  
                                  115                      120                      125  
 45    Ile His Gly Asn His Asp Asp Pro Thr Gly Ala Asp Ala Leu Cys Ala  
                                  130                      135                      140  
 Leu Asp Ile Leu Ser Cys Ala Gly Phe Val Asn His Phe Gly Thr Val  
                                  145                      150                      155                      160  
 50    Gln Trp Leu Trp Glu Lys Ile Asp Ile Xaa Ser Gly Phe Cys Phe Lys  
                                  165                      170                      175  
 Lys Gly Ser Pro Lys Gly Met Ala Leu Leu Leu Gly Leu Arg Xaa Pro  
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 Phe Xaa Glu  
                                  195

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       <213> Homo sapiens

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Arg Ala Lys Leu Ser Ile Met Lys Asp Glu Pro Glu Glu Ala Glu Leu  
 20 25 30  
 Ile Leu His Asp Ala Leu Arg Leu Ala Tyr Gln Thr Asp Asn Lys Lys  
 35 40 45  
 5 Ala Ile Thr Tyr Thr Tyr Asp Leu Met Ala Asn Leu Ala Phe Ile Arg  
 50 55 60  
 Gly Gln Leu Glu Asn Ala Glu Gln Leu Phe Lys Ala Thr Met Ser Tyr  
 65 70 75 80  
 10 Leu Leu Gly Gly Gly Met Lys Gln Glu Asp Asn Ala Ile Ile Glu Ile  
 85 90 95  
 Ser Leu Lys Leu Ala Ser Ile Tyr Ala Ala Gln Asn Arg Gln Glu Phe  
 100 105 110  
 Ala Val Ala Gly Tyr Glu Phe Cys Ile Ser Thr Leu Glu Glu Lys Ile  
 115 120 125  
 15 Glu Arg Glu Lys Glu Leu Ala Glu Asp Ile Met Ser Val Glu Glu Lys  
 130 135 140  
 Ala Asn Thr His Leu Leu Glu Gly Met Cys Leu Asp Ala Cys Ala Arg  
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 20 Tyr Leu Leu Phe Ser Lys Gln Pro Val Thr Gly Thr Lys Asp Val  
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&lt;211&gt; 937

&lt;212&gt; PRT

25 &lt;213&gt; Homo sapiens

&lt;400&gt; 602

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 30 Gly Trp Trp Ala Ser Glu Arg Arg Gly Met Val Asp Tyr His Ala Ala  
 20 25 30  
 Asn Gln Ser Tyr Gln Tyr Gly Pro Ser Ser Ala Ala Met Ala Trp Arg  
 35 35 40 45  
 Arg Gly Ser Met Gly Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg  
 50 55 60  
 Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln Gln Arg Lys Thr Phe  
 65 70 75 80  
 Thr Ala Trp Ser Asn Ser His Leu Arg Lys Ala Gly Thr Gln Ile Glu  
 85 90 95  
 40 Asn Ile Asp Glu Asp Phe Arg Asp Gly Leu Lys Leu Met Leu Leu Leu  
 100 105 110  
 Glu Val Ile Ser Gly Glu Arg Leu Pro Lys Pro Glu Arg Gly Lys Met  
 115 120 125  
 Arg Val His Lys Ile Asn Asn Val Asn Lys Ala Leu Asp Phe Ile Ala  
 130 135 140  
 45 Ser Lys Gly Ile Lys Leu Asp Phe His Arg Ala Glu Glu Ile Val Asp  
 145 150 155 160  
 Gly Asn Ala Lys Met Thr Leu Gly Met Ile Trp Thr Ile Ile Leu Arg  
 165 170 175  
 50 Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr Ser Ala Lys Glu Gly  
 180 185 190  
 Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro Tyr Lys Asn Val Asn  
 195 200 205  
 Val Gln Asn Phe His Ile Ser Trp Lys Asp Gly Leu Ala Phe Asn Ala  
 210 215 220  
 55 Leu Ile His Arg His Arg Pro Glu Leu Ile Glu Tyr Asp Lys Leu Arg  
 225 230 235 240  
 Lys Asp Asp Pro Val Thr Asn Leu Asn Asn Ala Phe Glu Val Ala Glu  
 245 250 255  
 60 Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala Glu Asp Ile Val Asn  
 260 265 270  
 Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr Tyr Val Ser Ser Phe  
 275 280 285

	Tyr	His	Ala	Phe	Ser	Gly	Ala	Gln	Lys	Ala	Glu	Thr	Glu	Thr	Ala	Ala
	290						295					300				
	Asn	Arg	Ile	Cys	Lys	Val	Leu	Ala	Val	Asn	Gln	Glu	Asn	Cys	Ser	Thr
	305					310					315					320
5	Ser	Met	Glu	Asp	Tyr	Glu	Lys	Leu	Ala	Ser	Asp	Leu	Leu	Glu	Trp	Ile
				325						330					335	
	Arg	Arg	Thr	Ile	Pro	Trp	Leu	Glu	Asp	Arg	Val	Pro	Gln	Lys	Thr	Ile
				340					345					350		
10	Gln	Glu	Met	Gln	Gln	Lys	Leu	Glu	Asp	Phe	Arg	Asp	Tyr	Arg	Arg	Val
			355					360					365			
	His	Lys	Pro	Pro	Lys	Val	Gln	Glu	Lys	Cys	Gln	Leu	Glu	Ile	Asn	Phe
		370					375					380				
	Asn	Ser	Val	Gln	Thr	Lys	Leu	Arg	Leu	Ser	Asn	Arg	Pro	Ala	Phe	Met
	385					390					395					400
15	Pro	Ser	Glu	Gly	Lys	Met	Val	Ser	Asp	Ile	Asn	Asn	Gly	Trp	Gln	His
					405					410					415	
	Leu	Glu	Gln	Ala	Glu	Lys	Gly	Tyr	Glu	Glu	Trp	Leu	Leu	Asn	Glu	Ile
				420					425					430		
20	Arg	Arg	Leu	Glu	Arg	Leu	Asp	His	Leu	Ala	Glu	Lys	Phe	Arg	Gln	Lys
			435					440					445			
	Ala	Ser	Ile	His	Glu	Ala	Trp	Thr	Asp	Gly	Lys	Glu	Ala	Met	Leu	Lys
		450					455					460				
	His	Arg	Asp	Tyr	Glu	Thr	Ala	Thr	Leu	Ser	Asp	Ile	Lys	Ala	Leu	Ile
	465					470					475					480
25	Arg	Lys	His	Glu	Ala	Phe	Glu	Ser	Asp	Leu	Ala	Ala	His	Gln	Asp	Arg
					485					490					495	
	Val	Glu	Gln	Ile	Ala	Ala	Ser	Ala	Gln	Glu	Leu	Asn	Glu	Leu	Asp	Tyr
				500					505				510			
30	Tyr	Asp	Ser	His	Asn	Val	Asn	Thr	Arg	Cys	Gln	Lys	Ile	Cys	Asp	Gln
		515						520					525			
	Trp	Asp	Ala	Leu	Gly	Ser	Leu	Thr	His	Ser	Arg	Arg	Glu	Ala	Leu	Glu
		530					535					540				
	Lys	Thr	Glu	Lys	Gln	Leu	Glu	Ala	Ile	Ile	Asp	Gln	Leu	His	Leu	Glu
	545					550					555					560
35	Tyr	Ala	Lys	Pro	Ala	Ala	Pro	Phe	Asn	Asn	Trp	Met	Glu	Ser	Ala	Met
					565					570					575	
	Glu	Asp	Leu	Gln	Asp	Met	Phe	Ile	Val	His	Thr	Ile	Glu	Glu	Ile	Glu
				580					585				590			
40	Gly	Leu	Ile	Ser	Ala	His	Asp	Gln	Phe	Lys	Ser	Thr	Leu	Pro	Asp	Ala
		595						600					605			
	Asp	Arg	Glu	Arg	Glu	Ala	Ile	Leu	His	Pro	Gln	Gly	Gly	Gln	Arg	Ile
		610					615					620				
	Ala	Glu	Ser	Asn	His	Ile	Lys	Leu	Ser	Gly	Ser	Asn	Pro	Tyr	Thr	Thr
	625					630					635					640
45	Val	Thr	Pro	Gln	Ile	Ile	Asn	Ser	Lys	Trp	Glu	Lys	Val	Gln	Gln	Leu
					645					650					655	
	Val	Pro	Lys	Arg	Asp	His	Ala	Leu	Leu	Glu	Glu	Gln	Ser	Lys	Gln	Gln
				660					665					670		
50	Gln	Ser	Asn	Glu	His	Leu	Arg	Arg	Gln	Phe	Ala	Ser	Gln	Ala	Asn	Val
		675						680					685			
	Val	Gly	Pro	Trp	Ile	Gln	Thr	Lys	Met	Glu	Glu	Ile	Ala	Ile	Ser	Ile
		690					695					700				
	Glu	Met	Asn	Gly	Thr	Leu	Glu	Asp	Gln	Leu	Ser	His	Leu	Lys	Gln	Tyr
	705					710					715					720
55	Glu	Arg	Ser	Ile	Val	Asp	Tyr	Lys	Pro	Asn	Leu	Asp	Leu	Leu	Glu	Gln
					725					730					735	
	Gln	His	Gln	Leu	Ile	Gln	Glu	Ala	Leu	Ile	Phe	Asp	Asn	Lys	His	Thr
				740					745					750		
60	Asn	Tyr	Thr	Met	Glu	His	Ile	Arg	Val	Gly	Trp	Glu	Gln	Leu	Leu	Thr
		755						760					765			
	Thr	Ile	Ala	Arg	Thr	Ile	Asn	Glu	Val	Glu	Asn	Gln	Ile	Leu	Thr	Arg
		770					775					780				
	Asp	Ala	Lys	Gly	Ile	Ser	Gln	Glu	Gln	Met	Gln	Glu	Phe	Arg	Ala	Ser



		785				790					795				800		
		Phe	Asn	His	Phe	Asp	Lys	Asp	His	Gly	Gly	Ala	Leu	Gly	Arg	Gly	Val
					805						810					815	
5		Gln	Gly	Leu	Pro	His	Gln	Pro	Gly	Leu	Arg	Arg	Gly	Glu	Arg	Pro	Ala
					820					825					830		
		Gly	Glu	Ala	Glu	Phe	Asn	Arg	Ile	Met	Ser	Leu	Val	Asp	Pro	Asn	His
					835				840					845			
		Ser	Gly	Leu	Val	Thr	Phe	Gln	Ala	Phe	Ile	Asp	Phe	Met	Ser	Arg	Glu
								855					860				
10		Thr	Thr	Asp	Thr	Asp	Thr	Ala	Asp	Gln	Val	Ile	Thr	Ser	Phe	Lys	Val
							870					875					880
		Leu	Ala	Gly	Asp	Lys	Asn	Phe	Ile	Thr	Ala	Glu	Glu	Leu	Arg	Arg	Glu
						885					890					895	
		Leu	Pro	Pro	Asp	Gln	Ala	Glu	Tyr	Cys	Ile	Ala	Arg	Met	Ala	Pro	Tyr
					900					905					910		
15		Gln	Gly	Pro	Asp	Gly	Val	Arg	Gly	Ala	Leu	Asp	Tyr	Lys	Ser	Phe	Ser
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		Thr	Ala	Leu	Tyr	Gly	Glu	Ser	Asp	Leu							
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					20					25					30		
		Glu	Lys	Ala	Phe	Gln	Gln	Ser	Val	Glu	Gln	Asp	Asn	Leu	Phe	Asp	Ile
					35				40					45			
		Ser	Thr	Glu	Glu	Gly	Ser	Thr	Lys	Arg	Lys	Lys	Ser	Gln	Lys	Gly	Pro
					50			55					60				
35		Ala	Lys	Thr	Lys	Lys	Leu	Lys	Ile	Glu	Lys	Arg	Glu	Ser	Ser	Lys	Ser
		65					70					75					80
		Ala	Arg	Glu	Lys	Phe	Glu	Ile	Leu	Ser	Val	Glu	Ser	Leu	Cys	Glu	Gly
					85						90					95	
40		Met	Arg	Ile	Leu	Gly	Cys	Val	Lys	Glu	Val	Asn	Glu	Leu	Glu	Leu	Val
					100					105					110		
		Ile	Ser	Leu	Pro	Asn	Gly	Leu	Gln	Gly	Phe	Val	Gln	Val	Thr	Glu	Ile
					115												

		290				295				300							
		Thr 305	Pro	Phe	Gly	Leu	Thr 310	Leu	Asn	Phe	Leu	Thr 315	Phe	Phe	Thr	Gly	Val 320
5		Val	Asp	Phe	Met	His 325	Leu	Asp	Pro	Lys	Lys	Ala	Gly	Thr	Tyr	Phe	Ser
		Asn	Gln	Ala	Val	Arg	Ala	Cys	Ile	Leu	Cys	Val	His	Pro	Arg	Thr	Arg
		Val	Val	His	Leu	Ser	Leu	Arg	Pro	Ile	Phe	Leu	Gln	Pro	Gly	Arg	Pro
10		Leu	Thr	Arg	Leu	Ser	Cys	Gln	Asn	Leu	Gly	Ala	Val	Leu	Asp	Asp	Val
		Pro	Val	Gln	Gly	Phe	Phe	Lys	Lys	Ala	Gly	Ala	Thr	Phe	Arg	Leu	Lys
		Asp	Gly	Val	Leu	Ala	Tyr	Ala	Arg	Leu	Ser	His	Leu	Ser	Asp	Ser	Lys
15		Asn	Val	Phe	Asn	Pro	Glu	Ala	Phe	Lys	Pro	Gly	Asn	Thr	His	Lys	Cys
		Arg	Ile	Ile	Asp	Tyr	Ser	Gln	Met	Asp	Glu	Leu	Ala	Leu	Leu	Ser	Leu
		Arg	Thr	Ser	Ile	Ile	Glu	Ala	Gln	Tyr	Leu	Arg	Tyr	His	Asp	Ile	Glu
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		Met	Leu	Val	Lys	Val	Gly	Glu	Gln	Met	Arg	Gly	Leu	Val	Pro	Pro	Met
		His	Leu	Ala	Asp	Ile	Leu	Met	Lys	Asn	Pro	Glu	Lys	Lys	Tyr	His	Ile
25		Gly	Asp	Glu	Val	Lys	Cys	Arg	Val	Leu	Leu	Cys	Asp	Pro	Glu	Ala	Lys
		Lys	Leu	Met	Met	Thr	Leu	Lys	Lys	Thr	Leu	Ile	Glu	Ser	Lys	Leu	Pro
		Val	Ile	Thr	Cys	Tyr	Ala	Asp	Ala	Lys	Pro	Gly	Leu	Gln	Thr	His	Gly
30		Phe	Ile	Ile	Arg	Val	Lys	Asp	Tyr	Gly	Cys	Ile	Val	Lys	Phe	Tyr	Asn
		Asn	Val	Gln	Gly	Leu	Val	Pro	Lys	His	Glu	Leu	Ser	Thr	Glu	Tyr	Ile
		Pro	Asp	Pro	Glu	Arg	Val	Phe	Tyr	Thr	Gly	Gln	Val	Val	Lys	Val	Val
40		Val	Leu	Asn	Cys	Glu	Pro	Ser	Lys	Glu	Arg	Met	Leu	Leu	Ser	Phe	Lys
		Leu	Ser	Ser	Asp	Pro	Glu	Pro	Lys	Lys	Glu	Pro	Ala	Gly	His	Ser	Gln
		Lys	Lys	Gly	Lys	Ala	Ile	Asn	Ile	Gly	Gln	Leu	Val	Asp	Val	Lys	Val
45		Leu	Glu	Lys	Thr	Lys	Asp	Gly	Leu	Glu	Val	Ala	Val	Leu	Pro	His	Asn
		Ile	Arg	Ala	Phe	Leu	Pro	Thr	Ser	His	Leu	Ser	Asp	His	Val	Ala	Asn
		Gly	Pro	Leu	Leu	His	His	Trp	Leu	Gln	Ala	Gly	Asp	Ile	Leu	His	Arg
50		Val	Leu	Cys	Leu	Ser	Gln	Ser	Glu	Gly	Arg	Val	Leu	Leu	Cys	Arg	Lys
		Pro	Ala	Leu	Val	Ser	Thr	Val	Glu	Gly	Gly	Gln	Asp	Pro	Lys	Asn	Phe
		Ser	Glu	Ile	His	Pro	Gly	Met	Leu	Leu	Ile	Gly	Phe	Val	Lys	Ser	Ile
55		Lys	Asp	Tyr	Gly	Val	Phe	Ile	Gln	Phe	Pro	Ser	Gly	Leu	Ser	Gly	Leu
		Ala	Pro	Lys	Ala	Ile	Met	Ser	Asp	Lys	Phe	Val	Thr	Ser	Thr	Ser	Asp
		His	Phe	Val	Glu	Gly	Gln	Thr	Val	Ala	Ala	Lys	Val	Thr	Asn	Val	Asp
60		Thr	Pro	Phe	Gly	Leu	Thr	Leu	Asn	Phe	Leu	Thr	Phe	Thr	Tyr	Phe	Ser
		Val	Asp	Phe	Met	His	Leu	Asp	Pro	Lys	Lys	Ala	Gly	Thr	Tyr	Thr	Arg
		Asn	Gln	Ala	Val	Arg	Ala	Cys	Ile	Leu	Cys	Val	His	Pro	Arg	Thr	Arg
		Val	Val	His	Leu	Ser	Leu	Arg	Pro	Ile	Phe	Leu	Gln	Pro	Gly	Arg	Pro
		Leu	Thr	Arg	Leu	Ser	Cys	Gln	Asn	Leu	Gly	Ala	Val	Leu	Asp	Asp	Val

	Glu	Glu	Lys	Gln	Arg	Met	Leu	Leu	Ser	Leu	Arg	Leu	Ser	Asp	Cys	Gly
					805					810					815	
	Leu	Gly	Asp	Leu	Ala	Ile	Thr	Ser	Leu	Leu	Leu	Leu	Asn	Gln	Cys	Leu
				820					825					830		
5	Glu	Glu	Leu	Gln	Gly	Val	Arg	Ser	Leu	Met	Ser	Asn	Arg	Asp	Ser	Val
			835					840					845			
	Leu	Ile	Gln	Thr	Leu	Ala	Glu	Met	Thr	Pro	Gly	Met	Phe	Leu	Asp	Leu
		850					855					860				
	Val	Val	Gln	Glu	Val	Leu	Glu	Asp	Gly	Ser	Val	Val	Phe	Ser	Gly	Gly
10		865				870					875					880
	Pro	Val	Pro	Asp	Leu	Val	Leu	Lys	Ala	Ser	Arg	Tyr	His	Arg	Ala	Gly
					885				890						895	
	Gln	Glu	Val	Glu	Ser	Gly	Gln	Lys	Lys	Lys	Val	Val	Ile	Leu	Asn	Val
				900				905						910		
15	Asp	Leu	Leu	Lys	Leu	Glu	Val	His	Val	Ser	Leu	His	Gln	Asp	Leu	Val
		915						920					925			
	Asn	Arg	Lys	Ala	Arg	Lys	Leu	Arg	Lys	Gly	Ser	Glu	His	Gln	Ala	Ile
		930					935					940				
	Val	Gln	His	Leu	Glu	Lys	Ser	Phe	Ala	Ile	Ala	Ser	Leu	Val	Glu	Thr
20		945				950					955					960
	Gly	His	Leu	Ala	Ala	Phe	Ser	Leu	Thr	Ser	His	Leu	Asn	Asp	Thr	Phe
				965					970						975	
	Arg	Phe	Asp	Ser	Glu	Lys	Leu	Gln	Val	Gly	Gln	Gly	Val	Ser	Leu	Thr
				980				985						990		
25	Leu	Lys	Thr	Thr	Glu	Pro	Gly	Val	Thr	Gly	Leu	Leu	Leu	Ala	Val	Glu
		995					1000						1005			
	Gly	Pro	Ala	Ala	Lys	Arg	Thr	Met	Arg	Pro	Thr	Gln	Lys	Asp	Ser	Glu
		1010					1015					1020				
	Thr	Val	Asp	Glu	Asp	Glu	Glu	Val	Asp	Pro	Ala	Leu	Thr	Val	Gly	Thr
30		1025				1030					1035					104
	Ile	Lys	Lys	His	Thr	Leu	Ser	Ile	Gly	Asp	Met	Val	Thr	Gly	Thr	Val
				1045					1050						1055	
	Lys	Ser	Ile	Lys	Pro	Thr	His	Val	Val	Val	Thr	Leu	Glu	Asp	Gly	Ile
				1060				1065						1070		
35	Ile	Gly	Cys	Ile	His	Ala	Ser	His	Ile	Leu	Asp	Asp	Val	Pro	Glu	Gly
		1075					1080						1085			
	Thr	Ser	Pro	Thr	Thr	Lys	Leu	Lys	Val	Gly	Lys	Thr	Val	Thr	Ala	Arg
		1090					1095					1100				
	Val	Ile	Gly	Gly	Arg	Asp	Met	Lys	Thr	Phe	Lys	Tyr	Leu	Pro	Ile	Ser
40		1105				1110					1115					112
	His	Pro	Arg	Phe	Val	Arg	Thr	Ile	Pro	Glu	Leu	Ser	Val	Arg	Pro	Ser
				1125						1130					1135	
	Glu	Leu	Glu	Asp	Gly	His	Thr	Ala	Leu	Asn	Thr	His	Ser	Val	Ser	Pro
				1140				1145						1150		
45	Met	Glu	Lys	Ile	Lys	Gln	Tyr	Gln	Ala	Gly	Gln	Thr	Val	Thr	Cys	Phe
		1155					1160						1165			
	Leu	Lys	Lys	Tyr	Asn	Val	Val	Lys	Lys	Trp	Leu	Glu	Val	Glu	Ile	Ala
		1170					1175					1180				
	Pro	Asp	Ile	Arg	Gly	Arg	Ile	Pro	Leu	Leu	Leu	Thr	Ser	Leu	Ser	Phe
50		1185				1190					1195					120
	Lys	Val	Leu	Lys	His	Pro	Asp	Lys	Lys	Phe	Arg	Val	Gly	Gln	Ala	Leu
				1205						1210					1215	
	Arg	Ala	Thr	Val	Val	Gly	Pro	Asp	Ser	Ser	Lys	Thr	Phe	Leu	Cys	Leu
				1220				1225						1230		
55	Ser	Leu	Thr	Gly	Pro	His	Lys	Leu	Glu	Glu	Gly	Glu	Val	Ala	Met	Gly
		1235					1240						1245			
	Arg	Val	Val	Lys	Val	Thr	Pro	Asn	Glu	Gly	Leu	Thr	Val	Ser	Phe	Pro
		1250					1255					1260				
	Phe	Gly	Lys	Ile	Gly	Thr	Val	Ser	Ile	Phe	His	Met	Ser	Asp	Ser	Tyr
60		1265				1270					1275					128
	Ser	Glu	Thr	Pro	Leu	Glu	Asp	Phe	Val	Pro	Gln	Lys	Val	Val	Arg	Cys
				1285						1290					1295	
	Tyr	Ile	Leu	Ser	Thr	Ala	Asp	Asn	Val	Leu	Thr	Leu	Ser	Leu	Arg	Ser

		1300		1305		1310	
	Ser	Arg	Thr	Asn	Pro	Glu	Thr
		1315		1320		1325	
	Asn	Ser	Ile	Gln	Asp	Ile	Lys
5		1330		1335		1340	
	Gly	Ser	Ile	Gln	Pro	His	Gly
	1345			1350		1355	
	Val	Gly	Leu	Ala	Arg	Tyr	Ser
		1365		1370		1375	
10	Lys	Ala	Leu	Tyr	Asn	Lys	His
		1380		1385		1390	
	Arg	Val	Leu	Arg	Leu	Asn	His
		1395		1400		1405	
	Leu	Pro	Gly	Asp	Thr	Gly	Lys
15		1410		1415		1420	
	Gly	Gln	Leu	Thr	Lys	Gln	Glu
	1425			1430		1435	
	Asp	Gln	Lys	Gly	Glu	Lys	Lys
		1445		1450		1455	
20	Gln	Lys	Gly	Gln	Glu	Glu	Val
		1460		1465		1470	
	Pro	Gln	Lys	Pro	Gln	Ala	Gln
		1475		1480		1485	
	Ser	Gly	Ser	Glu	Gln	Glu	Arg
25		1490		1495		1500	
	Leu	Ser	Glu	Glu	Asp	Asp	Ser
	1505			1510		1515	
	Lys	Glu	Glu	Ala	Glu	Glu	Thr
		1525		1530		1535	
30	Lys	Pro	Ala	Glu	Ala	Pro	Arg
		1540		1545		1550	
	Asn	Val	Gly	Leu	Asp	Ser	Leu
		1555		1560		1565	
	Ser	Ser	Asp	Ser	Glu	Glu	Asp
35		1570		1575		1580	
	Lys	Ser	Lys	Lys	Glu	Arg	Glu
	1585			1590		1595	
	Leu	Ser	Arg	Ile	Glu	Glu	Ala
		1605		1610		1615	
40	Ser	Ala	Asp	Asp	Phe	Asp	Arg
		1620		1625		1630	
	Ile	Leu	Trp	Leu	Gln	Tyr	Met
		1635		1640		1645	
	Glu	Lys	Ala	Arg	Ala	Val	Ala
45		1650		1655		1660	
	Arg	Glu	Glu	Gln	Glu	Lys	Leu
	1665			1670		1675	
	Glu	Asn	Met	Tyr	Gly	Ser	Gln
		1685		1690		1695	
50	Ala	Val	Gln	Tyr	Asn	Glu	Pro
		1700		1705		1710	
	Ile	Tyr	Ala	Lys	Ser	Glu	Lys
		1715		1720		1725	
	Arg	Met	Leu	Lys	Arg	Phe	Arg
55		1730		1735		1740	
	Gly	Ala	Phe	Leu	Leu	Arg	Arg
	1745			1750		1755	
	Leu	Gln	Arg	Ala	Leu	Glu	Cys
		1765		1770		1775	
60	Ile	Ala	Lys	Phe	Ala	Gln	Leu
		1780		1785		1790	
	Ala	Lys	Ala	Ile	Phe	Glu	Asn
		1795		1800		1805	

Asp Val Trp Ser Val Tyr Ile Asp Met Thr Ile Lys His Gly Ser Gln  
 1810 1815 1820  
 Lys Asp Val Arg Asp Ile Phe Glu Arg Val Ile His Leu Ser Leu Ala  
 1825 1830 1835 184  
 5 Pro Lys Arg Met Lys Phe Phe Phe Lys Arg Tyr Leu Asp Tyr Glu Lys  
 1845 1850 1855  
 Gln His Gly Thr Glu Lys Asp Val Gln Ala Val Lys Ala Lys Ala Leu  
 1860 1865 1870  
 10 Glu Tyr Val Glu Ala Lys Ser Ser Val Leu Glu Asp  
 1875 1880

&lt;210&gt; 604

&lt;211&gt; 192

&lt;212&gt; PRT

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 604

Asp Ala Leu Leu Arg Glu Phe Gln Glu Glu Ile Ala Arg Leu Lys Ala  
 1 5 10 15  
 20 Gln Leu Glu Lys Arg Ser Ile Glu Glu Lys Met Arg Leu Leu Lys Glu  
 20 25 30  
 Lys Glu Lys Lys Met Glu Asp Leu Arg Arg Glu Lys Asp Ala Ala Glu  
 35 40 45  
 Met Leu Gly Ala Lys Ile Lys Ala Met Glu Ser Lys Leu Leu Val Gly  
 50 55 60  
 25 Gly Lys Asn Ile Val Asp His Thr Asn Glu Gln Lys Ile Leu Glu  
 65 70 75 80  
 Gln Lys Arg Gln Glu Ile Ala Glu Gln Lys Arg Xaa Glu Arg Glu Ile  
 85 90 95  
 30 Gln Gln Gln Met Glu Ser Arg Asp Glu Glu Thr Leu Glu Leu Lys Glu  
 100 105 110  
 Thr Tyr Ser Ser Leu Gln Gln Glu Val Asp Ile Lys Thr Lys Lys Leu  
 115 120 125  
 Lys Lys Leu Phe Xaa Lys Leu Gln Ala Val Lys Ala Glu Ile His Asp  
 130 135 140  
 35 Leu Gln Glu Glu His Xaa Lys Glu Arg Gln Glu Leu Xaa Gln Thr Gln  
 145 150 155 160  
 Asn Glu Leu Thr Arg Glu Leu Lys Leu Lys His Leu Ile Ile Glu Asn  
 165 170 175  
 40 Phe Ile Pro Leu Glu Glu Lys Ser Lys Ile Met Asn Arg Ala Phe Phe  
 180 185 190

&lt;210&gt; 605

&lt;211&gt; 186

&lt;212&gt; PRT

45 &lt;213&gt; Homo sapiens

&lt;400&gt; 605

Lys Pro Gly Arg Glu Lys Gln Glu Gly Thr Met Ala Ser Ser Ser Gly  
 1 5 10 15  
 Asn Asp Asp Asp Leu Thr Ile Pro Arg Ala Ala Ile Asn Lys Met Ile  
 20 25 30  
 Lys Glu Thr Leu Pro Asn Val Arg Val Ala Asn Asp Ala Arg Glu Leu  
 35 40 45  
 55 Val Val Asn Cys Cys Thr Glu Phe Ile His Leu Ile Ser Ser Glu Ala  
 50 55 60  
 Asn Glu Ile Cys Asn Lys Ser Glu Lys Lys Thr Ile Ser Pro Glu His  
 65 70 75 80  
 Val Ile Gln Ala Leu Glu Ser Leu Gly Phe Gly Ser Tyr Ile Ser Glu  
 85 90 95  
 60 Val Lys Glu Val Leu Gln Glu Cys Lys Thr Val Ala Leu Lys Arg Arg  
 100 105 110  
 Lys Ala Ser Ser Arg Leu Glu Asn Leu Gly Ile Pro Glu Glu Glu Leu

115 120 125  
 Leu Arg Gln Gln Gln Glu Leu Phe Ala Lys Ala Arg Gln Gln Gln Ala  
 130 135 140  
 Glu Leu Ala Gln Gln Glu Trp Leu Gln Met Gln Gln Ala Ala Gln Gln  
 5 145 150 155 160  
 Ala Gln Leu Ala Ala Ala Ser Ala Ser Ala Ser Asn Gln Ala Gly Ser  
 165 170 175  
 Ser Gln Asp Glu Glu Asp Asp Asp Asp Ile  
 180 185  
 10  
 <210> 606  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 606  
 Glu Pro Val Val Leu Arg Phe Met Ile Phe Cys Arg Leu Leu Ala Lys  
 1 5 10 15  
 Met Ala Asn Asn Asp Ala Val Leu Lys Arg Leu Glu Gln Lys Gly Ala  
 20 20 25 30  
 Glu Ala Asp Gln Ile Ile Glu Tyr Leu Lys Gln Gln Val Ser Leu Leu  
 35 40 45  
 Lys Glu Lys Ala Ile Leu Gln Ala Thr Leu Arg Glu Glu Lys Lys Leu  
 50 55 60  
 25 Arg Val Glu Asn Ala Lys Leu Lys Lys Glu Ile Glu Glu Leu Lys Gln  
 65 70 75 80  
 Glu Leu Ile Gln Ala Glu Ile Gln Asn Gly Val Lys Gln Ile Ala Phe  
 85 90 95  
 Pro Ser Gly Thr Pro Leu His Ala Asn Ser Met Val Ser Glu Asn Val  
 100 105 110  
 30 Ile Gln Ser Thr Ala Val Thr Thr Val Ser Ser Gly Thr Lys Glu Gln  
 115 120 125  
 Ile Lys Gly Gly Thr Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu  
 130 135 140  
 35 Lys Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser  
 145 150 155 160  
 Ala Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly  
 165 170 175  
 Cys Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val  
 180 185 190  
 40 Glu Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly  
 195 200 205  
 Leu Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile  
 210 215 220  
 45 Leu Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln  
 225 230 235 240  
 Ala Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala  
 245 250 255  
 Pro Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe  
 260 265 270  
 50 Pro Gly Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu  
 275 280 285  
 Gln Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr  
 290 295 300  
 55 Lys Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln  
 305 310 315 320  
 Thr Met Ser Asn Ser Gly Ile Lys  
 325  
 60  
 <210> 607  
 <211> 347  
 <212> PRT  
 <213> Homo sapiens

<400> 607

	Ala	Pro	Val	Arg	Glu	Ala	Ala	Arg	Ala	Arg	Gly	Arg	Arg	Ala	Gly	Trp
	1				5					10					15	
5	Gly	Ser	Ala	Ala	Gln	Cys	Gln	Arg	Gln	Arg	Gln	Thr	Arg	Ala	Pro	Arg
			20				25							30		
	Ser	Pro	Ala	Arg	Arg	Leu	Pro	Trp	Asp	Ser	Arg	Ala	Arg	Thr	Pro	Ala
			35				40						45			
10	Leu	Pro	Val	Arg	Cys	Pro	Ser	Met	Glu	Leu	Leu	Cys	Cys	Glu	Gly	Thr
		50					55					60				
	Arg	His	Ala	Pro	Arg	Ala	Gly	Pro	Asp	Pro	Arg	Leu	Leu	Gly	Asp	Gln
		65				70					75					80
	Arg	Val	Leu	Gln	Ser	Leu	Leu	Arg	Leu	Glu	Glu	Arg	Tyr	Val	Pro	Arg
				85						90					95	
15	Ala	Ser	Tyr	Phe	Gln	Cys	Val	Gln	Arg	Glu	Ile	Lys	Pro	His	Met	Arg
				100					105					110		
	Lys	Met	Leu	Ala	Tyr	Trp	Met	Leu	Glu	Val	Cys	Glu	Glu	Gln	Arg	Cys
			115					120					125			
20	Glu	Glu	Glu	Val	Phe	Pro	Leu	Ala	Met	Asn	Tyr	Leu	Asp	Arg	Tyr	Leu
		130					135					140				
	Ser	Cys	Val	Pro	Thr	Arg	Lys	Ala	Gln	Leu	Gln	Leu	Leu	Gly	Ala	Val
		145				150					155					160
	Cys	Met	Leu	Leu	Ala	Ser	Lys	Leu	Arg	Glu	Thr	Thr	Pro	Leu	Thr	Ile
					165					170					175	
25	Glu	Lys	Leu	Cys	Ile	Tyr	Thr	Asp	His	Ala	Val	Ser	Pro	Arg	Gln	Leu
				180					185					190		
	Arg	Asp	Trp	Glu	Val	Leu	Val	Leu	Gly	Lys	Leu	Lys	Trp	Asp	Leu	Ala
			195					200					205			
30	Ala	Val	Ile	Ala	His	Asp	Phe	Leu	Ala	Phe	Ile	Leu	His	Arg	Leu	Ser
		210					215					220				
	Leu	Pro	Arg	Asp	Arg	Gln	Ala	Leu	Val	Lys	Lys	His	Ala	Gln	Thr	Phe
		225				230					235					240
	Leu	Ala	Leu	Cys	Ala	Thr	Asp	Tyr	Thr	Phe	Ala	Met	Tyr	Pro	Pro	Ser
				245						250					255	
35	Met	Ile	Ala	Thr	Gly	Ser	Ile	Gly	Ala	Ala	Val	Gln	Gly	Leu	Gly	Ala
				260				265						270		
	Cys	Ser	Met	Ser	Gly	Asp	Glu	Leu	Thr	Glu	Leu	Leu	Ala	Gly	Ile	Thr
			275				280						285			
40	Gly	Thr	Glu	Val	Asp	Cys	Leu	Arg	Ala	Cys	Gln	Glu	Gln	Ile	Glu	Ala
		290					295				300					
	Ala	Leu	Arg	Glu	Ser	Leu	Arg	Glu	Ala	Ser	Gln	Thr	Ser	Ser	Ser	Pro
					310					315						320
	Ala	Pro	Lys	Ala	Pro	Arg	Gly	Ser	Ser	Ser	Gln	Gly	Pro	Ser	Gln	Thr
					325					330					335	
45	Ser	Thr	Pro	Thr	Asp	Val	Thr	Ala	Ile	His	Leu					
				340					345							

&lt;210&gt; 608

&lt;211&gt; 526

50 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 608

55	Ser	Gly	Ala	Ala	Lys	Met	Pro	Leu	Glu	Leu	Thr	Gln	Ser	Arg	Val
	1				5				10					15	
	Gln	Lys	Ile	Trp	Val	Pro	Val	Asp	His	Arg	Pro	Ser	Leu	Pro	Arg
			20					25					30		
	Cys	Gly	Pro	Lys	Leu	Thr	Asn	Ser	Pro	Thr	Val	Ile	Val	Met	Val
			35				40					45			
60	Leu	Pro	Ala	Arg	Gly	Lys	Thr	Tyr	Ile	Ser	Lys	Lys	Leu	Thr	Arg
		50				55					60				
	Leu	Asn	Trp	Ile	Gly	Val	Pro	Thr	Lys	Val	Phe	Asn	Val	Gly	Glu
		65				70					75				80

	Arg	Arg	Glu	Ala	Val	Lys	Gln	Tyr	Ser	Ser	Tyr	Asn	Phe	Phe	Arg	Pro
					85					90					95	
	Asp	Asn	Glu	Glu	Ala	Met	Lys	Val	Arg	Lys	Gln	Cys	Ala	Leu	Ala	Ala
				100					105					110		
5	Leu	Arg	Asp	Val	Lys	Ser	Tyr	Leu	Ala	Lys	Glu	Gly	Gly	Gln	Ile	Ala
			115					120					125			
	Val	Phe	Asp	Ala	Thr	Asn	Thr	Thr	Arg	Glu	Arg	Arg	His	Met	Ile	Leu
			130				135					140				
10	His	Phe	Ala	Lys	Glu	Asn	Asp	Phe	Lys	Ala	Phe	Phe	Ile	Glu	Ser	Val
	145					150					155				160	
	Cys	Asp	Asp	Pro	Thr	Val	Val	Ala	Ser	Asn	Ile	Met	Glu	Val	Lys	Ile
					165					170					175	
	Ser	Ser	Pro	Asp	Tyr	Lys	Asp	Cys	Asn	Ser	Ala	Glu	Ala	Met	Asp	Asp
				180					185					190		
15	Phe	Met	Lys	Arg	Ile	Ser	Cys	Tyr	Glu	Ala	Ser	Tyr	Gln	Pro	Leu	Asp
			195					200					205			
	Pro	Asp	Lys	Cys	Asp	Arg	Asp	Leu	Ser	Leu	Ile	Lys	Val	Ile	Asp	Val
			210				215						220			
20	Gly	Arg	Arg	Phe	Leu	Val	Asn	Arg	Val	Gln	Asp	His	Ile	Gln	Ser	Arg
	225					230					235					240
	Ile	Val	Tyr	Tyr	Leu	Met	Asn	Ile	His	Val	Gln	Pro	Arg	Thr	Ile	Tyr
					245					250					255	
	Leu	Cys	Arg	His	Gly	Glu	Asn	Glu	His	Asn	Leu	Gln	Gly	Arg	Ile	Gly
				260					265					270		
25	Gly	Asp	Ser	Gly	Leu	Ser	Ser	Arg	Gly	Lys	Lys	Phe	Ala	Ser	Ala	Leu
			275					280					285			
	Ser	Lys	Phe	Val	Glu	Glu	Gln	Asn	Leu	Lys	Asp	Leu	Arg	Val	Trp	Thr
			290				295					300				
30	Ser	Gln	Leu	Lys	Ser	Thr	Ile	Gln	Thr	Ala	Glu	Ala	Leu	Arg	Leu	Pro
	305					310					315					320
	Tyr	Glu	Gln	Trp	Lys	Ala	Leu	Asn	Glu	Ile	Asp	Ala	Gly	Val	Cys	Glu
					325					330					335	
	Glu	Leu	Thr	Tyr	Glu	Glu	Ile	Arg	Asp	Thr	Tyr	Pro	Glu	Glu	Tyr	Ala
				340					345					350		
35	Leu	Arg	Glu	Gln	Asp	Lys	Tyr	Tyr	Tyr	Arg	Tyr	Pro	Thr	Gly	Glu	Ser
			355					360					365			
	Tyr	Gln	Asp	Leu	Val	Gln	Arg	Leu	Glu	Pro	Val	Ile	Met	Glu	Leu	Glu
			370				375					380				
40	Arg	Gln	Glu	Asn	Val	Leu	Val	Ile	Cys	His	Gln	Ala	Val	Leu	Arg	Cys
	385					390					395					400
	Leu	Leu	Ala	Tyr	Phe	Leu	Asp	Lys	Ser	Ala	Glu	Glu	Met	Pro	Tyr	Leu
					405					410					415	
	Lys	Cys	Pro	Leu	His	Thr	Val	Leu	Lys	Leu	Thr	Pro	Val	Ala	Tyr	Gly
				420					425					430		
45	Cys	Arg	Val	Glu	Ser	Ile	Tyr	Leu	Asn	Val	Glu	Ser	Val	Cys	Thr	His
			435					440					445			
	Arg	Glu	Arg	Ser	Glu	Asp	Ala	Lys	Lys	Gly	Pro	Asn	Pro	Leu	Met	Arg
			450				455					460				
50	Arg	Asn	Ser	Val	Thr	Pro	Leu	Ala	Ser	Pro	Glu	Pro	Thr	Lys	Lys	Pro
	465					470					475					480
	Arg	Ile	Asn	Ser	Phe	Glu	Glu	His	Val	Ala	Ser	Thr	Ser	Ala	Ala	Leu
					485					490					495	
	Pro	Ser	Cys	Leu	Pro	Pro	Glu	Val	Pro	Thr	Gln	Leu	Pro	Gly	Gln	Asn
				500					505					510		
55	Met	Lys	Gly	Ser	Arg	Ser	Ser	Ala	Asp	Ser	Ser	Arg	Lys	His		
			515					520					525			

&lt;210&gt; 609

&lt;211&gt; 205

60 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 609



Asn Ile Ser Cys Asn Leu Leu Asn Ile Val Leu Lys Val Lys Asn Arg  
 1 5 10 15  
 Met Val Val Trp Glu Leu Glu Ala Leu Phe Pro Leu Leu Gln Asn Ala  
 20 25 30  
 5 Tyr Leu Ser Cys Ile Ile Val Lys Trp Lys Cys His Lys Leu Pro Ile  
 35 40 45  
 Ile His Trp Xaa Pro Leu Tyr Phe Thr Gln Leu Thr Leu Thr Trp Glu  
 50 55 60  
 Ile Pro His Asn His Ser Ile Arg Glu Ala Ser Xaa Ser Pro Gln Gln  
 65 70 75 80  
 10 Leu Arg Leu Ile Gly Leu Phe Gln Pro Gly Ile Ile Arg Ser Arg Leu  
 85 90 95  
 Pro Gln Ser Gln Lys Gly Glu Glu Ala Xaa Pro Val Trp Ala Pro Gly  
 100 105 110  
 15 Cys Leu Val Gln Pro Arg Val His Ser Trp Met Pro Arg Ser Pro Xaa  
 115 120 125  
 Trp Val Ser Xaa Glu Cys Ser Ala Leu Gln Gly Ala Gly Leu Val Ala  
 130 135 140  
 Gln Gly Pro Phe Gln Glu Phe His Ser Leu Thr Leu Val Gln Ala Ala  
 145 150 155 160  
 20 Ala Trp Ala Pro Pro Gly Ala Gly Ser Trp Ala Gly Arg Pro Xaa Trp  
 165 170 175  
 Arg Pro Met Leu Leu Lys Ala Val Asp Ala Arg Leu Phe Trp Trp Val  
 180 185 190  
 25 Arg Gly Leu Ala Xaa Arg Gly Asp Thr Ile Xaa Val Ser  
 195 200 205

&lt;210&gt; 610

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 610

Val Ile Pro Ser Thr Gly Ile Lys Leu Pro Ser Ser Val Phe Ala Ser  
 1 5 10 15  
 Glu Phe Glu Glu Asp Val Gly Leu Leu Asn Lys Ala Ala Pro Val Ser  
 20 25 30  
 Gly Pro Arg Leu Asp Phe Asp Pro Asp Ile Val Ala Ala Leu Asp Asp  
 35 40 45  
 40 Asp Phe Asp Phe Asp Asp Pro Asp Asn Leu Leu Glu Asp Asp Phe Ile  
 50 55 60  
 Leu Gln Ala Asn Lys Ala Thr Gly Glu Glu Glu Gly Met Asp Ile Gln  
 65 70 75 80  
 Lys Ser Glu Asn Glu Asp Asp Ser Glu Trp Glu Asp Val Asp Asp Glu  
 85 90 95  
 45 Lys Gly Asp Ser Asn Asp Asp Tyr Asp Ser Ala Gly Leu Leu Ser Asp  
 100 105 110  
 Glu Asp Cys Met Ser Val Pro Gly Lys Thr His Arg Ala Ile Ala Asp  
 115 120 125  
 50 His Leu Phe Trp Ser Glu Glu Thr Lys Ser Arg Phe Thr Glu Tyr Ser  
 130 135 140  
 Met Thr Ser Ser Val Met Arg Arg Asn Glu Gln Leu Thr Leu His Asp  
 145 150 155 160  
 Glu Arg Phe Glu Lys Phe Tyr Glu Gln Tyr Asp Asp Asp Glu Ile Gly  
 165 170 175  
 55 Ala Leu Asp Asn Ala Glu Leu Glu Gly Ser Ile Gln Val Gly Gln Gln  
 180 185 190  
 Ser Leu Thr Gly Ser Phe Glu  
 195

&lt;210&gt; 611

&lt;211&gt; 117

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 611

5 Ser Cys Ser Gly Ala Gly Thr Pro Arg Thr Gly Thr Arg Ser Pro Met  
 1 5 10 15  
 Glu Ala Trp His Ala Gly Arg Gly Asn Arg Pro Thr Pro Pro Ser Ala  
 20 25 30  
 Leu Ser Pro Ala Arg Lys Arg Gly Lys Asn Cys Asn Ser Ser Gly Lys  
 35 40 45  
 10 Leu Ser Ser Lys Ser Leu Pro Thr Ser Asp Asp Tyr Glu Leu Gly Ala  
 50 55 60  
 Gly Ile Arg Lys Arg His Lys Gly Pro Lys Glu Glu His Asn Ala Leu  
 65 70 75 80  
 Ile Gly Thr Gly Lys Ala Arg Glu Arg Asn Gln Thr Trp Asp Glu His  
 15 85 90 95  
 Glu Ala Ser Ser Lys Phe Ile Ser Gln Leu Lys Ile Lys Lys Lys Lys  
 100 105 110  
 Met Asp Ser Asp Gln  
 115

20

&lt;210&gt; 612

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

25

&lt;400&gt; 612

Ser Leu Leu Ala Ala Gly Ser His Met Leu Arg Glu Val Leu Asp Gly  
 1 5 10 15  
 Pro Val Val Gly Pro Ala Gln Glu Pro Ala Ala Pro Thr Gly Ala Glu  
 20 25 30  
 Ala His Asn Lys Tyr Ser Trp Met Arg Lys Lys Glu Glu Arg Met Tyr  
 35 40 45  
 Pro Met Lys Ser Ser Val Glu Asp Met Asp Val Leu Glu Leu Asp Phe  
 50 55 60  
 35 Arg Met Trp Arg Ala Glu Val Gln His Gln Tyr Lys Glu Lys Gln His  
 65 70 75 80  
 Glu Leu Val Lys Leu Gln Arg Arg Arg Asp Ser Glu Asp Arg His Glu  
 85 90 95  
 Glu Ser His Gly Ser Leu Ala Arg Arg Pro Trp Lys Gln Thr His Ala  
 100 105 110  
 40 Pro Glu Arg Pro Val Ala Arg Pro Gln Glu Gly Glu Glu Leu Gln Gln  
 115 120 125

45

&lt;210&gt; 613

&lt;211&gt; 197

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 613

50 Ala Arg Ala Leu Glu Lys Leu Glu Ala Ala Glu Ser Leu Val Leu Glu  
 1 5 10 15  
 Gln Ser Phe Leu His Gly Ile Thr Leu Leu Ser Glu Ile Ala Glu Leu  
 20 25 30  
 Glu Leu Glu Arg Arg Ser Gln Glu Met Gly Gly Ala Glu Arg Ala Leu  
 35 40 45  
 55 Val Ala Arg Pro Ser Leu Glu Ser Leu Leu Ala Ala Gly Ser His Met  
 50 55 60  
 Leu Arg Glu Val Leu Asp Gly Pro Val Val Asp Pro Leu Lys Asn Leu  
 65 70 75 80  
 60 Arg Leu Pro Arg Glu Leu Lys Pro Asn Lys Lys Tyr Ser Trp Met Arg  
 85 90 95  
 Lys Lys Glu Glu Arg Met Tyr Ala Met Lys Ser Ser Leu Glu Asp Met  
 100 105 110

Asp Ala Leu Glu Leu Asp Phe Arg Met Arg Leu Ala Glu Val Gln Arg  
           115                          120                          125  
 Gln Tyr Lys Glu Lys Gln Arg Glu Leu Val Lys Leu Gln Arg Arg Arg  
           130                          135                          140  
 5 Asp Ser Glu Asp Arg Arg Glu Glu Pro His Arg Ser Leu Ala Arg Arg  
    145                          150                          155                          160  
 Gly Pro Gly Arg Pro Arg Lys Arg Thr His Ala Pro Ser Ala Leu Ser  
                           165                          170                          175  
 10 Pro Pro Arg Lys Arg Gly Lys Ser Gly His Ser Ser Gly Lys Leu Ser  
           180                          185                          190  
 Ser Lys Val Ser Cys  
           195  
  
       <210> 614  
 15       <211> 184  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 614  
 20 Leu Lys Met Asn Ser Ile Cys Leu Ile Lys Leu Gly Ile Thr Lys Ile  
    1                          5                          10                          15  
 Ala Val Gln Thr Ser Ser His Thr Pro Thr Arg Gln Asn Ser Ile Tyr  
           20                          25                          30  
 Lys Met Phe Xaa Gly Lys Pro Xaa Pro Asn Pro Cys Pro Lys Arg Ala  
 25       35                          40                          45  
 Arg Thr Lys Pro Gly Val Ser Gly Trp Ala Xaa Asn Val Ser Ala Gly  
    50                          55                          60  
 Val Gly Gly Thr Arg Gly Arg Gly Arg Arg Ala Gly Arg Arg Ala Ser  
    65                          70                          75                          80  
 30 Gly Xaa Lys Arg Arg Xaa Lys Ser Ser His Ile Thr Ala Gln Lys Glu  
           85                          90  
 Pro Ala Gly Asp Ile Ile Thr Met Ile Gln Ser Asn Xaa Ser Lys Asn  
           100                          105                          110  
 Gln Asn His Ser Ala Asp Asn Ser Lys Leu Arg Cys Gln Glu Pro Ile  
 35       115                          120                          125  
 Trp Gln Pro Ser Cys Xaa His Ser His Gly Pro Phe Thr His His Xaa  
    130                          135                          140  
 Ser Arg Ala Pro Thr Arg Phe Pro Phe Ala Tyr Leu His Ala Phe Phe  
    145                          150                          155                          160  
 40 Ala Arg Lys His Gly Arg Phe Phe Gly Phe Gly Ala Ser Asn Leu Gly  
           165                          170                          175  
 Lys Pro Phe Pro Pro Xaa Ser Cys  
           180  
  
 45       <210> 615  
       <211> 188  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 615  
 50 Ala Arg Ala Glu Val Gln Glu Lys Lys Lys Lys Met Lys Asn Glu Asn  
    1                          5                          10                          15  
 Ala Asp Lys Leu Leu Lys Ser Glu Lys Gln Met Lys Lys Ser Glu Lys  
           20                          25                          30  
 55 Lys Ser Lys Gln Glu Lys Glu Lys Ser Lys Lys Lys Lys Gly Gly Lys  
    35                          40                          45  
 Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr Asn Lys His Phe Thr Gln  
    50                          55                          60  
 Ser Pro Lys Lys Ser Val Ala Asp Leu Leu Gly Ser Phe Glu Gly Lys  
 60     65                          70                          75                          80  
 Arg Arg Leu Leu Leu Ile Thr Ala Pro Lys Ala Glu Asn Asn Met Tyr  
           85                          90                          95  
 Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser Phe Cys Lys Met Ala Thr

100 105 110  
 Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro Val Asn Asn Ser Thr  
 115 120 125  
 Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu Lys Pro Met Arg Val  
 130 135 140  
 Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu Ile Ser Glu Leu Arg  
 145 150 155 160  
 Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe Met Val Leu Thr Asp  
 165 170 175  
 10 Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val Gln  
 180 185  
  
 <210> 616  
 <211> 129  
 15 <212> PRT  
 <213> Homo sapiens  
  
 <400> 616  
 Ala Arg Gly Gly Gly Gly Ala Arg Leu Arg Arg Gly Asp Ala Ser Pro  
 1 5 10 15  
 Val Arg Pro Arg Arg Gly Leu His Ala Pro Leu Ala Arg Ser Leu Pro  
 20 25 30  
 Pro Pro Ala Pro Arg Pro Ala Met Ala Glu Pro Ser Ser Ala Arg Arg  
 35 40 45  
 25 Pro Val Pro Leu Ile Glu Ser Glu Leu Tyr Phe Leu Ile Ala Arg Tyr  
 50 55 60  
 Leu Ser Ala Gly Pro Cys Arg Arg Ala Ala Gln Val Leu Val Gln Glu  
 65 70 75 80  
 Leu Glu Gln Tyr Gln Leu Leu Pro Lys Arg Leu Asp Trp Glu Gly Asn  
 85 90 95  
 30 Glu His Asn Arg Ser Tyr Xaa Glu Leu Val Leu Ser Asn Lys His Val  
 100 105 110  
 Ala Pro Asp His Leu Leu Gln Ile Cys Glu Arg Ile Gly Ser Tyr Val  
 115 120 125  
 35 Gly  
  
 <210> 617  
 <211> 215  
 40 <212> PRT  
 <213> Homo sapiens  
  
 <400> 617  
 Arg Arg Gly Arg Pro Gly Pro Gly Gly Ala Ala Leu His Ala Gly His  
 1 5 10 15  
 Val Gly Val Gly Pro Leu Arg Pro Pro Ala Leu His Gly Pro Gln Ala  
 20 25 30  
 Gly Pro Pro Gly Ala Gly Ala Leu Pro Ala Pro Gly Pro Gln Ile Arg  
 35 40 45  
 50 Arg Ser Gly Ala Glu Pro Arg Gly Gln Ala Val Arg Val Pro Arg Arg  
 50 55 60  
 Gln Thr Ala Gly Gly Ala Val Trp Gly Arg Arg His Arg Leu Leu Leu  
 65 70 75 80  
 Gly Gln Ala Gly Arg Asp Thr Val Trp Glu Asp Ala Arg Glu Pro Leu  
 85 90 95  
 55 Ala Pro Val Ala Leu Pro Gly Gly Arg Asn Pro Val Asn Tyr Gly Arg  
 100 105 110  
 Pro Tyr Arg Leu Ser Cys Val Glu Xaa Phe Ala Ala Thr Phe Leu His  
 115 120 125  
 60 Xaa Arg Leu Xaa Gln Thr Leu Leu Ser Phe Cys Cys Gly Lys Phe Lys  
 130 135 140  
 Trp Gly Lys Gly Leu Leu Gly Pro Glu Xaa Ala Lys Xaa Leu Asp Lys  
 145 150 155 160

Xaa Pro Val Leu Xaa Xaa Pro Arg Xaa Lys Cys Phe Lys Ala Xaa Gln  
                                   165                                  170                                  175  
 Xaa Phe Leu Gly Lys Leu Pro Met Glu Lys Pro Pro Arg Xaa Glu Glu  
                                   180                                  185                                  190  
 5 Asn Arg Ile Pro Xaa Asn Val Gly Phe Lys Gly Lys Lys Ile Leu Glu  
                                   195                                  200                                  205  
 Asn Pro Lys Arg Xaa Phe Trp  
                                   210                                  215  
  
 10 <210> 618  
       <211> 137  
       <212> PRT  
       <213> Homo sapiens  
  
 15 <400> 618  
 Pro Arg His Leu Pro Thr Arg Ser Leu Glu Ala Phe Ala Glu Glu Val  
   1                                  5                                  10                                  15  
 Gly Ala Ala Leu Gln Ala Ser Val Glu Pro Gly Ala Ala Asp Gly Glu  
                                   20                                  25                                  30  
 20 Gly Gly Pro Gly Pro Ala Ala Leu Pro Cys Thr Leu Ala Met Trp Glu  
                                   35                                  40                                  45  
 Leu Gly His Cys Asp Pro Arg Arg Cys Thr Gly Arg Lys Leu Ala Arg  
                                   50                                  55                                  60  
 Leu Gly Leu Val Arg Cys Leu Arg Leu Gly His Arg Phe Gly Gly Leu  
 25 65                                  70                                  75                                  80  
 Val Leu Ser Pro Val Gly Lys Gln Tyr Ala Ser Pro Ala Asp Arg Gln  
                                   85                                  90                                  95  
 Leu Val Ala Gln Ser Gly Val Ala Val Ile Asp Cys Ser Trp Ala Arg  
                                   100                                  105                                  110  
 30 Leu Asp Glu Thr Pro Phe Gly Lys Met Arg Gly Ser His Leu Arg Leu  
                                   115                                  120                                  125  
 Leu Pro Tyr Leu Val Ala Ala Thr Pro  
                                   130                                  135  
  
 35 <210> 619  
       <211> 227  
       <212> PRT  
       <213> Homo sapiens  
  
 40 <400> 619  
 Gly Thr Ser Ile Tyr Ser Gly Arg Leu Leu Ser Arg Ala Asn Thr Glu  
   1                                  5                                  10                                  15  
 Lys Ser Tyr Gly Ile Asp Glu Asn Gly Arg Asp Glu Asn Thr Met Lys  
                                   20                                  25                                  30  
 45 Asn Ile Phe Ser Lys Lys Arg Lys Leu Glu Val Ala Cys Ser Asp Cys  
                                   35                                  40                                  45  
 Glu Val Glu Val Leu Pro Leu Gly Leu Glu Thr His Pro Arg Thr Ala  
                                   50                                  55                                  60  
 Lys Thr Glu Lys Cys Pro Pro Lys Phe Ser Asn Asn Pro Lys Glu Leu  
 50 65                                  70                                  75                                  80  
 Thr Met Glu Thr Lys Tyr Asp Asn Ile Ser Arg Ile Gln Tyr His Ser  
                                   85                                  90                                  95  
 Val Ile Arg Asp Pro Glu Ser Lys Thr Ala Ile Phe Gln His Asn Gly  
                                   100                                  105                                  110  
 55 Lys Lys Met Glu Phe Val Ser Ser Glu Ser Val Thr Pro Glu Asp Asn  
                                   115                                  120                                  125  
 Asp Gly Phe Lys Pro Pro Arg Glu His Leu Asn Ser Lys Thr Lys Gly  
                                   130                                  135                                  140  
 Ala Gln Lys Asp Ser Ser Ser Asn His Val Asp Glu Phe Glu Asp Asn  
 60 145                                  150                                  155                                  160  
 Leu Leu Ile Glu Ser Asp Val Ile Asp Ile Thr Lys Tyr Arg Glu Glu  
                                   165                                  170                                  175  
 Thr Pro Pro Arg Ser Arg Cys Asn Gln Ala Thr Thr Leu Asp Asn Gln  
                                   215

180 185 190  
 Asn Ile Lys Lys Ala Ile Glu Val Gln Ile Gln Lys Pro Pro Arg Gly  
 195 200 205  
 Thr Ile Tyr Ser Met Ser Lys Thr Ser Xaa Tyr Phe Val Met Lys Lys  
 210 215 220  
 Leu Leu Lys  
 225

5  
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 15  
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<210> 620  
 <211> 227  
 <212> PRT  
 <213> Homo sapiens  
 <400> 620  
 Ile Pro Xaa Gln Pro Phe Phe Lys Pro Asn Gly Lys Lys Met Glu Phe  
 1 5 10 15  
 Val Ser Ser Glu Ser Val Thr Pro Glu Asp Asn Asp Gly Phe Lys Pro  
 20 25 30  
 Pro Arg Glu His Leu Asn Ser Lys Thr Lys Gly Ala Gln Lys Asp Ser  
 35 40 45  
 Ser Ser Asn His Val Asp Glu Phe Glu Asp Asn Leu Leu Ile Glu Ser  
 50 55 60  
 Asp Val Ile Asp Ile Thr Lys Tyr Arg Glu Glu Thr Pro Pro Arg Ser  
 65 70 75 80  
 Arg Cys Asn Gln Ala Thr Thr Leu Asp Asn Gln Asn Ile Lys Lys Ala  
 85 90 95  
 Ile Glu Val Gln Ile Gln Lys Pro Gln Glu Gly Arg Ser Thr Ala Cys  
 100 105 110  
 Gln Arg Gln Gln Val Phe Cys Asp Glu Glu Leu Leu Ser Glu Thr Lys  
 115 120 125  
 Asn Thr Ser Ser Asp Ser Leu Thr Lys Phe Asn Lys Gly Asn Val Phe  
 130 135 140  
 Leu Leu Asp Ala Thr Lys Glu Gly Asn Val Gly Arg Phe Leu Asn His  
 145 150 155 160  
 Ser Cys Cys Pro Asn Leu Leu Val Gln Asn Val Phe Val Glu Thr His  
 165 170 175  
 Asn Arg Asn Phe Pro Leu Val Ala Phe Phe Thr Asn Arg Tyr Val Lys  
 180 185 190  
 Ala Arg Thr Glu Leu Thr Trp Asp Tyr Gly Tyr Glu Ala Gly Thr Val  
 195 200 205  
 Pro Glu Lys Glu Ile Phe Cys Gln Cys Gly Val Asn Lys Cys Arg Lys  
 210 215 220  
 Lys Ile Leu  
 225

<210> 621  
 <211> 204  
 <212> PRT  
 <213> Homo sapiens  
 <400> 621  
 Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu Cys Lys  
 1 5 10 15  
 Lys Tyr Ala Asp Leu Leu Glu Glu Ser Arg Ser Val Gln Lys Gln Met  
 20 25 30  
 Lys Ile Leu Gln Lys Lys Gln Ala Gln Ile Val Lys Glu Lys Val His  
 35 40 45  
 Leu Gln Ser Glu His Ser Lys Ala Ile Leu Ala Arg Ser Lys Leu Glu  
 50 55 60  
 Ser Leu Cys Arg Glu Leu Gln Arg His Asn Lys Thr Leu Lys Glu Glu  
 65 70 75 80  
 Asn Met Gln Gln Ala Arg Glu Glu Glu Glu Arg Arg Lys Glu Ala Thr  
 85 90 95

Ala His Phe Gln Ile Thr Leu Asn Glu Ile Gln Ala Gln Leu Glu Gln  
                   100                  105                  110  
 His Asp Ile His Asn Ala Lys Leu Arg Gln Glu Asn Ile Glu Leu Gly  
                   115                  120                  125  
 5 Glu Lys Leu Lys Lys Leu Ile Glu Gln Tyr Ala Leu Arg Glu Glu His  
                   130                  135                  140  
 Ile Asp Lys Val Phe Lys His Lys Glu Leu Gln Gln Gln Leu Val Asp  
                   145                  150                  155                  160  
 10 Ala Lys Leu Gln Gln Thr Thr Gln Leu Ile Lys Glu Ala Asp Glu Lys  
                                   165                  170                  175  
 His Gln Arg Glu Arg Glu Phe Leu Leu Lys Glu Ala Thr Glu Ser Arg  
                                   180                  185                  190  
 His Lys Tyr Glu Gln Met Lys Gln Gln Glu Val His  
                   195                  200  
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     <210> 622  
     <211> 187  
     <212> PRT  
     <213> Homo sapiens  
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     <400> 622  
 Glu Leu Gly Pro Glu Thr Arg Gly Arg Ala Val Gly Pro Arg Asn Glu  
   1                  5                  10                  15  
 25 Ala Lys Met Leu Glu Gly Asp Leu Val Ser Lys Met Leu Arg Ala Val  
                   20                  25                  30  
 Leu Gln Ser His Lys Asn Gly Val Ala Leu Pro Arg Leu Gln Gly Glu  
                   35                  40                  45  
 Tyr Arg Ser Leu Thr Gly Asp Trp Ile Pro Phe Lys Gln Leu Gly Phe  
                   50                  55                  60  
 30 Pro Thr Leu Glu Ala Tyr Leu Arg Ser Val Pro Ala Val Val Arg Ile  
                   65                  70                  75                  80  
 Glu Thr Ser Arg Ser Gly Glu Ile Thr Cys Tyr Ala Met Ala Cys Thr  
                                   85                  90                  95  
 Glu Thr Ala Arg Ile Ala Gln Leu Val Ala Arg Gln Arg Ser Ser Lys  
                                   100                  105                  110  
 35 Arg Lys Thr Gly Arg Gln Val Asn Cys Gln Met Arg Val Lys Lys Thr  
                   115                  120                  125  
 Met Pro Phe Phe Leu Glu Gly Lys Pro Lys Ala Thr Leu Arg Gln Pro  
                   130                  135                  140  
 40 Gly Phe Ala Ser Asn Phe Ser Val Gly Lys Lys Pro Asn Pro Ala Pro  
                   145                  150                  155                  160  
 Leu Arg Asp Lys Gly Asn Ser Ala Gly Val Lys Pro Asp Ala Glu Met  
                                   165                  170                  175  
 Ser Pro Tyr Met Leu His Thr Thr Leu Trp Lys  
                   180                  185  
 45  
     <210> 623  
     <211> 141  
     <212> PRT  
     <213> Homo sapiens  
 50  
     <400> 623  
 Gln Trp Arg Lys Thr Lys Cys Met Leu Gln Lys Trp Lys Ile Ser Gly  
   1                  5                  10                  15  
 55 Thr Gly Cys Phe Leu Lys Gly Ile Leu Thr Asn Gly Leu Val Ser Val  
                   20                  25                  30  
 Tyr Glu Leu Asp Tyr Gly Lys His Glu Leu Val Asn Ile Arg Lys Val  
                   35                  40                  45  
 Gln Pro Leu Val Asp Met Phe Arg Lys Leu Pro Phe Gln Ala Val Thr  
                   50                  55                  60  
 60 Ala Gln Leu Ala Gly Val Lys Cys Asn Gln Trp Ser Glu Glu Ala Ser  
                   65                  70                  75                  80  
 Met Val Phe Arg Asn His Val Glu Lys Lys Pro Leu Val Ala Leu Val

85 90 95  
 Gln Thr Val Ile Glu Asn Ala Asn Pro Trp Asp Arg Lys Val Val Val  
 100 105 110  
 Tyr Leu Val Asp Thr Ser Leu Pro Asp Thr Asp Thr Trp Ile His Asp  
 115 120 125  
 5 Phe Met Ser Glu Tyr Leu Ile Glu Leu Ser Lys Val Asn  
 130 135 140  
  
 <210> 624  
 10 <211> 201  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 624  
 15 Met Val Ser Gly Asn Val Arg Val Met Ser Glu Met Leu Thr Glu Leu  
 1 5 10 15  
 Val Pro Thr Gln Ala Glu Pro Ala Asp Leu Glu Leu Leu Gln Glu Leu  
 20 20 25 30  
 Asn Arg Thr Cys Arg Ala Met Gln Gln Arg Val Leu Glu Leu Ile Pro  
 35 40 45  
 20 Gln Ile Ala Asn Glu Gln Leu Thr Glu Glu Leu Leu Ile Val Asn Asp  
 50 55 60  
 Asn Leu Asn Asn Val Phe Leu Arg His Glu Arg Phe Glu Arg Phe Arg  
 65 70 75 80  
 25 Thr Gly Gln Thr Thr Lys Ala Pro Ser Glu Ala Glu Pro Ala Ala Asp  
 85 90 95  
 Leu Ile Asp Met Gly Pro Asp Pro Ala Ala Thr Gly Asn Leu Ser Ser  
 100 105 110  
 Gln Leu Ala Gly Met Asn Leu Gly Ser Ser Ser Val Arg Ala Gly Leu  
 115 120 125  
 30 Gln Ser Leu Glu Ala Ser Gly Arg Leu Glu Asp Glu Phe Asp Met Phe  
 130 135 140  
 Ala Leu Thr Arg Gly Ser Ser Leu Ala Asp Gln Arg Lys Glu Val Lys  
 145 150 155 160  
 35 Tyr Glu Ala Pro Gln Ala Thr Asp Gly Leu Ala Gly Ala Leu Asp Ala  
 165 170 175  
 Arg Gln Gln Ser Thr Gly Arg Asp Pro Ser His Pro Gly Leu Pro His  
 180 185 190  
 40 Gly Gly His Xaa Ala Val Ala Val His  
 195 200  
  
 <210> 625  
 <211> 244  
 <212> PRT  
 45 <213> Homo sapiens  
  
 <400> 625  
 Glu Ala Arg Ser Ala Ala Gln Val Ala Leu Cys Ile Gln Gln Leu Gln  
 1 5 10 15  
 50 Lys Ser Ile Ala Trp Glu Lys Ser Ile Met Lys Val Tyr Cys Gln Ile  
 20 25 30  
 Cys Arg Lys Gly Asp Asn Glu Glu Leu Leu Leu Leu Cys Asp Gly Cys  
 35 40 45  
 Asp Lys Gly Cys His Thr Tyr Cys His Arg Pro Lys Ile Thr Thr Ile  
 50 55 60  
 Pro Asp Gly Asp Trp Phe Cys Pro Ala Cys Ile Ala Lys Ala Ser Gly  
 65 70 75 80  
 Gln Thr Leu Lys Ile Lys Lys Leu His Val Lys Gly Lys Lys Thr Asn  
 85 90 95  
 60 Glu Ser Lys Lys Gly Lys Lys Val Thr Leu Thr Gly Asp Thr Glu Asp  
 100 105 110  
 Glu Asp Ser Ala Ser Thr Ser Ser Ser Leu Lys Arg Gly Asn Lys Asp  
 115 120 125



Leu Lys Lys Arg Lys Met Glu Glu Asn Thr Ser Ile Asn Leu Ser Lys  
 130 135 140  
 Gln Glu Ser Phe Thr Ser Val Lys Lys Pro Lys Arg Asp Asp Ser Lys  
 145 150 155 160  
 5 Asp Leu Ala Leu Cys Ser Met Ile Leu Thr Glu Met Glu Thr His Glu  
 165 170 175  
 Asp Ala Trp Pro Phe Leu Leu Pro Val Asn Leu Lys Leu Val Pro Gly  
 180 185 190  
 Tyr Lys Lys Val Ile Lys Lys Pro Met Asp Phe Ser Thr Ile Arg Glu  
 195 200 205  
 10 Lys Leu Ser Ser Gly Gln Tyr Pro Asn Leu Glu Thr Phe Ala Leu Asp  
 210 215 220  
 Val Arg Leu Val Phe Asp Thr Val Lys His Leu Met Glu Asp Asp Ser  
 225 230 235 240  
 15 Asp Ile Gly Arg

<210> 626  
 <211> 208  
 20 <212> PRT  
 <213> Homo sapiens

<400> 626  
 Ala Arg Gly Lys Pro Ser Leu Val Arg Glu Thr Ser Arg Ile Thr Val  
 1 5 10 15  
 Leu Glu Ala Leu Arg His Pro Ile Gln Val Ser Arg Arg Leu Leu Ser  
 20 25 30  
 Arg Pro Gln Asp Ala Leu Glu Gly Val Val Leu Ser Pro Ser Leu Glu  
 35 40 45  
 30 Ala Arg Val Arg Asp Ile Ala Ile Ala Thr Arg Asn Thr Lys Lys Asn  
 50 55 60  
 Arg Ser Leu Tyr Arg Asn Ile Leu Met Tyr Gly Pro Pro Gly Thr Gly  
 65 70 75 80  
 Lys Thr Leu Phe Ala Lys Lys Leu Ala Leu His Ser Gly Met Asp Tyr  
 85 90 95  
 35 Ala Ile Met Thr Gly Gly Asp Val Ala Pro Met Gly Arg Glu Gly Val  
 100 105 110  
 Thr Ala Met His Lys Leu Phe Asp Trp Ala Asn Thr Ser Arg Arg Gly  
 115 120 125  
 40 Leu Leu Leu Phe Val Asp Glu Ala Asp Ala Phe Leu Arg Lys Arg Ala  
 130 135 140  
 Thr Glu Lys Ile Ser Glu Asp Leu Arg Ala Thr Leu Asn Ala Phe Leu  
 145 150 155 160  
 Tyr Arg Thr Gly Gln His Ser Asn Lys Phe Met Leu Val Leu Ala Ser  
 165 170 175  
 45 Asn Gln Pro Glu Gln Phe Asp Trp Ala Ile Asn Asp Arg Xaa Asn Glu  
 180 185 190  
 Met Val His Phe Asp Leu Xaa Arg Ala Xaa Arg Asn Gly Ser Ala Trp  
 195 200 205

50 <210> 627  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

55 <400> 627  
 Val Asn Arg Pro Gln Leu Gln Pro Gln Ala Trp Thr Gly Gln Leu Thr  
 1 5 10 15  
 Val Arg Pro Xaa Thr Pro Pro Pro Gly Ser Leu Leu Pro Pro Xaa Ser  
 20 25 30  
 60 Gly Ser Pro Val Cys Glu Xaa Ser Gly His Ala Gly His Arg Gly Lys  
 35 40 45  
 Gln Gly Ser Gly Cys Pro Thr Trp Val Trp Pro Trp Gln Ala Pro Pro

50 55 60  
 His Leu Ala Leu Leu Trp Glu Pro Arg Thr Lys Thr Ser Pro Ala Trp  
 65 70 75 80  
 Leu Leu Leu Pro Arg Gly Xaa Xaa Gln His Pro Pro Xaa Gln Xaa Pro  
 85 90 95  
 5 Gly Gln Gly Leu Gly Cys Lys Ala Ser Pro Ser Pro Cys Glu Pro Xaa  
 100 105 110  
 Gly Lys Cys Ile Ser Gln Xaa Cys Leu Glu Gly Gln Glu Gly Gly Leu  
 115 120 125  
 10 Pro Leu Pro Ser Gln Xaa Leu Gln Gln Gly Val Pro Trp Gly Ala Lys  
 130 135 140  
 Arg Pro Thr Ala Thr Thr Arg His Pro Gly Gly Gln Arg Pro Trp Ala  
 145 150 155 160  
 Gln Pro Asn Pro His Pro Gly Ala Xaa Pro Lys Cys Ala Gly Ala Gly  
 165 170 175  
 15 Lys Ala Gly Val Gly Xaa Gly Pro Xaa Pro Gly Phe Arg Glu Leu Trp  
 180 185 190  
 Ile Ser Leu Xaa Thr Ser Xaa Xaa Gly Gly Leu Arg Xaa His Ala Gln  
 195 200 205  
 20 Ala Leu Ser Leu Xaa Pro Ala Gln Ser Ser Xaa Gly Ala Xaa Gly Gln  
 210 215 220  
 Tyr Phe Ser Pro Gly Cys  
 225 230  
 25 <210> 628  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens  
 30 <400> 628  
 Gln Cys Gly Leu Xaa His Pro Arg Gln Val Pro Ser Ser Leu Xaa Xaa  
 1 5 10 15  
 Gln Gly His Gln Cys Val Lys Xaa Arg Gly Met Pro Ala Thr Gly Gly  
 20 25 30  
 35 Ser Arg Val Gln Ala Ala Pro Pro Gly Ser Gly Pro Gly Arg Arg Pro  
 35 40 45  
 Leu Thr Trp Leu Cys Cys Gly Ser Arg Glu Gln Arg His His Leu Pro  
 50 55 60  
 Gly Ser Cys Cys Pro Gly Gly Xaa Xaa Ser Thr His Pro Xaa Xaa Gly  
 65 70 75 80  
 40 Leu Gly Arg Gly Trp Gly Ala Lys Pro His Pro Pro Pro Val Ser Xaa  
 85 90 95  
 Thr Glu Asn Ala Phe Pro Xaa Ser Val Ser Arg Gly Arg Lys Glu Ala  
 100 105 110  
 45 Cys Pro Ser Leu Ala Xaa Ala Tyr Asn Arg Gly Cys Pro Gly Gly Gln  
 115 120 125  
 Asn Asp Arg Pro Pro Pro Gln Asp Ile Leu Gly Asp Lys Gly Pro Gly  
 130 135 140  
 His Ser Pro Ile Pro Ile Gln Glu Xaa Ile Leu Asn Val Gln Gly Pro  
 145 150 155 160  
 50 Ala Arg Gln Gly Trp Xaa Gly Val Arg Xaa Gln Ala Ser Val Ser Cys  
 165 170 175  
 Gly Ser Pro Xaa Gly Leu Xaa Asp Xaa Glu Gly Phe Xaa Pro Thr Pro  
 180 185 190  
 55 Arg Pro Phe Arg Xaa Xaa Gln His Asn Leu Leu Xaa Val Leu Xaa Asp  
 195 200 205  
 Ser Ile Phe His Pro Gly Val  
 210 215  
 60 <210> 629  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens

<400> 629

	Ala	Arg	Ala	Glu	Val	Glu	Lys	Gln	Thr	Ser	Leu	Thr	Pro	Arg	Glu	Leu
	1				5					10					15	
5	Glu	Ile	Arg	Arg	Arg	Glu	Asp	Glu	Tyr	Arg	Phe	Thr	Lys	Leu	Leu	Gln
				20				25						30		
	Ile	Ala	Gly	Ile	Ser	Pro	His	Gly	Asn	Ala	Leu	Gly	Ala	Ser	Met	Gln
			35					40					45			
	Gln	Gln	Val	Asn	Gln	Gln	Ile	Pro	Gln	Glu	Lys	Arg	Gly	Gly	Glu	Val
10		50					55					60				
	Leu	Asp	Ser	Ser	His	Asp	Asp	Ile	Lys	Leu	Glu	Lys	Ser	Asn	Ile	Leu
	65				70						75				80	
	Leu	Leu	Gly	Pro	Thr	Gly	Ser	Gly	Lys	Thr	Leu	Leu	Ala	Gln	Thr	Leu
					85					90					95	
15	Ala	Lys	Cys	Leu	Asp	Val	Pro	Phe	Ala	Ile	Cys	Asp	Cys	Thr	Thr	Leu
				100					105					110		
	Thr	Gln	Ala	Gly	Tyr	Val	Gly	Glu	Asp	Ile	Glu	Ser	Val	Ile	Ala	Lys
				115				120					125			
	Leu	Leu	Gln	Asp	Ala	Asn	Tyr	Asn	Val	Glu	Lys	Ala	Gln	Gln	Gly	Ile
20		130					135					140				
	Val	Phe	Leu	Asp	Glu	Val	Asp	Lys	Ile	Gly	Ser	Val	Pro	Gly	Ile	His
	145					150					155				160	
	Gln	Leu	Arg	Asp	Val	Gly	Gly	Glu	Gly	Val	Gln	Gln	Gly	Leu	Leu	Lys
					165					170					175	
25	Leu	Leu	Glu	Gly	Thr	Ile	Val	Asn	Val	Pro	Glu	Lys	Asn	Ser	Arg	Lys
				180				185					190			
	Leu	Arg	Gly	Glu	Thr	Val	Gln	Val	Asp	Thr	Thr	Asn	Ile	Leu	Phe	Val
			195					200					205			
	Ala	Ser	Gly	Ala	Phe	Asn	Gly	Phe	Arg	Gln	Asn	His	Gln	Xaa	Gly	Gly
30		210					215					220				
	Lys	Asn	Glu	Lys	Tyr	Leu	Gly	Phe	Xaa	Thr	Pro	Ile				
	225					230					235					

35 <210> 630  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 630

40	Ser	Arg	Ala	Cys	Arg	Ser	Thr	Leu	Val	Asp	Pro	Lys	Glu	Asn	Met	Asp
	1				5					10					15	
	Thr	Ser	Asn	Thr	Ser	Ile	Ser	Lys	Met	Lys	Arg	Ser	Arg	Pro	Thr	Ser
				20				25						30		
45	Glu	Gly	Ser	Asp	Ile	Glu	Ser	Thr	Glu	Pro	Gln	Lys	Gln	Cys	Ser	Lys
			35					40					45			
	Lys	Lys	Lys	Lys	Arg	Asp	Arg	Val	Glu	Ala	Ser	Ser	Leu	Pro	Glu	Val
		50					55					60				
	Arg	Thr	Gly	Lys	Arg	Lys	Arg	Ser	Ser	Ser	Glu	Asp	Ala	Glu	Ser	Leu
	65				70						75				80	
50	Ala	Pro	Arg	Ser	Lys	Val	Lys	Lys	Ile	Ile	Gln	Lys	Asp	Ile	Ile	Lys
					85					90					95	
	Glu	Ala	Ser	Glu	Ala	Ser	Lys	Glu	Asn	Arg	Asp	Ile	Glu	Ile	Ser	Thr
				100				105						110		
	Glu	Glu	Glu	Lys	Asp	Thr	Gly	Asp	Leu	Lys	Asp	Ser	Ser	Leu	Leu	Lys
55				115				120					125			
	Thr	Lys	Arg	Lys	His	Lys	Lys	Lys	His	Lys	Glu	Arg	His	Lys	Met	Gly
		130					135					140				
	Glu	Glu	Val	Ile	Pro	Leu	Arg	Val	Leu	Ser	Lys	Ser	Glu	Trp	Met	Asp
	145					150					155				160	
60	Leu	Lys	Lys	Glu	Tyr	Leu	Ala	Leu	Gln	Lys	Ala	Ser	Met	Ala	Ser	Leu
					165					170					175	
	Lys	Lys	Thr	Ile	Ser	Gln	Xaa	Lys	Ser	Glu	Ser	Glu	Met	Glu	Thr	Asp
				180					185					190		

Ser Gly Val Pro Gln Asn Thr Gly Met Lys Asn Glu Lys Thr Ala Asn  
 195 200 205  
 Arg Glu Glu Cys Arg Thr Gln Glu Lys Val Asn Ala Thr Gly Pro Gln  
 210 215 220  
 5 Phe Val Ser Gly Val Ile Val Lys Ile Ile Ser Thr Glu Pro Leu Leu  
 225 230 235 240  
 Ala Gly Asn Lys Ser Gly Ile Phe Gly Ser Asn Leu Arg Lys Phe Phe  
 245 250 255  
 Tyr Val Asp Leu Leu Glu Xaa Glu Pro Xaa Trp Pro Ala Arg Leu Lys  
 260 265 270  
 10 Thr Xaa Glu Asp Ala Gln Xaa Val Ile Asn Ala Phe Pro  
 275 280 285  
  
 <210> 631  
 15 <211> 593  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 631  
 20 Leu Asp Met Ala Pro Glu Ile Asn Leu Pro Gly Pro Met Ser Leu Ile  
 1 5 10 15  
 Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro Glu Ala Leu Lys Ile  
 20 25 30  
 Leu Ser Ala Ile Thr Gln Pro Val Val Val Val Ala Ile Val Gly Leu  
 35 40 45  
 25 Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys  
 50 55 60  
 Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser His Thr Lys Gly Ile  
 65 70 75 80  
 30 Trp Met Trp Cys Val Pro His Pro Lys Lys Pro Glu His Thr Leu Val  
 85 90 95  
 Leu Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu Lys Gly Asp Asn Glu  
 100 105 110  
 Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu Leu Ser Ser Thr Phe  
 115 120 125  
 35 Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu  
 130 135 140  
 His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys Ala Asn Ser Ser Pro  
 145 150 155 160  
 40 Gly Asn Asn Ser Val Asp Asp Ser Ala Asp Phe Val Ser Phe Phe Pro  
 165 170 175  
 Ala Phe Val Trp Thr Leu Arg Asp Phe Thr Leu Glu Leu Glu Val Asp  
 180 185 190  
 Gly Glu Pro Ile Thr Ala Asp Asp Tyr Leu Glu Leu Ser Leu Lys Leu  
 195 200 205  
 45 Arg Lys Gly Thr Asp Lys Lys Ser Lys Ser Phe Asn Asp Pro Arg Leu  
 210 215 220  
 Cys Ile Arg Lys Phe Phe Pro Lys Arg Lys Cys Phe Val Phe Asp Trp  
 225 230 235 240  
 50 Pro Ala Pro Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu  
 245 250 255  
 Glu Leu Asn Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr  
 260 265 270  
 Ile Leu Ser His Ser Asn Val Lys Thr Leu Ser Gly Gly Ile Ala Val  
 275 280 285  
 55 Asn Gly Pro Arg Leu Glu Ser Leu Val Leu Thr Tyr Val Asn Ala Ile  
 290 295 300  
 Ser Ser Gly Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala  
 305 310 315 320  
 60 Gln Ile Glu Asn Ser Ala Ala Val Glu Lys Ala Ile Ala His Tyr Glu  
 325 330 335  
 Gln Gln Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu Gln Glu  
 340 345 350

Leu Leu Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu Val Phe  
 355 360 365  
 Met Lys Asn Ser Phe Lys Asp Val Asp Gln Met Phe Gln Arg Lys Leu  
 370 375 380  
 5 Gly Ala Gln Leu Glu Ala Arg Arg Asp Asp Phe Cys Lys Gln Asn Ser  
 385 390 395 400  
 Lys Ala Ser Ser Asp Cys Cys Met Ala Leu Leu Gln Asp Ile Phe Gly  
 405 410 415  
 10 Pro Leu Glu Glu Asp Val Lys Gln Gly Thr Phe Ser Lys Pro Gly Gly  
 420 425 430  
 Tyr Arg Leu Phe Thr Gln Lys Leu Gln Glu Leu Lys Asn Lys Tyr Tyr  
 435 440 445  
 Gln Val Pro Arg Lys Gly Ile Gln Ala Lys Glu Val Leu Lys Lys Tyr  
 450 455 460  
 15 Leu Glu Ser Lys Glu Asp Val Ala Asp Ala Leu Leu Gln Thr Asp Gln  
 465 470 475 480  
 Ser Leu Ser Glu Lys Glu Lys Ala Ile Glu Val Glu Arg Ile Lys Ala  
 485 490 495  
 20 Glu Ser Ala Glu Ala Ala Lys Lys Met Leu Glu Glu Ile Gln Lys Lys  
 500 505 510  
 Asn Glu Glu Met Met Glu Gln Lys Glu Lys Ser Tyr Gln Glu His Val  
 515 520 525  
 Lys Gln Leu Thr Glu Lys Met Glu Arg Asp Arg Ala Gln Leu Met Ala  
 530 535 540  
 25 Glu Gln Glu Lys Thr Leu Ala Leu Lys Leu Gln Glu Gln Glu Arg Leu  
 545 550 555 560  
 Leu Lys Glu Gly Phe Glu Asn Glu Ser Lys Arg Leu Gln Lys Asp Ile  
 565 570 575  
 30 Trp Asp Ile Gln Met Arg Ser Lys Ser Leu Glu Pro Ile Cys Asn Ile  
 580 585 590  
 Leu

35 <210> 632  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<400> 632  
 40 Arg Arg Pro Ala Ala Gly Leu Arg Asp Xaa Val Xaa Ser Ala Pro Arg  
 1 5 10 15  
 Gly Met Ala Ser Glu Gly Pro Xaa Glu Pro Glu Ser Glu Gly Ile Lys  
 20 25 30  
 45 Leu Ser Gly Ile Cys Gln Thr Ile Cys Pro Gln Ile Cys Arg Ala Gln  
 35 40 45  
 Cys Gly Met Val Arg Val Leu Arg Ser Met Cys Leu Pro Gln Leu Cys  
 50 55 60  
 Ser His Ile Leu Ser Val Cys Ser Gly Thr Thr Ser Asp Arg Asn Xaa  
 65 70 75 80  
 50 Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro Ser Cys Tyr  
 85 90 95  
 Arg Gly Phe Gln Thr Xaa Lys His Arg Asn Glu Asn Thr Cys Pro Leu  
 100 105 110  
 Pro Gln Glu Met Lys Ala Leu Phe Lys Lys Lys Thr Xaa Asp Glu Lys  
 115 120 125  
 55 Lys Thr Tyr Asp Gln Gln Lys Phe Asp Ser Glu Arg Ala Asp Gly Thr  
 130 135 140  
 Ile Ser Ser Glu Ile Lys Ser Ala Arg Gly Ser His His Leu Ser Ile  
 145 150 155 160  
 60 Tyr Ala Glu Asn Ser Leu Lys Ser Asp Gly Tyr His Lys Arg Thr Asp  
 165 170 175  
 Arg Lys Ser Arg Ile Ile Cys Lys Lys Trp Ile Tyr Leu Gln Thr  
 180 185 190

<210> 633  
 <211> 149  
 <212> PRT  
 5 <213> Homo sapiens  
  
 <400> 633  
 Leu Gln Val Cys Leu Pro Ala Gly Gly Pro Cys Xaa Val Cys Pro Gln  
 1 5 10 15  
 10 Lys Val Met Xaa Leu Leu Pro Ile Phe Xaa Leu Xaa Lys Met Xaa Pro  
 20 25 30  
 Pro Val Xaa Arg Ala Val Val Thr Ser Pro Trp Xaa Gly Phe Thr Ser  
 35 40 45  
 15 Leu Leu Xaa Xaa Xaa Asn Phe Gln Thr Asn Xaa Xaa Leu Gly Asn Pro  
 50 55 60  
 Pro Gly Gly Leu Glu Lys Pro Xaa Gln Val Ala Val Pro Pro Pro Pro  
 65 70 75 80  
 Leu Pro Phe Xaa Ala Xaa Gly Glu Pro Xaa Pro Ser Ile Phe Trp Ala  
 85 90 95  
 20 Pro Phe Xaa Trp Gly Asn Xaa Val Gly Gly Leu Phe Xaa Ser Pro Leu  
 100 105 110  
 Lys Lys Xaa Gly Phe Leu Glu Xaa Pro Xaa Ile Xaa Xaa Xaa Pro Leu  
 115 120 125  
 Xaa Phe Leu Asp Gly Pro Pro Lys Phe Phe Phe Gln Xaa Phe Phe Gly  
 130 135 140  
 25 Pro Phe Phe Lys Xaa  
 145  
  
 <210> 634  
 30 <211> 124  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 634  
 35 Val Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu  
 1 5 10 15  
 Ala Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala  
 20 25 30  
 Asn Leu Pro Leu Leu Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala  
 35 40 45  
 40 Lys Gln Asn Pro Ala Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu  
 50 55 60  
 Asp Ala Ser Thr Thr Ser Pro Val Asp Ser Ser Glu Leu Leu Leu Asp  
 65 70 75 80  
 45 Val Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg Thr Lys Glu Asn  
 85 90 95  
 Gly Phe Asp Arg Glu Pro Leu His Ser Glu His Pro Ser Lys Arg Pro  
 100 105 110  
 Cys Thr Ile Ser Pro Gly Gln Arg Tyr Lys Ser Lys  
 115 120  
 50  
  
 <210> 635  
 <211> 187  
 <212> PRT  
 55 <213> Homo sapiens  
  
 <400> 635  
 Arg Thr Lys Ala Lys Lys Asp Lys Ala Gln Arg Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 60 Xaa Xaa Gly Xaa Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu  
 20 25 30  
 Glu Glu Ile Leu Gly Ser Asp Asp Asp Glu Gln Glu Asp Pro Asn Asp  
 35 40 45

Tyr Cys Lys Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn  
 50 55 60  
 Gly Arg Tyr His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr  
 65 70 75 80  
 5 Val Trp Leu Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys  
 85 90 95  
 Xaa Val Lys Ser Ala Glu His Tyr Thr Glu Thr Ala Leu Asp Glu Ile  
 100 105 110  
 Xaa Leu Leu Lys Ser Val Arg Asn Ser Asp Pro Asn Asp Pro Asn Arg  
 115 120 125  
 10 Glu Met Val Val Gln Leu Leu Asp Asp Phe Lys Ile Ser Gly Val Asn  
 130 135 140  
 Gly Thr His Ile Cys Met Val Phe Glu Val Leu Gly His His Leu Leu  
 145 150 155 160  
 15 Lys Trp Ile Ile Lys Ser Asn Tyr Xaa Gly Leu Pro Leu Pro Cys Xaa  
 165 170 175  
 Lys Lys Ile Ile Xaa Xaa Val Phe Thr Gly Xaa  
 180 185  
 20 <210> 636  
 <211> 275  
 <212> PRT  
 <213> Homo sapiens  
 25 <400> 636  
 Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Arg Val Cys Lys  
 1 5 10 15  
 Gly Ile Leu Glu Tyr Leu Thr Val Ala Glu Val Val Glu Thr Met Glu  
 20 25 30  
 30 Asp Leu Val Thr Tyr Thr Lys Asn Leu Gly Pro Gly Met Thr Lys Met  
 35 40 45  
 Ala Lys Met Ile Asp Glu Arg Gln Gln Glu Leu Thr His Gln Glu His  
 50 55 60  
 Arg Val Met Leu Val Asn Ser Met Asn Thr Val Lys Glu Leu Leu Pro  
 65 70 75 80  
 35 Val Leu Ile Ser Ala Met Lys Ile Phe Val Thr Thr Lys Asn Ser Lys  
 85 90 95  
 Asn Gln Gly Ile Glu Glu Ala Leu Lys Asn Arg Asn Phe Thr Val Glu  
 100 105 110  
 40 Lys Met Ser Ala Glu Ile Asn Glu Ile Ile Arg Val Leu Gln Leu Thr  
 115 120 125  
 Ser Trp Asp Glu Asp Ala Trp Ala Ser Lys Asp Thr Glu Ala Met Lys  
 130 135 140  
 Arg Ala Leu Ala Ser Ile Asp Ser Lys Leu Asn Gln Ala Lys Gly Trp  
 145 150 155 160  
 45 Leu Arg Asp Pro Ser Ala Ser Pro Gly Asp Ala Gly Glu Gln Ala Ile  
 165 170 175  
 Arg Gln Ile Leu Asp Glu Ala Gly Lys Val Gly Glu Leu Cys Ala Gly  
 180 185 190  
 50 Lys Lys Arg Arg Glu Xaa Leu Gly Asn Leu Gln Asn Ala Xaa Ala Asp  
 195 200 205  
 Asp Cys Gln Ser Gly Leu Thr Ser Val Pro Arg Gly Gln Gly Ser Leu  
 210 215 220  
 Pro Xaa Gly Pro Cys Xaa Lys Ser Xaa Thr Xaa Tyr Xaa Gln Gly Leu  
 225 230 235 240  
 55 Gly Xaa Cys Ser Pro Ala Lys Xaa Glu Lys Ala Ser Phe Gln Ser Trp  
 245 250 255  
 Glu Ser Leu Ala His Xaa Lys Pro Lys His Leu Xaa Xaa Lys Xaa Thr  
 260 265 270  
 60 Met Leu Val  
 275

&lt;210&gt; 637

<211> 162  
 <212> PRT  
 <213> Homo sapiens

5           <400> 637  
 Gln Lys Leu Val Ile Glu Asn Phe Asp Asp Glu Gln Ile Trp Gln Gln  
   1                  5                  10                  15  
 Leu Glu Leu Gln Asn Glu Pro Ile Leu Gln Tyr Phe Gln Asn Ala Val  
                   20                  25                  30  
 10 Ser Glu Thr Ile Asn Asp Glu Asp Ile Ser Leu Leu Pro Glu Ser Glu  
                   35                  40                  45  
 Glu Gln Glu Arg Glu Glu Asp Gly Ser Glu Ile Glu Ala Asp Asp Lys  
                   50                  55                  60  
 Glu Asp Leu Glu Asp Leu Glu Glu Glu Glu Val Ser Asp Met Gly Asn  
 15 65                  70                  75                  80  
 Asp Asp Pro Glu Met Gly Glu Arg Ala Glu Asn Ser Ser Lys Ser Asp  
                   85                  90                  95  
 Leu Arg Lys Ser Pro Val Phe Ser Asp Glu Asp Ser Asp Leu Asp Phe  
                   100                  105                  110  
 20 Asp Ile Ser Lys Leu Glu Gln Gln Ser Lys Val Gln Asn Lys Gly Gln  
                   115                  120                  125  
 Gly Lys Pro Arg Glu Lys Ser Ile Val Asp Asp Lys Phe Phe Lys Leu  
                   130                  135                  140  
 Ser Glu Met Glu Ala Tyr Leu Glu Asn Ile Glu Lys Glu Glu Glu Pro  
 25 145                  150                  155                  160  
 Lys Arg

<210> 638  
 <211> 171  
 <212> PRT  
 <213> Homo sapiens

30           <400> 638  
 Lys Met Ala Ala Gly Phe Lys Thr Val Glu Pro Xaa Glu Tyr Tyr Arg  
   1                  5                  10                  15  
 Arg Phe Leu Lys Glu Asn Cys Arg Pro Asp Gly Arg Glu Leu Gly Glu  
                   20                  25                  30  
 40 Phe Arg Thr Thr Thr Val Asn Ile Gly Ser Ile Ser Thr Ala Asp Gly  
                   35                  40                  45  
 Ser Ala Leu Val Lys Leu Gly Asn Xaa Thr Xaa Ile Cys Gly Val Lys  
                   50                  55                  60  
 Ala Glu Phe Ala Ala Pro Ser Thr Asp Ala Pro Asp Lys Gly Tyr Val  
                   65                  70                  75                  80  
 45 Val Pro Asn Val Asp Leu Pro Pro Leu Cys Ser Ser Arg Phe Arg Ser  
                   85                  90                  95  
 Gly Pro Pro Gly Glu Glu Ala Gln Val Ala Ser Gln Phe Ile Ala Asp  
                   100                  105                  110  
 Val Ile Glu Asn Ser Gln Ile Ile Gln Lys Glu Asp Leu Cys Ile Ser  
                   115                  120                  125  
 50 Pro Gly Lys Leu Val Trp Val Leu Tyr Cys Asp Leu Ile Cys Leu Asp  
                   130                  135                  140  
 Tyr Asp Gly Asn Ile Leu Asp Ala Cys Thr Phe Xaa Leu Leu Ala Ala  
                   145                  150                  155                  160  
 55 Leu Lys Asn Val Gln Val Ala Leu Lys Leu Leu  
                   165                  170

<210> 639  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 639



Xaa Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Leu Lys Ala  
 1 5 10 15  
 Lys Asp Gln Gly Lys Pro Glu Val Gly Glu Tyr Ala Lys Leu Glu Lys  
 20 25 30  
 5 Ile Asn Ala Glu Gln Gln Leu Lys Ile Gln Glu Leu Gln Glu Lys Leu  
 35 40 45  
 Glu Lys Ala Val Lys Ala Ser Thr Glu Ala Thr Glu Leu Leu Gln Asn  
 50 55 60  
 10 Ile Arg Gln Ala Lys Glu Arg Ala Glu Arg Glu Leu Glu Lys Leu Gln  
 65 70 75 80  
 Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys Lys Leu Val Glu Ala  
 85 90 95  
 Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val Lys Arg Leu Glu Thr  
 100 105 110  
 15 Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp Ile Gln Thr Lys Ser  
 115 120 125  
 Gln Gln Ile Gln Gln Met Ala Asp Lys Ile Leu Glu Leu Glu Glu Lys  
 130 135 140  
 His Arg Glu Ala Gln Val Ser Ala Gln His Leu Glu Val His Leu Lys  
 145 150 155 160  
 20 Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys Val Leu Asp Asn Gln  
 165 170 175  
 Ile Lys Lys Asp Leu Ala Asp Lys Glu Thr Leu Glu Asn Met Met Gln  
 180 185 190  
 25 Arg His Glu Glu Ala His Glu Xaa Gly Lys Ile Leu Gln Arg Thr  
 195 200 205  
 Glu Gly Asp Asp Gln Cys Tyr Gly Phe Gln Asp Gln Ile Pro Gly Thr  
 210 215 220  
 Xaa Asp Cys Gly Thr Val  
 225 230  
 30

&lt;210&gt; 640

&lt;211&gt; 256

&lt;212&gt; PRT

35 &lt;213&gt; Homo sapiens

&lt;400&gt; 640

Phe Glu Lys Asp Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg  
 1 5 10 15  
 40 Trp Gly Leu Val Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu  
 20 25 30  
 Gln Phe Asn Thr Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg  
 35 40 45  
 Ser Phe Lys Val Pro Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala  
 50 55 60  
 45 Asp Gly Phe Tyr Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln  
 65 70 75 80  
 Pro Tyr Phe Ile Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser  
 85 90 95  
 50 Ile Gly Ala Ala Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn  
 100 105 110  
 Trp Arg Leu Leu Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro  
 115 120 125  
 Glu Gly Gly Asp Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser  
 130 135 140  
 55 Cys Lys Gly Leu Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp  
 145 150 155 160  
 Gly Glu Glu Ala Val Ser Lys Trp Leu Asp Phe Gly Glu Val Ser Thr  
 165 170 175  
 60 Xaa Glu Ala Leu Lys Leu Ile His Pro Thr Glu Asn Ile Thr Phe His  
 180 185 190  
 Ala Val Ser Ser Val Xaa Asn Asn Ser Arg Asn Asn Thr Ser Glu Cys  
 195 200 205

Leu Ala Xaa Val Asp Leu Val Val Lys Xaa Glu Leu Lys Ala Ser Gly  
 210 215 220  
 Asn Xaa Pro Lys Asp Val Ala Met Gly Trp Xaa Gln Ser Xaa Pro Lys  
 225 230 235 240  
 5 Lys Glu Asp Ser Lys Thr Leu Gln Lys Glu Lys Val Arg Cys Xaa Pro  
 245 250 255  
  
 <210> 641  
 <211> 178  
 10 <212> PRT  
 <213> Homo sapiens  
  
 <400> 641  
 15 Gln Ser Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp  
 1 5 10 15  
 Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val  
 20 25 30  
 Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr  
 35 40 45  
 20 Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val  
 50 55 60  
 Pro Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr  
 65 70 75 80  
 Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile  
 85 90 95  
 25 Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala  
 100 105 110  
 Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu  
 115 120 125  
 30 Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp  
 130 135 140  
 Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu  
 145 150 155 160  
 35 Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala  
 165 170 175  
 Ser Phe  
  
 <210> 642  
 40 <211> 235  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 642  
 45 Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu  
 1 5 10 15  
 Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu  
 20 25 30  
 Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Met  
 35 40 45  
 50 Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val  
 50 55 60  
 Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser Glu Cys  
 65 70 75 80  
 55 Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met Asp Phe  
 85 90 95  
 Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr Asp Thr  
 100 105 110  
 Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu Met Gln  
 115 120 125  
 60 Asn Leu Gly Pro Leu Pro Asn Asp Val Cys Leu Thr Met Lys Leu Phe  
 130 135 140  
 Tyr Tyr Asp Glu Val Thr Pro Pro Asp Tyr Gln Pro Pro Gly Phe Lys

	145				150					155					160	
	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met	Tyr	Leu
					165					170					175	
5	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val	Lys	Val
				180					185					190		
	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Xaa	Leu	Ser
			195				200					205				
	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp	Lys	Asp
		210				215						220				
10	Val	Xaa	Xaa	Glu	Gln	Asp	Xaa	Tyr	Ile	Ser	Gly					
		225				230					235					

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15      <210> 643
        <211> 301
        <212> PRT
        <213> Homo sapiens

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[illegible]

60           <210> 644  
              <211> 163  
              <212> PRT  
              <213> Homo sapiens

<400> 644

Pro Ile Met Ser Xaa Xaa Thr Xaa Ser Thr Leu Val Asp Pro Lys Leu  
 1 5 10 15  
 Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp Arg Leu  
 20 25 30  
 5 Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg Cys Lys  
 35 40 45  
 Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu Asn His  
 50 55 60  
 His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp Glu Ala  
 65 70 75 80  
 10 Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser Glu Lys  
 85 90 95  
 Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr  
 100 105 110  
 15 Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile  
 115 120 125  
 Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala  
 130 135 140  
 Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys Arg Arg  
 145 150 155 160  
 Asn Xaa Arg

25 <210> 645  
 <211> 155  
 <212> PRT  
 <213> Homo sapiens

<400> 645  
 30 Asp Tyr Arg Xaa Ile Glu Ile Thr Ile Cys Lys Asn Asp Glu Cys Val  
 1 5 10 15  
 Leu Glu Asp Asn Ser Gln Arg Thr Lys Trp Lys Val Ile Ser Pro Thr  
 20 25 30  
 Gly Asn Glu Ala Xaa Val Pro Xaa Val Cys Phe Leu Ile Pro Pro Pro  
 35 35 40 45  
 Asn Lys Asp Ala Ile Xaa Met Ala Ser Arg Val Glu Gln Ser Tyr Xaa  
 50 55 60  
 Lys Val Met Ala Leu Trp His Gln Leu His Val Asn Thr Lys Ser Leu  
 65 70 75 80  
 40 Xaa Ser Trp Asn Tyr Leu Arg Lys Asp Leu Asp Leu Val Gln Thr Trp  
 85 90 95  
 Asn Leu Glu Lys Leu Arg Ser Ser Ala Pro Gly Glu Cys His Gln Ile  
 100 105 110  
 Met Xaa Asn Leu Gln Ala His Tyr Glu Asp Phe Xaa Gln Asp Ser Arg  
 115 120 125  
 45 Asp Ser Val Leu Val Ser Val Ala Asp Arg Leu Arg Leu Glu Glu Glu  
 130 135 140  
 Xaa Glu Ala Cys Lys Ala Arg Phe Gln His Leu  
 145 150 155

50 <210> 646  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<400> 646  
 Arg Gly Asn Xaa Gln Gly Lys Ala Xaa Ser Ser Glu Thr Lys Glu Ser  
 1 5 10 15  
 Thr Asp Ile Glu Lys Ala Ile Leu Glu Gln Gln Val Leu Ser Glu Glu  
 20 25 30  
 60 Leu Thr Thr Lys Lys Glu Gln Val Phe Glu Ala Ile Lys Thr Ser Gln  
 35 40 45  
 Ile Phe Leu Ala Lys His Gly His Lys Leu Ser Glu Lys Glu Lys Lys

50 55 60  
 Gln Ile Ser Glu Gln Leu Asn Ala Leu Asn Lys Ala Tyr His Asp Leu  
 65 70 75 80  
 Cys Asp Gly Ser Ala Asn Gln Leu Gln Gln Leu Gln Ser Gln Leu Ala  
 85 90 95  
 5 His Gln Thr Glu Gln Lys Glu Cys Arg Ala Val Ala Gly Val Ile Asp  
 100 105 110  
 Leu Gly Thr Val Glu Ile Phe Pro Ile Phe Lys Ala Met Gln Lys Gly  
 115 120 125  
 10 Leu Leu Asp Gln Asp Thr Gly Leu Val Leu Leu Glu Ser Gln Val Ile  
 130 135 140  
 Met Ser Gly Leu Ile Ala Pro Glu Thr Gly Glu Asn Leu Ser Leu Glu  
 145 150 155 160  
 Glu Gly Val Ala Arg Asn Leu Ile Asn Pro Gln Met Tyr Gln Gln Leu  
 15 165 170 175  
 Arg Glu Leu Gln Asp Ala Leu Ala Leu Ile Ser Arg Leu Thr Glu Ser  
 180 185 190  
 Arg Gly Pro Leu Ser Val Val Glu  
 195 200  
 20  
 <210> 647  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens  
 25  
 <400> 647  
 Lys Glu Gln Arg Lys Glu Asn Glu Pro Glu Ala Glu Lys Thr His Leu  
 1 5 10 15  
 Phe Ala Lys Gln Glu Lys Ala Phe Tyr Pro Lys Ser Phe Lys Ser Lys  
 20 25 30  
 30 Lys Gln Lys Pro Ser Arg Val Leu Tyr Ser Ser Thr Glu Ser Ser Asp  
 35 40 45  
 Glu Glu Ala Leu Gln Asn Lys Lys Ile Ser Thr Ser Cys Ser Val Ile  
 50 55 60  
 35 Pro Glu Thr Ser Asn Ser Asp Met Gln Thr Lys Lys Glu Tyr Val Val  
 65 70 75 80  
 Ser Gly Glu His Lys Gln Lys Gly Lys Val Lys Arg Lys Leu Lys Asn  
 85 90 95  
 Gln Asn Lys Asn Lys Glu Asn Gln Glu Leu Lys Gln Glu Lys Glu Gly  
 100 105 110  
 40 Lys Glu Asn Thr Arg Ile Thr Asn Leu Thr Val Asn Thr Gly Leu Asp  
 115 120 125  
 Cys Ser Glu Lys Thr Arg Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser  
 130 135 140  
 45 Pro Lys Asp Asp Thr Ser Leu His Leu Phe His Ile Ser Thr Gly Lys  
 145 150 155 160  
 Ser Pro Lys His Ser Cys Gly Leu Lys  
 165  
 50  
 <210> 648  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens  
 55  
 <400> 648  
 Ala Phe Leu Phe Pro Ser Xaa Tyr Ala Ser Ile Tyr Val Phe Leu Met  
 1 5 10 15  
 Xaa Tyr Leu Xaa Tyr Pro Phe Phe Ser Xaa Gly Asn Leu Asn Phe Gln  
 20 25 30  
 60 Met Xaa Asp Tyr Asp Leu His Pro Leu Phe Trp His Leu Ile Phe His  
 35 40 45  
 Gln Ile Leu Xaa Gly Asn Leu Ser Asp Val Xaa Phe Phe Pro Tyr Ala  
 50 55 60

Tyr Xaa Ile Leu Xaa Leu Asn Phe Xaa Ala Xaa Ile Gln Ile Leu Xaa  
 65 70 75 80  
 Tyr His Xaa Xaa Gln Xaa Gln Ala Val Met Thr Phe Gln Asn Phe Leu  
 85 90 95  
 5 Gly Ile Asn Met Phe Xaa Tyr Val Leu Xaa Leu Gly Gly Xaa Thr Xaa  
 100 105 110  
 Phe His Leu Ile Xaa Xaa Asn Val Trp Xaa Ile Tyr Xaa Xaa Lys Tyr  
 115 120 125  
 10 Glu Ile Asn Val Met Lys Xaa His Xaa Leu Gly  
 130 135

&lt;210&gt; 649

&lt;211&gt; 321

&lt;212&gt; PRT

15 <213> Homo sapiens

&lt;400&gt; 649

Gly Lys Asp Leu Leu Asn Met Tyr Ile Glu Thr Glu Gly Lys Met Ile  
 1 5 10 15  
 20 Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val  
 20 25 30  
 Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys Leu Cys Gly Pro Tyr Glu  
 35 40 45  
 25 Lys Phe Ile Cys Glu Gln Asp His Gln Asn Phe Leu Arg Leu Leu Thr  
 50 55 60  
 Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly Glu Asp Gln Ala Lys Gln  
 65 70 75 80  
 Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys Ile Gly Thr Pro Val  
 85 90 95  
 30 Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro Lys Met Phe Glu Glu  
 100 105 110  
 Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile Ala Ala Asp Phe Arg  
 115 120 125  
 35 Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu Ser Glu Met Lys Lys  
 130 135 140  
 Val Glu Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys  
 145 150 155 160  
 Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro  
 165 170 175  
 40 Lys Met Phe Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile  
 180 185 190  
 Ala Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu  
 195 200 205  
 45 Ser Glu Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu Trp  
 210 215 220  
 Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln Asp  
 225 230 235 240  
 Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu Asn  
 245 250 255  
 50 Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser  
 260 265 270  
 Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu  
 275 280 285  
 55 Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His Gln  
 290 295 300  
 Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu  
 305 310 315 320  
 Asp

60

&lt;210&gt; 650

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 650

5 Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Val Thr  
 1 5 10 15  
 Asp Ala Val Pro Phe Pro Ile Ser Leu Ile Trp Asn His Asp Ser Glu  
 20 25 30  
 Asp Thr Gly Val His Glu Val Phe Ser Arg Asn His Ala Ala Pro  
 35 40 45  
 10 Phe Ser Lys Val Leu Thr Phe Leu Arg Arg Gly Pro Phe Glu Leu Glu  
 50 55 60  
 Ala Phe Tyr Ser Asp Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile  
 65 70 75 80  
 Gly Arg Phe Val Val Gln Asn Val Ser Ala Gln Lys Asp Gly Glu Lys  
 15 85 90 95  
 Ser Arg Val Lys Val Lys Val Arg Val Asn Thr His Gly Ile Phe Thr  
 100 105 110  
 Ile Ser Thr Ala Ser Met Val Glu Lys Val Pro Thr Glu Glu Asn Glu  
 115 120 125  
 20 Met Ser Ser Glu Ala Asp Met Glu Cys Leu Asn Gln Arg Pro Pro Glu  
 130 135 140  
 Asn Pro Asp Thr Asp Ala Asn Glu Lys Lys Val Asp Gln Pro Pro Glu  
 145 150 155 160  
 Ala Lys Lys Pro Lys Ile Lys Val Val Asn Val Glu Leu Pro Ile Glu  
 25 165 170 175  
 Ala Asn Leu Val Trp Gln Leu Gly Glu Arg Pro Ser  
 180 185

&lt;210&gt; 651

30 &lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 651

35 Xaa Ile Xaa Lys Xaa Ile Gly Lys Xaa Xaa Xaa Gly Leu Lys Pro Val  
 1 5 10 15  
 Gly Asn Leu Val Xaa Val Xaa Xaa Xaa Leu Xaa Gly Xaa Tyr Glu Lys  
 20 25 30  
 Phe Ile Cys Glu Xaa Val Phe Lys Xaa Xaa Asp Asp Ala Xaa Gln Xaa  
 40 35 40 45  
 Leu Xaa Xaa Ala Val Ser Gly Xaa Gly Gly Xaa Ser Xaa Xaa Xaa Xaa  
 50 55 60  
 Arg Cys Xaa Val Ala Gly Leu Arg Xaa Xaa Gly Xaa Pro Val Lys Val  
 65 70 75 80  
 45 Xaa Phe Xaa Glu His Xaa Asn Gly Gln Lys Cys Phe Xaa Thr Xaa Gln  
 85 90 95  
 Xaa Leu Gln Xaa Tyr Pro Lys Ile Ala Ala Asp Phe Arg Asn Lys Xaa  
 100 105 110  
 Xaa Lys Ser Xaa Xaa Ile Asp Glu Phe Glu Met Lys Lys Val Glu Lys  
 50 115 120 125  
 Xaa Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala Gln  
 130 135 140  
 Ala Lys Xaa Ser Phe Asp Gln Asp Pro Val Xaa Arg Ala Gln Glu Ile  
 145 150 155 160  
 55 Lys Thr Lys Ile Lys Glu Leu Xaa Thr His Val Asn Pro Leu  
 165 170

&lt;210&gt; 652

60 &lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 652

Gly Asn Ile Xaa His Ser Asp Xaa Xaa Val Xaa Xaa Gln Asn Xaa Phe  
 1 5 10 15  
 Trp Leu Leu Asn Leu Leu Pro Phe Xaa Gln Tyr Xaa Gly His Leu Glu  
 20 25 30  
 5 Phe Phe Pro Val Xaa Xaa Ile Gln Phe Leu Val Ser Xaa Gly Leu Gln  
 35 40 45  
 Arg Val His Met Cys Xaa Gln Phe Leu Asp Phe Cys Phe Asn Phe Leu  
 50 55 60  
 Ser Pro Xaa Asn Trp Ile Leu Ile Lys Thr Xaa Phe Ser Leu Ser Ile  
 65 70 75 80  
 10 His Asp Ile Ile His Pro Phe His His Phe Ile Asn Xaa Leu Leu His  
 85 90 95  
 Phe Phe His Phe Lys Leu Ile Asn Xaa Xaa Gly Phe Xaa Xaa Leu Ile  
 100 105 110  
 15 Ser Glu Val Ser Cys Tyr Leu Gly Ile Xaa Leu Gln Xaa Leu Xaa Ser  
 115 120 125  
 Xaa Lys Thr Phe Leu Ala Val Xaa Met Phe Xaa Lys Xaa Asn Phe His  
 130 135 140  
 Trp Xaa Ala Xaa Xaa Pro  
 145 150  
 20

&lt;210&gt; 653

&lt;211&gt; 155

&lt;212&gt; PRT

25 &lt;213&gt; Homo sapiens

&lt;400&gt; 653

Ala Glu Xaa Ala Ala Leu Cys Gln Asp Ser Ser Cys Phe Arg Asn Lys  
 1 5 10 15  
 30 Asp Glu Lys Xaa Thr His Ile Asp Glu Xaa Glu Met Lys Lys Val Glu  
 20 25 30  
 Lys Ser Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala  
 35 40 45  
 Gln Ala Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu  
 50 55 60  
 35 Ile Lys Pro Lys Ile Lys Glu Leu Asn Asn Thr Cys Glu Pro Val Val  
 65 70 75 80  
 Thr Xaa Pro Lys Pro Lys Ile Glu Xaa Pro Lys Leu Glu Arg Thr Pro  
 85 90 95  
 40 Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Xaa Lys Xaa  
 100 105 110  
 Asn Phe Gly Xaa Glu Pro Pro His Gln Asn Gly Glu Cys Tyr Pro Asn  
 115 120 125  
 Glu Lys Asn Ser Val Asn Met Asp Leu Asp Xaa Ile Xaa Leu Asn Trp  
 130 135 140  
 45 Pro Ile Pro Ser Ile Asn Lys Ile Phe Leu Pro  
 145 150 155

&lt;210&gt; 654

50 &lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 654

Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Val Thr  
 1 5 10 15  
 Asp Ala Val Pro Phe Pro Ile Ser Leu Ile Trp Asn His Asp Ser Glu  
 20 25 30  
 60 Asp Thr Glu Gly Val His Glu Val Phe Ser Arg Asn His Ala Ala Pro  
 35 40 45  
 Phe Ser Lys Val Leu Thr Phe Leu Arg Arg Gly Pro Phe Glu Leu Glu  
 50 55 60  
 Ala Phe Tyr Ser Asp Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile



65 70 75 80  
 Gly Arg Phe Val Val Gln Asn Val Ser Ala Gln Lys Asp Gly Glu Lys  
 85 90 95  
 Ser Arg Val Lys Val Lys Val Arg Val Asn Thr His Gly Ile Phe Thr  
 100 105 110  
 5 Ile Ser Thr Ala Ser Met Val Glu Lys Val Pro Thr Glu Glu Asn Glu  
 115 120 125  
 Met Ser Ser Glu Ala Asp Met Glu Cys Leu Asn Gln Arg Pro Pro Glu  
 130 135 140  
 10 Asn Pro Asp Thr Asp Ala Asn Glu Lys Lys Val Asp Gln Pro Pro Glu  
 145 150 155 160  
 Ala Lys Lys Pro Lys Ile Lys Val Val Asn Val Glu Leu Pro Ile Glu  
 165 170 175  
 15 Ala Asn Leu Val Trp Gln Leu Gly Glu Arg Pro Ser  
 180 185

&lt;210&gt; 655

&lt;211&gt; 138

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 655

Ala Glu Ala Ala Ala Leu Cys Gln Asp Ser Ser Cys Phe Arg Asn Lys  
 1 5 10 15  
 25 Asp Glu Lys Xaa Thr His Ile Asp Glu Ser Glu Met Lys Lys Val Glu  
 20 25 30  
 Lys Ser Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala  
 35 40 45  
 Gln Ala Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu  
 50 55 60  
 30 Ile Lys Thr Lys Ile Lys Glu Leu Thr Asn Thr Cys Glu Pro Val Val  
 65 70 75 80  
 Thr Xaa Pro Lys Pro Lys Ile Glu Ser Pro Lys Leu Glu Arg Thr Pro  
 85 90 95  
 35 Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Asp Lys Asn  
 100 105 110  
 Asn Phe Gly Ala Xaa Pro Pro His Gln Asn Gly Glu Cys Tyr Pro Asn  
 115 120 125  
 40 Glu Lys Asn Ser Val Asn Met Asp Leu Asp  
 130 135

&lt;210&gt; 656

&lt;211&gt; 110

&lt;212&gt; PRT

45 &lt;213&gt; Homo sapiens

&lt;400&gt; 656

Arg Xaa Arg Gln Arg Leu Gln His Tyr Ala Lys Ile Ala Ala Xaa Phe  
 1 5 10 15  
 50 Arg Asn Lys Asp Glu Lys Ser Pro Xaa Ile Asp Glu Phe Glu Met Lys  
 20 25 30  
 Lys Val Glu Lys Xaa Val Asn Glu Val Met Glu Trp Met Asn Asn Val  
 35 40 45  
 Met Asn Ala Gln Xaa Lys Xaa Ser Xaa Asp Gln Asp Pro Val Val Arg  
 50 55 60  
 55 Ala Gln Glu Ile Asn Xaa Lys Ser Arg Asn Xaa Xaa Thr His Val Xaa  
 65 70 75 80  
 Xaa Xaa Xaa Pro Asn Arg Xaa Xaa Lys Leu Asn Xaa Pro Xaa Xaa Lys  
 85 90 95  
 60 Glu Leu Gln Met Ala Gln Ile Leu Ile Lys Arg Lys Lys Ile  
 100 105 110

&lt;210&gt; 657

<211> 138  
 <212> PRT  
 <213> Homo sapiens

5           <400> 657  
 Ala Glu Ala Ala Ala Leu Cys Gln Asp Ser Ser Cys Phe Arg Asn Lys  
   1                           5                           10                           15  
 Asp Glu Lys Ser Pro His Ile Asp Glu Phe Glu Met Lys Lys Val Xaa  
                  20                           25                           30  
 10 Lys Xaa Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala  
                  35                           40                           45  
 Gln Ala Lys Xaa Ser Phe Asp Gln Asp Pro Val Val Xaa Ala Gln Glu  
                  50                           55                           60  
 Ile Lys Xaa Lys Ile Lys Glu Leu Xaa Xaa Xaa Cys Glu Pro Val Val  
 15 65                           70                           75                           80  
 Thr Xaa Pro Lys Xaa Lys Ile Glu Xaa Pro Xaa Leu Glu Arg Thr Xaa  
                  85                           90                           95  
 Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Xaa Xaa Xaa  
                  100                           105                           110  
 20 Xaa Phe Xaa Xaa Glu Xaa Xaa His Gln Asn Xaa Glu Cys Tyr Pro Asn  
                  115                           120                           125  
 Glu Lys Asn Xaa Val Asn Met Asp Leu Asp  
                  130                           135

25           <210> 658  
              <211> 133  
              <212> PRT  
              <213> Homo sapiens

30           <400> 658  
 Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala  
   1                           5                           10                           15  
 Lys Asn Ala Val Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys Leu Cys  
                  20                           25                           30  
 35 Gly Pro Tyr Glu Lys Phe Ile Cys Glu Gln Asp His Gln Asn Phe Leu  
                  35                           40                           45  
 Arg Leu Leu Thr Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly Glu Asp  
                  50                           55                           60  
 Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys Ile  
 40 65                           70                           75                           80  
 Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro Lys  
                  85                           90                           95  
 Met Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile Ala  
                  100                           105                           110  
 45 Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu Ser  
                  115                           120                           125  
 Glu Met Lys Lys Val  
                  130

50           <210> 659  
              <211> 118  
              <212> PRT  
              <213> Homo sapiens

55           <400> 659  
 Phe Leu Phe Ile Asn Ile Xaa Ala Ile Trp Ser Ser Phe Gln Xaa Gly  
   1                           5                           10                           15  
 Xaa Phe Asn Phe Trp Phe Arg Leu Gly Tyr Asn Gly Xaa Thr Cys Xaa  
                  20                           25                           30  
 60 Gly Gln Phe Leu Asp Phe Xaa Phe Asn Phe Leu Ser Xaa Tyr Asn Trp  
                  35                           40                           45  
 Ile Leu Ile Lys Thr Xaa Phe Ser Leu Ser Ile His Asp Ile Ile His  
                  50                           55                           60

Pro Phe His His Phe Ile Asn Arg Leu Xaa Xaa Phe Phe His Phe Xaa  
 65 70 75 80  
 Leu Ile Asn Met Xaa Gly Phe Leu Ile Leu Ile Xaa Glu Val Ser Cys  
 85 90 95  
 5 Xaa Leu Gly Ile Met Leu Xaa Pro Xaa Pro Ser Xaa Ser Asn Ile Leu  
 100 105 110  
 Gly Arg Ser Ser Ala Ser  
 115  
 10 <210> 660  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens  
 15 <400> 660  
 Xaa Thr Arg Xaa Arg Xaa Gln His Tyr Ala Lys Xaa Ala Ala Asp Phe  
 1 5 10 15  
 Xaa Asn Lys Asp Glu Lys Ser Xaa His Ile Asp Glu Xaa Glu Met Lys  
 20 20 25 30  
 Lys Xaa Xaa Lys Ser Val Asn Glu Val Met Glu Trp Met Asn Asn Val  
 35 40 45  
 Met Asn Ala Gln Ala Lys Xaa Ser Leu Asp Gln Asp Pro Val Val Xaa  
 50 55 60  
 Ala Gln Glu Ile Lys Xaa Lys Ile Lys Glu Leu Thr Xaa Thr Cys Xaa  
 25 65 70 75 80  
 Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Xaa Pro Xaa Leu Glu  
 85 90 95  
 Arg Thr Pro Asn Gly Xaa Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu  
 100 105 110  
 30 Xaa Lys Xaa Asn Phe Xaa Gly Glu Pro Pro His Gln Asn Gly Glu Cys  
 115 120 125  
 Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu Asp  
 130 135 140  
 35 <210> 661  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens  
 40 <400> 661  
 Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met Lys Ile Gly  
 1 5 10 15  
 Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro Lys Met  
 20 25 30  
 45 Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile Ala Ala  
 35 40 45  
 Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp Glu Ser Glu  
 50 55 60  
 Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu Trp Met Asn  
 50 65 70 75 80  
 Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln Asp Pro Val  
 85 90 95  
 Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu Asn Asn Thr  
 100 105 110  
 55 Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser Pro Lys  
 115 120 125  
 Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu Glu Asp  
 130 135 140  
 60 Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His Gln Asn Gly  
 145 150 155 160  
 Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu Asp  
 165 170 175

<210> 662  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

5

<400> 662  
 Glu Thr Glu Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg  
 1 5 10 15  
 Asn Asp Ala Lys Asn Ala Val Glu Glu Tyr Val Tyr Glu Phe Arg Asp  
 20 25 30  
 Lys Leu Cys Gly Pro Tyr Glu Lys Phe Ile Cys Glu Gln Asp His Gln  
 35 40 45  
 Asn Phe Leu Arg Leu Leu Thr Glu Thr Glu Asp Trp Leu Tyr Glu Glu  
 50 55 60  
 Xaa Glu Asp Gln Ala Lys Gln Xaa Xaa Val Asp Xaa Leu Glu Xaa Leu  
 65 70 75 80  
 Met Lys Xaa Xaa Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu  
 85 90 95  
 Arg Pro Lys Met Phe Glu Glu Leu Gly Gln Arg Leu Xaa His Tyr Ala  
 100 105 110  
 Lys Ile Ala Ala Asp Phe Lys Lys  
 115 120

25

<210> 663  
 <211> 79  
 <212> PRT  
 <213> Homo sapiens

30

<400> 663  
 Xaa Phe Gln Xaa Val Asp Xaa Xaa Leu Phe Ser Leu Val Leu Xaa Phe  
 1 5 10 15  
 Phe Ile Gln Pro Val Phe Ser Phe Cys Glu Glu Ser Gln Lys Ile Leu  
 20 25 30  
 Met Ile Leu Leu Thr Tyr Lys Phe Phe Ile Trp Ser Thr Gln Leu Val  
 35 40 45  
 Ser Glu Leu Ile His Ile Phe Leu Asn Cys Ile Phe Ser Ile Ile Pro  
 50 55 60  
 Phe Phe Phe Gln Phe Ile Leu His Tyr His Leu Thr Leu Cys Leu  
 65 70 75

40

<210> 664  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

45

<400> 664  
 Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln Asp  
 1 5 10 15  
 Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu Asn  
 20 25 30  
 Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser  
 35 40 45  
 Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu  
 50 55 60  
 Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His Gln  
 65 70 75 80  
 Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp Leu  
 85 90 95  
 Asp

60

<210> 665  
 <211> 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 665

5 Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met  
    1                  5                  10                  15  
    Lys Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg  
                   20                  25                  30  
 10 Pro Lys Met Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys  
           35                  40                  45  
    Ile Ala Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp  
           50                  55                  60  
    Glu Ser Glu Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu  
    65                  70                  75                  80  
 15 Trp Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln  
                   85                  90                  95  
    Asp Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu  
                   100                  105                  110  
    Asn Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu  
           115                  120                  125  
 20 Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys  
           130                  135                  140  
    Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His  
    145                  150                  155                  160  
 25 Gln Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp  
                   165                  170                  175  
    Leu Asp

&lt;210&gt; 666

&lt;211&gt; 198

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 666

35 Gly Arg Gln Pro Glu Val Arg Ser Asp Leu Arg Arg Leu Ser Pro Ala  
    1                  5                  10                  15  
    Phe Ser Gln Gly Phe Leu Ser Ala Ser Arg Arg Cys Pro Arg Gly Ser  
                   20                  25                  30  
 40 Arg Arg Leu Leu Thr Gly Arg Gly Cys Leu Cys Val Leu Leu Ser Val  
           35                  40                  45  
    Arg Gly Thr Ala Arg Pro Arg Gly Pro Glu Gln Asn Ala Ala Arg Ala  
           50                  55                  60  
    Glu Ser Gly Gly Arg Arg Ser Arg Gln Gly Ala Gly Gly Arg Arg Pro  
    65                  70                  75                  80  
    Arg Pro Glu Ala Glu Ala Asp Arg Glu Pro Ala Met Ser Val Val Gly  
                   85                  90                  95  
    Leu Asp Val Gly Ser Gln Ser Cys Tyr Ile Ala Val Ala Arg Ala Gly  
                   100                  105                  110  
 50 Gly Ile Glu Thr Ile Ala Asn Glu Phe Ser Asp Arg Cys Thr Pro Ser  
           115                  120                  125  
    Val Ile Ser Phe Gly Ser Lys Asn Arg Thr Ile Gly Val Ala Ala Lys  
           130                  135                  140  
    Asn Gln Gln Ile Thr His Ala Asn Asn Thr Val Ser Asn Phe Lys Arg  
    145                  150                  155                  160  
 55 Phe His Gly Arg Ala Phe Asn Asp Pro Phe Ile Gln Lys Glu Lys Gly  
                   165                  170                  175  
    Lys Leu Glu Leu Arg Phe Gly Ser Ile Glu Lys Trp Xaa Ser Trp Asn  
                   180                  185                  190  
 60 Lys Xaa Asn Val His Gly  
           195

&lt;210&gt; 667

<211> 100  
 <212> PRT  
 <213> Homo sapiens

5           <400> 667  
 Thr Ser Thr Pro Thr His Met Leu Asn Gly Glu Gln Asn Ala Arg Lys  
   1                   5                   10                   15  
 Leu Pro Trp Gln Glu Gln Met Leu Lys Asp Phe Asn His Ser Pro Leu  
           20                   25                   30  
 10 Glu Gln Xaa Val Gln Phe Phe Phe Ser Lys Arg Gln Lys Ser Val Ser  
           35                   40                   45  
 Ser Ser Xaa Met Gln Met Xaa Arg Leu His Arg Lys Leu Ser Met Asn  
   50                   55                   60  
 Ser Gln Phe His Arg Asn Xaa Lys Val Thr Lys Ala Ile Phe Pro Phe  
 15 65                   70                   75                   80  
 Arg Xaa Ile Lys Thr Thr Asp Leu Ser Phe Phe Leu Phe Pro Tyr Asn  
                   85                   90                   95  
 Xaa Gln Lys Phe  
                   100

20           <210> 668  
              <211> 141  
              <212> PRT  
              <213> Homo sapiens

25           <400> 668  
 Gly Arg Gln Pro Glu Val Arg Ser Asp Leu Arg Arg Leu Ser Pro Ala  
   1                   5                   10                   15  
 Phe Ser Gln Gly Phe Leu Ser Ala Ser Arg Arg Cys Pro Arg Gly Ser  
 30                   20                   25                   30  
 Arg Arg Leu Leu Thr Gly Arg Gly Cys Leu Cys Val Leu Leu Ser Val  
           35                   40                   45  
 Arg Gly Thr Ala Arg Pro Arg Gly Pro Glu Xaa Asn Ala Ala Arg Ala  
   50                   55                   60  
 35 Glu Ser Gly Gly Arg Arg Ser Xaa Gln Gly Ala Gly Gly Arg Arg Pro  
   65                   70                   75                   80  
 Arg Pro Glu Ala Xaa Ala Asp Arg Glu Pro Ala Met Ser Val Val Gly  
                   85                   90                   95  
 Leu Asp Val Gly Xaa Gln Ser Cys Tyr Ile Ala Val Ala Arg Ala Gly  
 40                   100                   105                   110  
 Gly Ile Glu Thr Ile Ala Xaa Glu Phe Xaa Asp Arg Xaa Thr Pro Xaa  
           115                   120                   125  
 Val Ile Ser Phe Xaa Ser Lys Asn Ile Asn Lys Ser Glu  
   130                   135                   140

45           <210> 669  
              <211> 116  
              <212> PRT  
              <213> Homo sapiens

50           <400> 669  
 Gln Leu Xaa Glu Pro Thr Ser Asn Pro Thr Thr Asp Met Ala Gly Ser  
   1                   5                   10                   15  
 Arg Ser Xaa Ser Ala Ser Gly Leu Gly Leu Arg Pro Pro Ala Pro Cys  
 55                   20                   25                   30  
 Xaa Leu Leu Leu Pro Pro Leu Ser Ala Leu Ala Ala Xaa Cys Ser Gly  
           35                   40                   45  
 Pro Arg Gly Leu Ala Val Pro Leu Thr Leu Arg Arg Thr His Arg Gln  
   50                   55                   60  
 60 Pro Arg Pro Val Arg Ser Leu Leu Leu Pro Arg Gly Gln Arg Arg Leu  
   65                   70                   75                   80  
 Ala Asp Lys Lys Pro Trp Glu Lys Ala Gly Leu Ser Leu Arg Arg Ser  
                   85                   90                   95

Leu Arg Thr Ser Gly Cys Leu Pro His Ser Ala Ala Ala Arg Thr Pro  
 100 105 110  
 Ala Pro Ala Leu  
 115

5

<210> 670  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

10

<400> 670  
 Tyr Asp Xaa Arg Gly Xaa Pro Val Xaa Glu Leu Xaa Gly Asp Gly Leu  
 1 5 10 15  
 Asp Ala Pro Gly Pro Gly Tyr Arg Asp Val Ala Ala Leu Xaa Ala His  
 20 25 30  
 Val Gln Pro His His Arg His Gly Arg Leu Ala Val Arg Xaa Arg Leu  
 35 40 45  
 Gly Ser Arg Ser Ala Ser Ser Gly Pro Leu Xaa Ala Ser Pro Ala Ala  
 50 55 60  
 Ala Phe Cys Pro Gly Arg Val Xaa Leu Arg Pro Ala Gly Ser Gly Arg  
 65 70 75 80  
 Ser Ser Asp Thr Gln Lys Asp Thr Gln Thr Ala Ala Ala Cys Gln Glu  
 85 90 95  
 Pro Pro Thr Pro Pro Gly Thr Ala Ala Gly  
 100 105

25

<210> 671  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

30

<400> 671  
 Gly Asn Val Cys Lys Trp Gly Pro Val His Val Ser Val Trp Cys Ala  
 1 5 10 15  
 Cys Gly Asn Val Cys Lys Trp Ala Pro Val Arg Val Cys Gly Val Cys  
 20 25 30  
 Val Gly Met Cys Ala Ser Gly Arg Leu Cys Glu Cys Val Val Arg Val  
 35 40 45  
 Trp Glu Cys Val Gln Val Gly Ala Cys Pro Cys Glu Cys Val Val Arg  
 50 55 60  
 Val Leu Glu Cys Val Gln Val Asp Ala Cys Ala Cys Glu Cys Val Val  
 65 70 75 80  
 Arg Val Gly Met Cys Ala Ser Gly His Leu Cys Glu Cys Val Val Arg  
 85 90 95  
 Val Trp Glu Cys Val Gln Val Gly Thr Cys Pro Trp Glu Cys Val Val  
 100 105 110  
 Arg Val Trp Glu Cys Val Gln Val Gly Ala Cys Ala Cys Glu Cys Glu  
 115 120 125  
 Asp Thr Ser Cys Ser Gly Val Thr Asn Pro Ile  
 130 135

50

<210> 672  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

55

<400> 672  
 Val Cys Gly Val His Val Gly Met Cys Ala Ser Gly Arg Leu Cys Glu  
 1 5 10 15  
 Cys Val Val Cys Val Trp Glu Cys Val Gln Val Gly Ala Cys Ala Ser  
 20 25 30  
 Val Trp Cys Val Cys Gly Asn Val Cys Lys Trp Ala Pro Ala His Val  
 35 40 45

60

271

Ser Val Trp Cys Val Cys Trp Asn Val Cys Lys Trp Thr Pro Ala His  
 50 55 60  
 Val Ser Val Trp Cys Val Trp Glu Cys Val Gln Val Gly Thr Cys Ala  
 65 70 75 80  
 5 Ser Val Trp Cys Ala Cys Gly Asn Val Cys Lys Trp Ala Pro Ala His  
 85 90 95  
 Gly Ser Val Trp Cys Ala Cys Gly Asn Val Cys Lys Trp Glu Pro Ala  
 100 105 110  
 His Val Ser Val Arg Thr Pro Arg Ala Gln Val Ser Pro Thr Pro Phe  
 115 120 125  
 10 Lys Lys Glu Ile Thr Met Met Thr Thr Ser Leu  
 130 135  
 <210> 673  
 15 <211> 134  
 <212> PRT  
 <213> Homo sapiens  
 <400> 673  
 20 His Leu Ser Thr Arg Cys Pro His Thr His Met Arg Arg Leu Pro Leu  
 1 5 10 15  
 Ala His Ile Pro Thr Arg Ala Pro His Thr Pro Met Gly Arg Cys Pro  
 20 25 30  
 Leu Ala His Ile Pro Thr Arg Ala Pro His Thr Arg Thr Gly Ala His  
 25 35 40 45  
 Leu His Thr Phe Pro His Ala Pro His Thr His Met Arg Arg Arg Pro  
 50 55 60  
 Leu Ala His Ile Pro Thr His Ala Pro His Thr His Met Gly Arg Arg  
 65 70 75 80  
 30 Pro Leu Ala His Ile Pro Thr His Ala Pro His Thr Arg Thr Gly Ala  
 85 90 95  
 His Leu His Thr Phe Pro His Thr His His Thr Leu Ala Gln Ala Pro  
 100 105 110  
 Thr Cys Thr His Ser His Met His Thr Thr His Ser His Ala Gln Ala  
 115 120 125  
 35 Pro Thr Cys Thr His Ser  
 130  
 <210> 674  
 40 <211> 132  
 <212> PRT  
 <213> Homo sapiens  
 <400> 674  
 45 Ala Arg Gly Val Leu Thr Leu Thr Cys Ala Gly Ser His Leu His Thr  
 1 5 10 15  
 Phe Pro His Ala His His Thr Leu Pro Trp Ala Gly Ala His Leu His  
 20 25 30  
 Thr Phe Pro His Ala His His Thr Leu Ala Gln Val Pro Thr Cys Thr  
 35 40 45  
 50 His Ser His Thr His His Thr Leu Thr Cys Ala Gly Val His Leu His  
 50 55 60  
 Thr Phe Gln His Thr His His Thr Leu Thr Trp Ala Gly Ala His Leu  
 65 70 75 80  
 55 His Thr Phe Pro His Thr His His Thr Leu Ala Gln Ala Pro Thr Cys  
 85 90 95  
 Thr His Ser His Thr His Thr Thr His Ser His Arg Arg Pro Leu Ala  
 100 105 110  
 His Ile Pro Thr Cys Thr Pro His Thr His Met His Arg Pro Pro Leu  
 115 120 125  
 60 Ala His Ile Pro  
 130



<210> 675  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

5

<400> 675

Met Gly Leu Val Thr Pro Glu His Glu Val Ser Ser His Ser His Ala  
 1 5 10 15  
 Gln Ala Pro Thr Cys Thr His Ser His Thr Arg Thr Thr His Ser His  
 10 20 25 30  
 Gly Gln Val Pro Thr Cys Thr His Ser His Thr Arg Thr Thr His Ser  
 35 40 45  
 His Arg Cys Pro Leu Ala His Ile Pro Thr Arg Thr Thr His Ser His  
 50 55 60  
 15 Ala Gln Ala Ser Thr Cys Thr His Ser Asn Thr Arg Thr Thr His Ser  
 65 70 75 80  
 His Gly Gln Ala Pro Thr Cys Thr His Ser His Thr Arg Thr Thr His  
 85 90 95  
 Ser His Arg Arg Pro Leu Ala His Ile Pro Thr His Thr Pro His Thr  
 100 105 110  
 20 Arg Thr Gly Ala His Leu His Thr Phe Pro His Ala His His Thr Leu  
 115 120 125  
 Thr Cys Thr Gly Pro His Leu His Thr Phe  
 130 135

25

<210> 676  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

30

<400> 676

Met Glu Ser Lys Met Gln Glu Asn Tyr Leu Gly Arg Asn Lys Cys Leu  
 1 5 10 15  
 Lys Ile Leu Ile Thr Ala Leu Leu Asn Lys Gln Tyr Lys Phe Phe Phe  
 20 25 30  
 35 Ser Lys Arg Gln Lys Ser Val Ser Ser Ser Val Met Gln Met Xaa Arg  
 35 40 45  
 Leu His Arg Lys Leu Ser Met Asn Ser Gln Phe His Arg Asn Leu Lys  
 50 55 60  
 40 Val Thr Lys Ala Ile Phe Pro Phe Arg Ile Ile Lys Thr Thr Xaa Leu  
 65 70 75 80  
 Lys Leu Phe Phe Phe Phe His Ile Ile His Lys Ile Ser Lys Tyr Pro  
 85 90 95

45

<210> 677  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

50

<400> 677

Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met  
 1 5 10 15  
 Lys Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg  
 20 25 30  
 55 Pro Lys Met Phe Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys  
 35 40 45  
 Ile Ala Ala Asp Phe Arg Asn Lys Asp Glu Lys Tyr Asn His Ile Asp  
 50 55 60  
 Glu Ser Glu Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu  
 65 70 75 80  
 60 Trp Met Asn Asn Val Met Asn Ala Gln Ala Lys Lys Ser Leu Asp Gln  
 85 90 95  
 Asp Pro Val Val Arg Ala Gln Glu Ile Lys Thr Lys Ile Lys Glu Leu

100 105 110  
 Asn Asn Thr Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu  
 115 120 125  
 Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys  
 130 135 140  
 5 Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe Gly Ala Glu Pro Pro His  
 145 150 155 160  
 Gln Asn Gly Glu Cys Tyr Pro Asn Glu Lys Asn Ser Val Asn Met Asp  
 165 170 175  
 10 Leu Asp

15 <210> 678  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 678  
 20 Glu Asn Glu Met Ser Ser Glu Ala Asp Met Glu Cys Leu Asn Gln Arg  
 1 5 10 15  
 Pro Pro Glu Asn Pro Asp Thr Asp Lys Asn Val Gln Gln Asp Asn Ser  
 20 25 30  
 Glu Ala Gly Thr Gln Pro Gln Val Gln Thr Asp Ala Gln Gln Thr Ser  
 35 40 45  
 25 Gln Ser Pro Pro Ser Pro Glu Leu Thr Ser Glu Glu Asn Lys Ile Pro  
 50 55 60  
 Asp Ala Asp Lys Ala Asn Glu Lys Lys Val Asp Gln Pro Pro Glu Ala  
 65 70 75 80  
 Lys Lys Pro Lys Ile Lys Val Val Asn Val Glu Leu Pro Ile Glu Ala  
 85 90 95  
 30 Asn Leu Val Trp Gln Leu Gly Lys Asp Leu Leu Asn Met Tyr Ile Glu  
 100 105 110  
 Thr Glu Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn  
 115 120 125  
 35 Asp Ala Lys Asn Ala Val Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys  
 130 135 140  
 Leu Cys Gly Pro Tyr Glu Lys Phe Ile Cys Glu Gln Asp His Gln Asn  
 145 150 155 160  
 Phe Leu Arg Leu Leu Thr Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly  
 165 170 175  
 40 Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp Lys Leu Glu Glu Leu Met  
 180 185 190  
 Lys Ile Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Arg Thr  
 195 200 205  
 45 Ala Gln Lys Cys Leu Lys Asn  
 210 215

50 <210> 679  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 679  
 55 Ser Asp Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile Gly Arg Phe  
 1 5 10 15  
 Val Val Gln Asn Val Ser Ala Gln Lys Asp Gly Glu Lys Ser Arg Val  
 20 25 30  
 Lys Val Lys Val Arg Val Asn Thr His Gly Ile Phe Thr Ile Ser Thr  
 35 40 45  
 60 Ala Ser Met Val Glu Lys Val Pro Thr Glu Glu Asn Glu Met Ser Ser  
 50 55 60  
 Glu Ala Asp Met Glu Cys Leu Asn Gln Arg Pro Pro Glu Asn Pro Asp  
 65 70 75 80

Thr Asp Lys Asn Val Gln Gln Asp Asn Ser Glu Ala Gly Thr Gln Pro  
 85 90 95  
 Gln Val Gln Thr Asp Ala Gln Gln Thr Ser Gln Ser Pro Pro Ser Pro  
 100 105 110  
 5 Glu Leu Thr Ser Glu Glu Asn Lys Ile Pro Asp Ala Asp Lys Ala Asn  
 115 120 125  
 Glu Lys Lys Val Asp Gln Pro Pro Glu Ala Lys Lys Pro Lys Ile Lys  
 130 135 140  
 Val Val Asn Val Glu Leu Pro Ile Glu Ala Asn Leu Val Trp Gln Leu  
 145 150 155 160  
 10 Gly Lys Asp Leu Leu Asn Met Tyr Ile Glu Thr Glu Gly Lys Met Ile  
 165 170 175  
 Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val  
 180 185 190  
 15 Glu Glu Tyr Val Tyr Glu Phe Arg Asp Lys Leu Cys Gly Pro Tyr Glu  
 195 200 205  
 Lys Phe Ile Cys Glu Gln Asp His Gln Lys Phe Phe Glu Asp Ser Ser  
 210 215 220  
 Gln Lys Thr Gly Arg Thr Gly Leu Phe  
 225 230  
 20  
 <210> 680  
 <211> 471  
 <212> PRT  
 25 <213> Homo sapiens  
 <400> 680  
 Leu Asp Met Ala Pro Glu Ile Asn Leu Pro Gly Pro Met Ser Leu Ile  
 1 5 10 15  
 30 Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro Glu Ala Leu Lys Ile  
 20 25 30  
 Leu Ser Ala Ile Thr Gln Pro Val Val Val Ala Ile Val Gly Leu  
 35 35 40 45  
 Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys  
 50 55 60  
 Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser His Thr Lys Gly Ile  
 65 70 75 80  
 Trp Met Trp Xaa Val Pro His Pro Lys Lys Pro Glu His Thr Leu Val  
 85 90 95  
 40 Leu Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu Lys Gly Asp Asn Glu  
 100 105 110  
 Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu Leu Ser Ser Thr Phe  
 115 120 125  
 Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu  
 130 135 140  
 45 His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys Ala Asn Ser Ser Pro  
 145 150 155 160  
 Gly Asn Asn Ser Val Asp Asp Ser Ala Asp Phe Val Ser Phe Phe Pro  
 165 170 175  
 50 Ala Phe Val Trp Thr Leu Arg Asp Phe Thr Leu Glu Leu Glu Val Asp  
 180 185 190  
 Gly Glu Pro Ile Thr Ala Asp Asp Tyr Leu Glu Leu Ser Leu Lys Leu  
 195 200 205  
 Arg Lys Gly Thr Asp Lys Lys Ser Lys Ser Phe Asn Asp Pro Arg Leu  
 210 215 220  
 55 Cys Ile Arg Lys Phe Phe Pro Lys Arg Lys Cys Phe Val Phe Asp Trp  
 225 230 235 240  
 Pro Ala Pro Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu  
 245 250 255  
 60 Glu Leu Asn Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr  
 260 265 270  
 Ile Leu Ser His Ser Asn Val Lys Thr Leu Ser Gly Gly Ile Ala Val  
 275 280 285  
 245

Asn Gly Pro Arg Leu Glu Ser Leu Val Leu Thr Tyr Val Asn Ala Ile  
 290 295 300  
 Ser Ser Gly Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala  
 305 310 315 320  
 5 Gln Ile Glu Asn Ser Ala Ala Val Glu Lys Ala Ile Ala His Tyr Glu  
 325 330 335  
 Gln Gln Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu Gln Glu  
 340 345 350  
 10 Leu Leu Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu Val Phe  
 355 360 365  
 Met Lys Asn Ser Phe Lys Asp Val Asp Gln Met Phe Gln Arg Lys Leu  
 370 375 380  
 Gly Ala Gln Leu Glu Ala Arg Arg Asp Asp Phe Cys Lys Gln Asn Ser  
 385 390 395 400  
 15 Lys Ala Ser Ser Asp Cys Cys Met Ala Leu Leu Gln Asp Ile Phe Gly  
 405 410 415  
 Pro Leu Glu Glu Asp Val Lys Gln Gly Thr Phe Ser Lys Pro Gly Gly  
 420 425 430  
 20 Tyr Arg Leu Phe Thr Gln Lys Leu Gln Glu Leu Lys Asn Lys Ser Thr  
 435 440 445  
 Arg Ala Lys Glu Gly Asp Thr Gly Gln Arg Gly Ala Glu Lys Ile Phe  
 450 455 460  
 Gly Val Gln Gly Gly Cys Gly  
 465 470  
 25  
 <210> 681  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens  
 30  
 <400> 681  
 Leu Asp Met Ala Pro Glu Ile Asn Leu Pro Gly Pro Met Ser Leu Ile  
 1 5 10 15  
 35 Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro Glu Ala Leu Lys Ile  
 20 25 30  
 Leu Ser Ala Ile Thr Gln Pro Val Val Val Val Ala Ile Val Gly Leu  
 35 40 45  
 Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys  
 50 55 60  
 40 Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser His Thr Lys Gly Ile  
 65 70 75 80  
 Trp Met Trp Xaa Val Pro His Pro Lys Lys Pro Glu His Thr Leu Val  
 85 90 95  
 45 Leu Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu Lys Gly Asp Asn Glu  
 100 105 110  
 Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu Leu Ser Ser Thr Phe  
 115 120 125  
 Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu  
 130 135 140  
 50 His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys Ala Asn Xaa Ser Pro  
 145 150 155 160  
 Gly Asn Asn Ser Val Asp Asp Ser Xaa Asp Phe Val Ser Phe Phe Pro  
 165 170 175  
 55 Ala Phe Val Trp Thr Leu Lys Xaa Phe Thr Leu Glu Leu Gly Ser Arg  
 180 185 190  
 Trp Arg Thr His His Cys  
 195  
 60  
 <210> 682  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 682  
 Ser Pro Gly Ala Lys Gly Arg Gly Tyr Lys Ala Lys Glu Val Xaa Lys  
 1 5 10 15  
 Lys Tyr Leu Glu Ser Lys Xaa Asp Val Ala Asp Ala Leu Leu Gln Thr  
 20 25 30  
 Asp Gln Ser Leu Ser Glu Lys Glu Lys Ala Ile Glu Val Glu Arg Ile  
 35 40 45  
 Lys Ala Glu Ser Ala Glu Ala Ala Lys Lys Met Leu Glu Glu Ile Xaa  
 50 55 60  
 Lys Lys Asn Glu Glu Met Met Glu Gln Lys Glu Lys Ser Tyr Gln Glu  
 65 70 75 80  
 His Val Lys Gln Leu Thr Glu Lys Met Glu Arg Asp Arg Ala Gln Leu  
 85 90 95  
 Met Ala Glu Gln Glu Lys Thr Leu Ala Leu Lys Leu Gln Glu Gln Glu  
 100 105 110  
 Arg Leu Leu Lys Glu Gly Phe Glu Asn Glu Ser Lys Arg Leu Gln Lys  
 115 120 125  
 Asp Ile Trp Asp Ile Gln Met Arg Ser Lys Ser Leu Glu Pro Ile Cys  
 130 135 140  
 Asn Ile Leu  
 145

<210> 683  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 683  
 Glu Arg Gly Ser Ser Leu Ala Leu Pro Leu Thr Gly Pro Cys Pro Ser  
 1 5 10 15  
 Pro Ser Ser Gln Ser Ile Val Ser His Val Pro Asp Asn Ser Ser Leu  
 20 25 30  
 Ser Val Pro Ser Ser Pro His Ser Ser Xaa Val Phe Pro Pro Thr Phe  
 35 40 45  
 Ser Leu Gln Leu Leu Gln Ile Gln Pro Leu Tyr Val Pro Leu Gln Ser  
 50 55 60  
 Leu Phe Pro Phe Leu Arg Val Thr Asp Gln Ser Val Glu Val His Gln  
 65 70 75 80  
 Pro His Pro Xaa Trp Thr Pro Asn Ile Phe Ser Xaa Pro Leu Trp Pro  
 85 90 95  
 Cys Ile Pro Phe Leu Trp His Leu Gly  
 100 105

<210> 684  
 <211> 274  
 <212> PRT  
 <213> Homo sapiens

<400> 684  
 Ile Leu Leu Ser Ser Thr Phe Val Tyr Asn Ser Met Gly Thr Ile Asn  
 1 5 10 15  
 Gln Gln Ala Met Asp Gln Leu His Tyr Val Thr Glu Leu Thr Asp Arg  
 20 25 30  
 Ile Lys Ala Asn Ser Ser Pro Gly Asn Asn Ser Val Asp Asp Ser Ala  
 35 40 45  
 Asp Phe Val Ser Phe Phe Pro Ala Phe Val Trp Thr Leu Arg Asp Phe  
 50 55 60  
 Thr Leu Glu Leu Glu Val Asp Gly Glu Pro Ile Thr Ala Asp Asp Tyr  
 65 70 75 80  
 Leu Glu Leu Ser Leu Lys Leu Arg Lys Gly Thr Asp Lys Lys Ser Lys  
 85 90 95  
 Ser Phe Asn Asp Pro Arg Leu Cys Ile Arg Lys Phe Phe Pro Lys Arg  
 100 105 110

Lys Cys Phe Val Phe Asp Trp Pro Ala Pro Lys Lys Tyr Leu Ala His  
           115                  120          125  
 Leu Glu Gln Leu Lys Glu Glu Leu Asn Pro Asp Phe Ile Glu Gln  
       130                  135          140  
 5 Val Ala Glu Phe Cys Ser Tyr Ile Leu Ser His Ser Asn Val Lys Thr  
    145                  150          155          160  
 Leu Ser Gly Gly Ile Ala Val Asn Gly Pro Arg Leu Glu Ser Leu Val  
                   165          170          175  
 Leu Thr Tyr Val Asn Ala Ile Gly Ser Gly Asp Leu Pro Cys Met Glu  
 10                  180          185          190  
 Asn Ala Val Leu Ala Leu Ala Gln Ile Glu Glu Leu Ser Pro Gln Xaa  
       195                  200          205  
 Lys Arg Leu Leu Xaa Thr Tyr Glu Gln Gln Asp Gly Ala Arg Arg Gly  
       210                  215          220  
 15 Ser Cys Pro Pro Glu Thr Leu Pro Gly Ala Xaa Gly Thr Cys Xaa Xaa  
    225                  230          235          240  
 Thr Val Arg Lys Xaa Ala Ile Glu Val Phe Ile Glu Xaa Thr Phe Phe  
                   245          250          255  
 Lys Asp Val Gly Pro Asn Gly Ser Lys Xaa Lys Leu Gly Gly Pro Ile  
 20                  260          265          270  
 Trp Glu

25       <210> 685  
           <211> 120  
           <212> PRT  
           <213> Homo sapiens

          <400> 685  
 30 Cys Thr Xaa Thr Ala Asp Gln Xaa Leu Ser Glu Lys Glu Lys Ala Ile  
    1                  5          10          15  
 Glu Val Glu Arg Ile Lys Val Xaa Ser Ala Glu Ala Ala Lys Lys Met  
       20                  25          30  
 Leu Glu Glu Ile Gln Lys Lys Asn Glu Glu Met Met Asp Gln Lys Glu  
 35                  35          40          45  
 Lys Xaa Tyr Gln Glu His Val Xaa Gln Leu Xaa Xaa Xaa Met Xaa Arg  
    50                  55          60  
 Xaa Arg Ala Gln Leu Met Ala Glu Gln Xaa Lys Pro Leu Xaa Xaa Lys  
    65                  70          75          80  
 40 Leu Gln Glu Gln Glu Xaa Leu Xaa Lys Glu Gly Xaa Glu Asn Glu Ser  
                   85          90          95  
 Lys Arg Xaa Gln Lys Asp Ile Trp Asp Ile Gln Met Arg Ser Lys Ser  
       100                  105          110  
 Leu Glu Pro Ile Cys Asn Ile Leu  
 45          115          120

50       <210> 686  
           <211> 205  
           <212> PRT  
           <213> Homo sapiens

          <400> 686  
 Pro Met Ser Leu Ile Asp Asn Thr Lys Gly Gln Leu Val Val Asn Pro  
    1                  5          10          15  
 55 Glu Ala Leu Lys Ile Leu Ser Ala Ile Thr Gln Pro Val Val Val  
       20                  25          30  
 Ala Ile Val Gly Leu Tyr Arg Thr Gly Lys Ser Tyr Leu Met Asn Lys  
    35                  40          45  
 Leu Ala Gly Lys Lys Asn Gly Phe Ser Leu Gly Ser Thr Val Lys Ser  
    50                  55          60  
 60 His Thr Lys Gly Ile Trp Met Trp Cys Val Pro His Pro Lys Lys Pro  
    65                  70          75          80  
 Glu His Thr Leu Val Leu Leu Asp Thr Glu Gly Leu Gly Asp Ile Glu

85 90 95  
 Lys Gly Asp Asn Glu Asn Asp Ser Trp Ile Phe Ala Leu Ala Ile Leu  
 100 105 110  
 5 Leu Ser Ser Thr Phe Val Tyr Asn Ser Met Gly Thr Ile Asn Gln Gln  
 115 120 125  
 Ala Met Asp Gln Leu His Tyr Val Thr Glu Leu Thr Asp Arg Ile Lys  
 130 135 140  
 Ala Asn Ser Ser Pro Gly Asn Asn Ser Val Asp Asp Ser Ala Asp Phe  
 145 150 155 160  
 10 Val Ser Phe Phe Pro Ala Phe Val Trp Thr Leu Arg Asp Phe Thr Leu  
 165 170 175  
 Glu Leu Glu Val Asp Gly Glu Pro Ile Thr Ala Asp Asp Tyr Leu Glu  
 180 185 190  
 15 Leu Ser Leu Lys Leu Arg Lys Gly Thr Asp Lys Glu Lys  
 195 200 205  
  
 <210> 687  
 <211> 111  
 <212> PRT  
 20 <213> Homo sapiens  
  
 <400> 687  
 Lys Arg Leu Ser Thr Gly Thr Ile Phe Leu Thr Gln Glu Val Pro Val  
 1 5 10 15  
 25 Xaa Xaa Ser Lys Cys Arg Ser Xaa Arg Ile Ser Xaa Pro Arg Val Pro  
 20 25 30  
 Lys Glu Gly Asp Thr Gly Asn Leu Pro Ala Lys Glu Val Xaa Lys Asn  
 35 40 45  
 30 Ile Trp Ser Pro Arg Xaa Met Gly Xaa Cys Thr Xaa Thr Asp Cys Gln  
 50 55 60  
 Ser Leu Phe Lys Lys Glu Lys Ala Ile Glu Val Asp Gly Ile Lys Ala  
 65 70 75 80  
 Glu Phe Ala Glu Ala Lys Lys Met Leu Glu Glu Xaa Gln Lys Lys  
 85 90 95  
 35 Asn Glu Glu Met Met Ala Arg Lys Arg Arg Val Ile Arg Asn Met  
 100 105 110  
  
 <210> 688  
 <211> 115  
 40 <212> PRT  
 <213> Homo sapiens  
  
 <400> 688  
 Lys Val Thr Asp Ser Leu Xaa Lys Cys Ile Xaa Pro Xaa Ser Leu Asp  
 1 5 10 15  
 45 Ser Lys Tyr Phe Phe Xaa Pro Leu Trp Pro Gly Gly Tyr Leu Tyr Pro  
 20 25 30  
 Leu Pro Trp Ala Pro Trp Xaa Asp Leu Phe Xaa Ser Ser Cys Thr Leu  
 35 40 45  
 50 Xaa Lys Xaa Pro Glu Pro Pro Gly Leu Lys Lys Trp Ser Leu Leu Thr  
 50 55 60  
 Ile Phe Phe Lys Arg Ala Gln Xaa Xaa Leu Glu Val Lys Xaa Cys His  
 65 70 75 80  
 Lys Ser Asp Asp Ala Phe Gly Ile Leu Leu Thr Lys Xaa Ile Xaa Pro  
 85 90 95  
 55 Leu Val Xaa Thr Gly Ala Leu Asn Ser Xaa Gly Gln Xaa Gly Pro His  
 100 105 110  
 Pro Trp Lys  
 115  
 60  
  
 <210> 689  
 <211> 133  
 <212> PRT





<211> 194  
 <212> PRT  
 <213> Homo sapiens

5       <400> 692  
 Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu Glu Leu Asn  
   1                  5                  10                  15  
 Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr Ile Leu Ser  
                   20                  25                  30  
 10 His Ser Asn Val Lys Thr Leu Ser Gly Leu Glu Ser Leu Val Leu Thr  
                   35                  40                  45  
 Tyr Val Asn Ala Ile Ser Ser Gly Asp Leu Pro Cys Met Glu Asn Ala  
   50                  55                  60  
 Val Leu Ala Leu Ala Gln Ile Glu Asn Ser Ala Ala Val Glu Lys Ala  
 15 65                  70                  75                  80  
 Ile Ala His Tyr Glu Gln Gln Met Gly Gln Lys Val Gln Leu Pro Thr  
                   85                  90                  95  
 Glu Thr Leu Gln Glu Leu Leu Asp Leu His Arg Asp Ser Glu Arg Glu  
                   100                  105                  110  
 20 Ala Ile Glu Val Phe Met Lys Asn Ser Phe Lys Asp Val Asp Gln Met  
                   115                  120                  125  
 Phe Gln Arg Lys Leu Gly Ala Gln Leu Glu Ala Arg Arg Asp Asp Phe  
   130                  135                  140  
 Cys Lys Gln Asn Ser Lys Ala Ser Ser Asp Cys Cys Met Ala Leu Leu  
 25 145                  150                  155                  160  
 Gln Asp Ile Phe Gly Pro Leu Glu Glu Asp Val Lys Gln Gly Thr Phe  
                   165                  170                  175  
 Ser Lys Pro Gly Gly Tyr Arg Leu Phe Thr Gln Lys Leu Gln Gly Ala  
                   180                  185                  190  
 30 Glu Glu

<210> 693  
 <211> 130  
 35 <212> PRT  
 <213> Homo sapiens

      <400> 693  
 Pro Pro Gly Asn Xaa Pro Glu Val Val Ala Leu Xaa Arg Ala Ser Lys  
 40 1                  5                  10                  15  
 Lys Gly Xaa Xaa Ser Xaa Asn Lys Asp Phe Phe Lys Xaa Gly Pro Lys  
                   20                  25                  30  
 Cys Ser Arg Glu Ile Arg Gly Pro Val Glu Ala Xaa Arg Asn Xaa Phe  
                   35                  40                  45  
 45 Cys Ser Gln Ile Pro Lys Leu Ile Arg Leu Trp Xaa Gly Phe Thr Ser  
   50                  55                  60  
 Arg Ile Tyr Trp Ala Xaa Xaa Lys Lys Met Ser Ser Arg Glu His Phe  
 65                  70                  75                  80  
 Leu Asn Pro Glu Gly Ser Gly Phe Phe Thr Gln Lys Leu Gln Glu Leu  
 50                  85                  90                  95  
 Lys Asn Lys Ser Thr Arg Ala Lys Lys Gly Ile Gln Ala Lys Glu Val  
                   100                  105                  110  
 Leu Lys Lys Tyr Leu Glu Ser Lys Glu Asp Val Ala Asp Ala Leu Leu  
   115                  120                  125  
 55 Gln Thr  
   130

<210> 694  
 <211> 89  
 60 <212> PRT  
 <213> Homo sapiens

<400> 694

Val Lys Lys Pro Glu Pro Ser Gly Leu Arg Lys Cys Ser Leu Leu Asp  
 1 5 10 15  
 Ile Phe Xaa Xaa Xaa Ala Gln Tyr Ile Leu Glu Val Lys Xaa Cys His  
 20 25 30  
 5 Asn Leu Met Ser Phe Gly Ile Trp Leu Gln Lys Xaa Phe Xaa Leu Ala  
 35 40 45  
 Ser Thr Gly Pro Leu Ile Ser Leu Glu His Leu Gly Pro Xaa Leu Lys  
 50 55 60  
 Lys Ser Leu Leu Xaa Leu Xaa Xaa Pro Phe Leu Leu Ala Leu Xaa Arg  
 10 65 70 75 80  
 Ala Thr Thr Ser Gly Xaa Phe Pro Gly  
 85

15 <210> 695  
 <211> 203  
 <212> PRT  
 <213> Homo sapiens

<400> 695  
 20 Pro Lys Lys Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu Glu Leu  
 1 5 10 15  
 Asn Pro Asp Phe Ile Glu Gln Val Ala Glu Phe Cys Ser Tyr Ile Leu  
 20 25 30  
 Ser His Ser Asn Val Lys Thr Leu Ser Gly Gly Ile Pro Val Asn Gly  
 35 40 45  
 25 Pro Arg Leu Glu Ser Leu Val Leu Thr Tyr Val Asn Ala Ile Ser Ser  
 50 55 60  
 Gly Asp Leu Pro Cys Met Glu Asn Ala Val Leu Ala Leu Ala Gln Ile  
 65 70 75 80  
 30 Glu Asn Ser Ala Ala Val Glu Lys Ala Ile Ala His Tyr Glu Gln Gln  
 85 90 95  
 Met Gly Gln Lys Val Gln Leu Pro Thr Glu Thr Leu Gln Glu Leu Leu  
 100 105 110  
 Asp Leu His Arg Asp Ser Glu Arg Glu Ala Ile Glu Val Phe Met Lys  
 35 115 120 125  
 Asn Ser Phe Lys Asp Val Asp Gln Met Phe Gln Arg Lys Leu Gly Ala  
 130 135 140  
 Gln Leu Glu Ala Arg Arg Asp Asp Phe Cys Lys Gln Asn Ser Lys Ala  
 145 150 155 160  
 40 Ser Ser Asp Cys Cys Met Ala Leu Leu Gln Asp Ile Phe Gly Pro Leu  
 165 170 175  
 Glu Glu Asp Val Lys Gln Gly Thr Phe Ser Lys Pro Gly Gly Tyr Arg  
 180 185 190  
 Leu Phe Thr Gln Lys Leu Ala Gly Ala Glu Glu  
 45 195 200

<210> 696  
 <211> 159  
 <212> PRT  
 50 <213> Homo sapiens

<400> 696  
 Gly Thr Ile Asn Gln Gln Ala Met Asp Gln Leu His Tyr Val Thr Glu  
 1 5 10 15  
 55 Leu Thr Asp Arg Ile Lys Ala Asn Ser Ser Pro Gly Asn Asn Ser Val  
 20 25 30  
 Asp Asp Ser Ala Asp Phe Val Ser Phe Phe Pro Ala Phe Val Trp Thr  
 35 40 45  
 Leu Arg Asp Phe Thr Leu Glu Leu Glu Val Asp Gly Glu Pro Ile Thr  
 60 50 55 60  
 Ala Asp Asp Tyr Leu Glu Leu Ser Leu Lys Leu Arg Lys Gly Thr Asp  
 65 70 75 80  
 Xaa Lys Ser Lys Ser Phe Asn Asp Pro Arg Leu Cys Ile Arg Lys Phe

85 90 95  
 Phe Pro Lys Arg Lys Cys Phe Val Phe Asp Trp Pro Ala Pro Lys Lys  
 100 105 110  
 Tyr Leu Ala His Leu Glu Gln Leu Lys Glu Glu Glu Leu Asn Pro Asp  
 115 120 125  
 Phe Ile Glu Gln Xaa Ala Glu Phe Cys Ser Tyr Ile Leu Xaa Xaa Ser  
 130 135 140  
 Asn Val Lys Thr Leu Ser Gly Xaa Ile Pro Ala Met Gly Leu Val  
 145 150 155

10

<210> 697  
 <211> 194  
 <212> PRT  
 <213> Homo sapiens

15

<400> 697  
 Tyr Gly Gln Gly Ile Asn Pro Ile Ser Arg Leu Ala Gln Ile Gln Gln  
 1 5 10 15  
 Ala Lys Lys Glu Lys Glu Pro Glu Tyr Thr Leu Leu Thr Glu Arg Gly  
 20 20 25 30  
 Leu Pro Arg Arg Arg Glu Phe Val Met Gln Val Lys Val Gly Asn His  
 35 40 45  
 Thr Ala Glu Gly Thr Gly Thr Asn Lys Lys Val Ala Lys Arg Asn Ala  
 50 55 60  
 Ala Glu Asn Met Leu Glu Ile Leu Gly Phe Lys Val Pro Gln Ala Gln  
 25 65 70 75 80  
 Pro Thr Lys Pro Ala Leu Lys Ser Glu Glu Lys Thr Pro Ile Lys Lys  
 85 90 95  
 Pro Gly Asp Gly Arg Lys Val Thr Phe Phe Glu Pro Gly Ser Gly Asp  
 30 100 105 110  
 Glu Asn Gly Thr Ser Asn Lys Glu Asp Glu Phe Arg Met Pro Tyr Leu  
 115 120 125  
 Ser His Gln Gln Leu Pro Ala Gly Ile Leu Pro Met Val Pro Glu Val  
 130 135 140  
 Ala Gln Ala Val Gly Val Ser Gln Gly His His Thr Lys Asp Phe Thr  
 35 145 150 155 160  
 Arg Ala Ala Pro Asn Pro Ala Lys Ala Thr Val Thr Ala Met Ile Ala  
 165 170 175  
 Arg Glu Leu Leu Tyr Gly Gly Thr Ser Pro Thr Ala Glu Thr Ile Leu  
 40 180 185 190  
 Lys Glu

45

<210> 698  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 698  
 Gln Tyr Arg Ala Leu Trp Lys Ile Thr Leu Gln Val Tyr Met Asp Tyr  
 1 5 10 15  
 Met Glu Ile Ile Ser Cys Ser Val Val Lys Ala Lys Ser Ser Arg Ala  
 20 25 30  
 Ile Cys Ile Asp Thr Gln Cys Phe Leu Ile Ile Phe Lys Thr Glu Ile  
 35 40 45  
 Lys Val His Leu Ser Pro Val Cys Ile Asn Lys Asn Lys Asn Glu Ile  
 50 55 60  
 Lys Met Glu Pro Asn Asp His Leu Lys Phe Lys Ile Pro Lys Leu Ser  
 65 70 75 80  
 Asn Leu Tyr Asn Cys Gly Arg Leu Ile Gln Gly Phe  
 85 90

&lt;210&gt; 699

<211> 395  
 <212> PRT  
 <213> Homo sapiens

5           <400> 699  
 His Lys Ser Asp Leu Pro Ala Phe Ser Ala Glu Val Glu Glu Glu Ser  
   1                   5                   10                   15  
 Glu Ala Gly Lys Glu Ser Glu Glu Thr Glu Thr Lys Gln Thr Leu Lys  
           20                   25                   30  
 10 Glu Phe Arg Cys Gln Val Ser Asp Cys Ser Arg Ile Phe Gln Ala Ile  
           35                   40                   45  
 Thr Gly Leu Ile Gln His Tyr Met Lys Leu His Glu Met Thr Pro Glu  
           50                   55                   60  
 Glu Ile Glu Ser Met Thr Ala Ser Val Asp Val Gly Lys Phe Pro Cys  
 15 65                   70                   75                   80  
 Asp Gln Leu Glu Cys Lys Ser Ser Phe Thr Thr Tyr Leu Asn Tyr Val  
           85                   90                   95  
 Val His Leu Glu Ala Asp His Gly Ile Gly Leu Arg Ala Ser Lys Thr  
           100                   105                   110  
 20 Glu Glu Asp Gly Val Tyr Lys Cys Asp Cys Glu Gly Cys Asp Arg Ile  
           115                   120                   125  
 Tyr Ala Thr Arg Ser Asn Leu Leu Arg His Ile Phe Asn Lys His Asn  
           130                   135                   140  
 Asp Lys His Lys Ala His Leu Ile Arg Pro Arg Arg Leu Thr Pro Gly  
 25 145                   150                   155                   160  
 Gln Glu Asn Met Ser Ser Lys Ala Asn Gln Glu Lys Ser Lys Ser Lys  
           165                   170                   175  
 His Arg Gly Thr Lys His Ser Arg Cys Gly Lys Glu Gly Ile Lys Met  
           180                   185                   190  
 30 Pro Lys Thr Lys Arg Lys Lys Lys Asn Asn Leu Glu Asn Lys Asn Ala  
           195                   200                   205  
 Lys Ile Val Gln Ile Glu Glu Asn Lys Pro Tyr Ser Leu Lys Arg Gly  
           210                   215                   220  
 Lys His Val Tyr Ser Ile Lys Ala Arg Asn Asp Ala Leu Ser Glu Cys  
 35 225                   230                   235                   240  
 Thr Ser Arg Phe Val Thr Gln Tyr Pro Cys Met Ile Lys Gly Cys Thr  
           245                   250                   255  
 Ser Val Val Thr Ser Glu Ser Asn Ile Ile Arg His Tyr Lys Cys His  
           260                   265                   270  
 40 Lys Leu Ser Lys Ala Phe Thr Ser Gln His Arg Asn Leu Leu Ile Val  
           275                   280                   285  
 Phe Lys Arg Cys Cys Asn Ser Gln Val Lys Glu Thr Ser Glu Gln Glu  
           290                   295                   300  
 Gly Ala Lys Asn Asp Val Lys Asp Ser Asp Thr Cys Val Ser Glu Ser  
 45 305                   310                   315                   320  
 Asn Asp Asn Ser Arg Thr Thr Ala Thr Val Ser Gln Lys Glu Val Glu  
           325                   330                   335  
 Lys Asn Glu Lys Asp Glu Met Asp Glu Leu Thr Glu Leu Phe Ile Thr  
           340                   345                   350  
 50 Lys Leu Ile Asn Glu Asp Ser Thr Ser Val Glu Thr Gln Ala Asn Thr  
           355                   360                   365  
 Ser Ser Asn Val Ser Asn Asp Phe Gln Gly Arg Tyr Leu Cys Gln Ser  
           370                   375                   380  
 Glu Arg Gln Lys Ala Ser Asn Leu Lys Lys Ser  
 55 385                   390                   395

<210> 700  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

60           <400> 700  
 Lys Glu Gly Ile Lys Met Pro Lys Thr Lys Arg Lys Lys Lys Asn Asn

[illegible]

Ala Gly Phe Phe Phe Gly Phe Xaa Cys Arg Leu Xaa Lys Asn Phe Lys  
                   35                  40                  45  
 Lys Xaa Thr Ser Ile Pro Ile Gly Leu Lys Glu Leu Gln Ser Lys Lys  
                   50                  55                  60  
 5 Gln Asn Ala Pro Gln Trp Leu Asn Ala Asn Ser Ser Xaa Phe Phe Xaa  
    65                  70                  75                  80  
 Thr Ala Arg Tyr Leu Thr Gln Leu Leu Met Leu Val Gln Leu Phe Gln  
                   85                  90                  95  
 Leu Ser Phe Phe Tyr Phe Val Arg His Phe Phe Xaa Leu Leu Thr Leu  
 10 Leu Gln Ile Thr Gly Phe Leu Ser Phe Gly Leu Ala Glu Val Ser Ser  
                   100                  105                  110  
                   115                  120                  125  
 Leu Lys Ile Ile Thr Tyr Ile  
                   130                  135  
 15  
       <210> 703  
       <211> 135  
       <212> PRT  
       <213> Homo sapiens  
 20  
       <400> 703  
 Phe Pro Leu Val Thr Ala Val Leu Ser Ile Phe Phe Leu Glu Phe Glu  
    1                  5                  10                  15  
 Trp Asp Pro Phe Leu Phe Pro Val Phe Gly Trp Xaa Leu Gln Tyr Phe  
 25 Ser Ser Ala Ser Leu Gln Thr Pro Gln Glu Thr Ser Glu Met Ile Phe  
                   20                  25                  30  
                   35                  40                  45  
 Lys Ser His Trp Leu Lys Lys Ser Xaa Ser Gln Lys Asp Ala Arg Xaa  
    50                  55                  60  
 30 Ser Ser Met Gly Xaa Met Ala Pro Ala Val Ser Xaa Ser Leu Pro Xaa  
    65                  70                  75                  80  
 Xaa Leu Asn Ser Ala Xaa Gly Cys Trp Val Asn Leu Phe Gln Leu Phe  
                   85                  90                  95  
 Leu Phe Leu Phe Xaa Glu Xaa Xaa Phe Ser Leu Leu Thr Leu Phe Lys  
 35 Tyr Leu Ala Phe Trp Leu Ser Asp Trp Ala Xaa Gly Phe Xaa Pro Glu  
                   100                  105                  110  
                   115                  120                  125  
 Asn His Ser Leu His Leu Lys  
                   130                  135  
 40  
       <210> 704  
       <211> 123  
       <212> PRT  
       <213> Homo sapiens  
 45  
       <400> 704  
 Gly Val Cys Ser Glu Ala Glu Glu Lys Tyr Cys Lys Xaa His Pro Asn  
    1                  5                  10                  15  
 Thr Gly Asn Lys Lys Gly Ser His Ser Asn Ser Arg Lys Asn Ile Asp  
 50 Lys Thr Ala Val Thr Ser Gly Asn His Val Cys Pro Cys Lys Glu Ser  
                   20                  25                  30  
                   35                  40                  45  
 Glu Thr Phe Val Gln Phe Ala Asn Pro Ser Gln Leu Gln Cys Ser Asp  
    50                  55                  60  
 55 Asn Val Lys Ile Val Leu Asp Lys Asn Leu Lys Asp Cys Thr Glu Leu  
    65                  70                  75                  80  
 Val Leu Lys Gln Leu Gln Glu Met Lys Pro Thr Val Ser Leu Lys Lys  
                   85                  90                  95  
 Leu Glu Val His Ser Asn Asp Pro Asp Met Ser Val Met Lys Asp Ile  
 60 Ser Ile Gly Lys Ala Thr Gly Arg Gly Gln Tyr  
                   100                  105                  110  
                   115                  120

<210> 705  
 <211> 242  
 <212> PRT  
 <213> Homo sapiens

5

<400> 705  
 His Glu Met Thr Pro Glu Glu Ile Glu Ser Met Thr Ala Ser Val Asp  
 1 5 10 15  
 Val Gly Lys Phe Pro Cys Asp Gln Leu Glu Cys Lys Ser Ser Phe Thr  
 10 20 25 30  
 Thr Tyr Leu Asn Tyr Val Val His Leu Glu Ala Asp His Gly Ile Gly  
 35 40 45  
 Leu Arg Ala Ser Lys Thr Glu Glu Asp Gly Val Tyr Lys Cys Asp Cys  
 50 55 60  
 15 Glu Gly Cys Asp Arg Ile Tyr Ala Thr Arg Ser Asn Leu Leu Arg His  
 65 70 75 80  
 Ile Phe Asn Lys His Asn Asp Lys His Lys Ala His Leu Ile Arg Pro  
 85 90 95  
 Arg Arg Leu Thr Pro Gly Gln Glu Asn Met Ser Ser Lys Ala Asn Gln  
 100 105 110  
 20 Glu Lys Ser Lys Ser Lys His Arg Gly Thr Lys His Ser Arg Cys Gly  
 115 120 125  
 Lys Glu Gly Ile Lys Met Pro Lys Thr Lys Arg Lys Lys Lys Asn Asn  
 130 135 140  
 25 Leu Glu Asn Lys Asn Ala Lys Ile Val Gln Ile Glu Glu Asn Lys Pro  
 145 150 155 160  
 Tyr Ser Leu Lys Arg Gly Lys His Val Tyr Ser Ile Lys Ala Xaa Asn  
 165 170 175  
 Asp Ala Leu Ser Glu Cys Thr Ser Arg Phe Val Thr Gln Tyr Pro Cys  
 180 185 190  
 30 Met Ile Lys Gly Cys Thr Ser Val Val Thr Ser Glu Ser Asn Ile Ile  
 195 200 205  
 Arg His Tyr Lys Xaa His Lys Leu Ser Lys Ala Leu His His Thr Pro  
 210 215 220  
 35 Glu Xaa Xaa Leu Leu Phe Ser Asn Xaa Val Cys Thr Pro Ser Lys Gly  
 225 230 235 240  
 Asn Val

40

<210> 706  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

45

<400> 706  
 His Lys Ser Asp Leu Pro Ala Phe Ser Ala Glu Val Glu Glu Glu Ser  
 1 5 10 15  
 Glu Ala Gly Xaa Glu Ser Xaa Glu Thr Glu Thr Lys Gln Thr Leu Lys  
 20 25 30  
 50 Glu Phe Arg Cys Xaa Xaa Ser Asp Cys Ser Arg Ile Phe Gln Ala Ile  
 35 40 45  
 Thr Gly Leu Ile Gln His Tyr Met Lys Leu His Glu Met Thr Pro Glu  
 50 55 60  
 Glu Ile Glu Ser Met Thr Ala Ser Val Asp Val Gly Lys Phe Pro Cys  
 65 70 75 80  
 55 Asp Xaa Leu Glu Cys Lys Ser Ser Phe Thr Thr Tyr Leu Asn Tyr Val  
 85 90 95  
 Val His Leu Glu Ala Asp His Gly Ile Gly Leu Arg Ala Ser Lys Thr  
 100 105 110  
 60 Glu Glu Asp Gly Val Tyr Lys Cys Asp Cys Glu Gly Cys Asp Arg Ile  
 115 120 125  
 Tyr Ala Thr Arg Thr Asn Leu Arg Xaa Ile Phe Asn Lys His Asn  
 130 135 140

Asp Lys His Lys Ala His Leu Ile Arg Pro Arg Arg Leu Thr Pro Gly  
 145 150 155 160  
 Gln Glu Asn Met Xaa Ser Lys Ala Asn Gln Glu Lys Ser Lys Ser Lys  
 165 170 175  
 5 His Arg Gly Thr Lys His Xaa Lys Cys Gly Lys Glu Gly Ile Lys Met  
 180 185 190  
 Pro Arg Pro Thr Lys Glu Xaa Lys  
 195 200

10 <210> 707  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

15 <400> 707  
 Xaa Ser Tyr Arg Asn Xaa Gly Leu Gln Ile Leu Leu Gly His Ser Asp  
 1 5 10 15  
 Arg Ala Ser Phe Xaa Ser Leu Asn Arg Ile Xaa Met Leu Pro Thr Phe  
 20 25 30  
 Gln Lys Ile Arg Leu Ile Xaa Phe Gln Phe Ala Gln Ser Leu His Ser  
 35 40 45  
 Cys Phe Leu Asn Tyr Xaa Phe Ser Phe Val Gly Arg Gly Ile Phe Ile  
 50 55 60  
 Pro Ser Phe Pro His Xaa Leu Cys Leu Val Pro Arg Cys Leu Asp Phe  
 65 70 75 80  
 25 Asp Phe Ser Trp Phe Ala Leu Leu Xaa Ile Phe Ser Trp Pro Gly Val  
 85 90 95  
 Asn Leu Leu Gly Arg Ile Lys  
 100

30 <210> 708  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

35 <400> 708  
 Met Gly Ser Phe Phe Val Ser Ser Ile Arg Met Val Phe Ala Val Phe  
 1 5 10 15  
 Phe Phe Cys Phe Thr Xaa Asp Xaa Ser Arg Asn Phe Arg Asn Asp Leu  
 40 20 25 30  
 Gln Ile Pro Leu Gly Leu Lys Xaa Leu Gln Ser Lys Arg Cys Xaa Asp  
 35 40 45  
 Ala Pro His Xaa Leu Asn Gly Asn Ser Lys Phe Xaa Xaa Leu Tyr Xaa  
 50 55 60  
 45 Arg Tyr Leu Thr Xaa Leu Xaa Met Leu Xaa Gln Leu Phe Gln Leu Ser  
 65 70 75 80  
 Phe Phe Ile Xaa Xaa Asp Xaa Phe Xaa Phe Tyr Leu Ser Ser Asn Thr  
 85 90 95  
 Cys Phe Trp Leu Ser Asp Gly Arg Gly Phe Phe Arg Lys His Phe Phe  
 100 105 110  
 50 Xaa Leu Xaa Lys Phe Asn Leu Gly Xaa Ser Xaa Gly Leu Ser Xaa Leu  
 115 120 125  
 Leu Ile Trp Lys Lys Gln Ser  
 130 135

55 <210> 709  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

60 <400> 709  
 Ser Ser Lys Pro Ile Gly Leu Lys Glu Leu Gln Ser Lys Asp Ala Xaa  
 1 5 10 15



Cys Ser Ser Met Gly Glu Trp His Ser Ser Phe Phe Phe Phe Thr Xaa  
                   20                  25                  30  
 Arg Tyr Leu Thr Xaa Leu Leu Met Ala Gly Ser Thr Phe Ser Thr Phe  
                   35                  40                  45  
 5 Leu Phe Tyr Leu Gly Arg His Phe Phe Leu Ile Thr Leu Ser Lys Thr  
                   50                  55                  60  
 Ala Phe Gly  
   65  
  
 10           <210> 710  
               <211> 131  
               <212> PRT  
               <213> Homo sapiens  
  
 15           <400> 710  
 Arg Ser Phe Leu Lys Phe Leu Glu Xaa Ser Ala Val Lys Gln Lys Lys  
   1                  5                  10                  15  
 Asn Xaa Xaa Lys Xaa His Pro Asn Thr Gly Asn Lys Lys Gly Ser His  
                   20                  25                  30  
 20 Ser Asn Ser Arg Lys Asn Ile Asp Lys Thr Ala Val Thr Ser Gly Asn  
                   35                  40                  45  
 His Val Cys Pro Cys Lys Glu Ser Glu Thr Phe Val Gln Phe Ala Asn  
                   50                  55                  60  
 Pro Ser Gln Leu Gln Cys Ser Asp Asn Val Lys Ile Val Leu Xaa Lys  
   25                  65                  70                  75                  80  
 Asn Leu Lys Asp Cys Xaa Glu Leu Val Leu Lys Gln Leu Gln Glu Met  
                   85                  90                  95  
 Lys Pro Xaa Val Ser Leu Lys Lys Leu Glu Val His Ser Asn Asp Pro  
                   100                  105                  110  
 30 Asp Met Ser Val Met Lys Asp Ile Ser Ile Gly Lys Ala Thr Gly Arg  
                   115                  120                  125  
 Gly Gln Tyr  
   130  
  
 35           <210> 711  
               <211> 528  
               <212> PRT  
               <213> Homo sapiens  
  
 40           <400> 711  
 Lys Asn Arg Ser Ile Gly Ala Ala Ala Lys Ser Gln Val Ile Ser Asn  
   1                  5                  10                  15  
 Ala Lys Asn Thr Val Gln Gly Phe Lys Arg Phe His Gly Arg Ala Phe  
                   20                  25                  30  
 45 Ser Asp Pro Phe Val Glu Ala Glu Lys Ser Asn Leu Ala Tyr Asp Ile  
                   35                  40                  45  
 Val Gln Leu Pro Thr Gly Leu Thr Gly Ile Lys Val Thr Tyr Met Glu  
                   50                  55                  60  
 Glu Glu Arg Asn Phe Thr Thr Glu Gln Val Thr Ala Met Leu Leu Ser  
   50                  65                  70                  75                  80  
 Lys Leu Lys Glu Thr Ala Glu Ser Val Leu Lys Lys Pro Val Val Asp  
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 Cys Val Val Ser Val Pro Cys Phe Tyr Thr Asp Ala Glu Arg Arg Ser  
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 55 Val Met Asp Ala Thr Gln Ile Ala Gly Leu Asn Cys Leu Arg Leu Met  
                   115                  120                  125  
 Asn Glu Thr Thr Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp  
                   130                  135                  140  
 Leu Pro Ala Leu Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met  
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 Gly His Ser Ala Tyr Gln Val Ser Val Cys Ala Phe Asn Arg Gly Lys  
                   165                  170                  175  
 Leu Lys Val Leu Ala Thr Ala Phe Asp Thr Thr Leu Gly Gly Arg Lys

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10	Thr	Met	Asn	Arg	Gly	Lys	Phe	Leu	Glu	Met	Cys	Asn	Asp	Leu	Leu	Ala
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	Thr	Thr	Leu	Asn	Ala	Asp	Glu	Ala	Val	Thr	Arg	Gly	Cys	Ala	Leu	Gln
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20	Cys	Ala	Ile	Leu	Ser	Pro	Ala	Phe	Lys	Val	Arg	Glu	Phe	Ser	Ile	Thr
				340					345					350		
	Asp	Val	Val	Pro	Tyr	Pro	Ile	Ser	Leu	Arg	Trp	Asn	Ser	Pro	Xaa	Glu
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	Glu	Gly	Ser	Ser	Asp	Cys	Glu	Val	Phe	Ser	Lys	Asn	His	Ala	Ala	Pro
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	Ala	Tyr	Tyr	Ser	Ser	Pro	Gln	Asp	Leu	Pro	Tyr	Pro	Asp	Pro	Ala	Ile
				405					410						415	
30	Ala	Gln	Phe	Ser	Val	Gln	Lys	Val	Thr	Pro	Gln	Ser	Asp	Gly	Ser	Ser
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	Ser	Lys	Val	Lys	Val	Lys	Val	Arg	Val	Asn	Val	His	Gly	Ile	Phe	Ser
			435					440					445			
	Val	Ser	Ser	Ala	Ser	Leu	Val	Glu	Val	His	Lys	Ser	Glu	Glu	Asn	Glu
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			465				470				475					480
	Val	Asp	Gln	Glu	Glu	Pro	His	Val	Glu	Glu	Gln	Gln	Gln	Gln	Thr	Pro
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			20						25					30		
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			35					40					45			
	Val	Gln	Lys	Val	Thr	Pro	Gln	Ser	Asp	Gly	Ser	Ser	Ser	Lys	Val	Lys
			50				55					60				
	Val	Lys	Val	Arg	Val	Asn	Val	His	Gly	Ile	Phe	Ser	Val	Ser	Ser	Ala
60			65				70				75					80
	Ser	Leu	Val	Glu	Val	His	Lys	Ser	Glu	Glu	Asn	Glu	Glu	Pro	Met	Glu
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	Thr	Asp	Gln	Asn	Ala	Lys	Glu	Glu	Glu	Lys	Met	Gln	Val	Asp	Gln	Glu
								260								

100 105 110  
 Glu Pro His Val Glu Glu Gln Gln Gln Thr Pro Ala Glu Asn Lys  
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 Ser Ser Phe Lys Asn Lys Glu Asp Gln Tyr Asp His Leu Asp Ala Ala  
 35 40 45  
 Asp Met Thr Lys Val Glu Lys Ser Thr Asn Glu Ala Met Glu Trp Met  
 50 55 60  
 Asn Asn Lys Leu Asn Leu Gln Asn Lys Gln Ser Leu Thr Met Asp Pro  
 65 70 75 80  
 25 Val Val Lys Ser Lys Glu Ile Glu Ala Lys Ile Lys Glu Leu Thr Ser  
 85 90 95  
 Thr Cys Ser Pro Ile Ile Ser Lys Pro Lys Pro Lys Val Glu Pro Pro  
 100 105 110  
 Lys Glu Gly Xaa Lys Met Xaa Xaa Arg Xaa Ala Xaa Trp Met Asp Lys  
 115 120 125  
 30 Glu Thr Thr Gln Ala Pro Arg Xaa Xaa Ser Arg Val Gln Thr Gln Leu  
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 Glu Thr Thr Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp Leu  
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 50 Pro Ala Leu Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met Gly  
 50 55 60  
 His Ser Ala Tyr Gln Val Ser Val Cys Ala Phe Asn Arg Gly Lys Leu  
 65 70 75 80  
 Lys Val Leu Ala Thr Ala Phe Asp Thr Thr Leu Gly Gly Arg Lys Phe  
 85 90 95  
 55 Asp Glu Val Leu Val Asn His Phe Cys Glu Glu Phe Gly Lys Lys Tyr  
 100 105 110  
 Lys Leu Asp Ile Lys Ser Lys Ile Arg Ala Leu Leu Arg Leu Ser Gln  
 115 120 125  
 60 Glu Cys Glu Lys Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp Leu  
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 Pro Leu Ser Ile Glu Cys Phe Met Asn Asp Val Asp Val Ser Gly Thr  
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Met Asn Arg Gly Lys Phe Leu Glu Met Cys Asn Asp Leu Leu Ala Arg  
 165 170 175  
 Val Glu Pro Pro Leu Arg Ser Val Leu Glu Gln Thr Lys Leu Lys Lys  
 180 185 190  
 5 Glu Asp Ile Tyr Ala Val Glu Ile Val Gly Gly Ala Thr Arg Ile Pro  
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 Ser Asp Pro Phe Val Glu Ala Glu Lys Ser Asn Leu Ala Tyr Asp Ile  
 35 40 45  
 Val Gln Leu Pro Thr Gly Leu Thr Gly Ile Lys Val Thr Tyr Met Glu  
 50 55 60  
 Glu Glu Arg Asn Phe Thr Thr Glu Gln Val Thr Ala Met Leu Leu Ser  
 65 70 75 80  
 25 Lys Leu Lys Glu Thr Ala Glu Ser Val Leu Lys Lys Pro Val Val Asp  
 85 90 95  
 Cys Val Val Ser Val Pro Cys Phe Tyr Thr Asp Ala Glu Arg Arg Ser  
 100 105 110  
 30 Val Met Asp Ala Thr Gln Ile Ala Gly Leu Asn Cys Leu Arg Leu Met  
 115 120 125  
 Asn Glu Thr Thr Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp  
 130 135 140  
 Leu Pro Ala Leu Glu Glu Lys Pro Arg Asn Val Val Phe Val Asp Met  
 145 150 155 160  
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 165 170 175  
 Leu Lys Val Ser Gly His Cys Ile  
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 Lys Val Thr Tyr Met Glu Glu Glu Arg Asn Phe Thr Thr Glu Gln Val  
 35 40 45  
 Thr Ala Met Leu Leu Ser Lys Leu Lys Glu Thr Ala Glu Ser Val Leu  
 50 55 60  
 55 Lys Lys Pro Val Val Asp Cys Val Val Ser Val Pro Cys Phe Tyr Thr  
 65 70 75 80  
 Asp Ala Glu Arg Arg Ser Val Met Asp Ala Thr Gln Ile Ala Gly Phe  
 85 90 95  
 Asn Cys Leu Arg Leu Met Asn Glu Thr Thr Ala Val Ala Leu Ala Tyr  
 100 105 110  
 60 Gly Ile Tyr Lys Gln Asp Leu Pro Ala Leu Glu Glu Lys Pro Arg Asn  
 115 120 125  
 Val Val Phe Val Asp Met Gly His Ser Ala Tyr Gln Val Ser Val Cys  
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130 135 140  
 Ala Phe Asn Arg Gly Lys Leu Lys Val Leu Ala Thr Ala Phe Asp Thr  
 145 150 155 160  
 Thr Leu Gly Gly Arg Lys Phe Asp Glu Val Leu Val Asn His Phe Cys  
 5 165 170 175  
 Glu Glu Phe Gly Lys Lys Tyr Lys Leu Asp Ile Lys Ser Lys Ile Arg  
 180 185 190  
 Ala Leu Leu Arg Leu Ser Gln Glu Cys Glu Lys Leu Lys Lys Ile Asp  
 195 200 205  
 10 Glu Val Gln Met Leu Gln Ile Ser Leu Leu Ser Ile Glu Trp Phe Met  
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 Glu Lys Val Pro Met Ile Ser  
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 Asp Val Ser Gly Thr Met Asn Arg Gly Lys Phe Leu Glu Met Cys Asn  
 35 40 45  
 Asp Leu Leu Ala Arg Val Glu Pro Pro Leu Arg Ser Val Leu Glu Gln  
 30 50 55 60  
 Thr Lys Leu Lys Lys Glu Asp Ile Tyr Ala Val Glu Ile Val Gly Gly  
 65 70 75 80  
 Ala Thr Arg Ile Pro Ala Val Lys Glu Lys Ile Ser Lys Phe Phe Gly  
 85 90 95  
 35 Lys Glu Leu Ser Thr Thr Leu Asn Ala Asp Glu Ala Val Thr Arg Gly  
 100 105 110  
 Cys Ala Leu Gln Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu  
 115 120 125  
 Phe Ser Ile Thr Asp Val Val Pro Tyr Pro Ile Ser Leu Arg Trp Asn  
 40 130 135 140  
 Ser Pro Xaa Glu Glu Gly Ser Ser Asp Cys Glu Val Phe Phe Lys Asn  
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 Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln Gln Glu Gln Phe Glu  
 35 40 45  
 His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn Gly Leu Ser Ala Trp  
 50 55 60  
 60 Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe Ser Lys Gly Met Asp  
 65 70 75 80  
 Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val Phe Asn Glu Leu Ile  
 85 90 95

Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys Lys Gly His Arg Arg  
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 Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys Pro Asn Ile Ile Ser  
                   115                  120                  125  
 5 Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys Gly Asp Ile Leu Leu  
                   130                  135                  140  
 Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp Lys Asp Gly Lys Lys  
                   145                  150                  155                  160  
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 Phe Arg

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 Gly Ile Ile Ser Ala Arg Cys Asn Leu Arg Leu Pro Arg Ser Ser Asp  
                   20                  25                  30  
 Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Ile Thr Gly Ala Arg His  
 25           35                  40                  45  
 Gln Ala Gln Leu Ile Phe Phe Val Phe Leu Val Glu Thr Gly Phe His  
           50                  55                  60  
 Gln Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Pro Pro  
           65                  70                  75                  80  
 30 Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Val Ser His His Ala  
                   85                  90                  95  
 Arg Pro Pro Lys Leu Phe Leu Leu Ser Leu Xaa  
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 Ile Gly Pro Phe Met Cys Cys Phe Tyr Phe Thr Ser Asn Cys Arg Tyr  
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                   20                  25                  30  
 Lys Arg Pro Val Leu Gly Tyr Arg Asn Leu Asn Leu Phe Lys Leu Phe  
                   35                  40                  45  
 60 Arg Leu Val His Lys Leu Gly Gly Phe Asp Asn Ile Glu Ser Gly Ala  
       50                  55                  60  
 Val Trp Lys Gln Val Tyr Gln Asp Leu Gly Ile Pro Val Leu Asn Ser  
       65                  70                  75                  80

	Ala	Ala	Gly	Tyr	Asn	Val	Lys	Cys	Ala	Tyr	Lys	Lys	Tyr	Leu	Tyr	Gly
					85					90					95	
	Phe	Glu	Glu	Tyr	Cys	Arg	Ser	Ala	Asn	Ile	Glu	Phe	Gln	Met	Ala	Leu
				100					105					110		
5	Pro	Glu	Lys	Val	Val	Asn	Lys	Gln	Cys	Lys	Glu	Cys	Glu	Asn	Val	Lys
			115					120					125			
	Glu	Ile	Lys	Val	Lys	Glu	Glu	Asn	Glu	Thr	Glu	Ile	Lys	Glu	Xaa	Lys
		130					135					140				
	Met	Glu	Glu	Glu	Arg	Asn	Ile	Ile	Pro	Arg	Glu	Glu	Lys	Pro	Ile	Glu
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	Asp	Glu	Ile	Glu	Arg	Lys	Glu	Asn	Ile	Lys	Pro	Ser	Leu	Gly	Ser	Lys
				165						170				175		
	Lys	Asn	Leu	Leu	Xaa	Ser	Ile	Pro	Thr	His	Ser	Asp	Gln	Glu	Lys	Glu
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	Pro	Xaa	Ala	Ser	Cys	Pro	Lys	Gly	Gly	Gly	Xaa	Glu	Glu	Ser	Leu	Gln
			20					25					30			
	Thr	Val	Val	Xaa	Glu	Glu	Ser	Cys	Ser	Pro	Ser	Val	Glu	Leu	Glu	Xaa
			35				40						45			
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	Cys	Leu	Asn	Thr	Pro	Pro	Thr	Thr	Pro	Glu	Ser	Pro	Ser	Ser	Val	Thr
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	Val	Thr	Xaa	Gly	Ser	Arg	Gln	Gln	Ser	Ser	Val	Thr	Val	Ser	Glu	Pro
				100					105					110		
	Leu	Ala	Pro	Asn	Gln	Glu	Glu	Val	Arg	Ser	Ile	Lys	Ser	Glu	Thr	Asp
			115					120					125			
40	Ser	Thr	Ile	Glu	Val	Asp	Ser	Val	Ala	Gly	Glu	Leu	Gln	Asp	Leu	Gln
	130						135					140				
	Ser	Glu	Gly	Asn	Ser	Ser	Pro	Ala	Gly	Phe	Asp	Ala	Ser	Val	Ser	Ser
	145					150				155					160	
	Ser	Ser	Ser	Asn	Gln	Pro	Glu	Pro	Glu	His	Pro	Glu	Lys	Ala	Cys	Thr
45					165					170					175	
	Gly	Gln	Lys	Arg	Val	Lys	Asp	Ala	Gln	Gly	Gly	Gly	Ser	Ser	Ser	Lys
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	Lys	Gln	Lys	Arg	Ser	His	Lys	Ala	Thr	Val	Val	Asn	Asn			
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60	Leu	Phe	Arg	Leu	Val	His	Lys	Leu	Gly	Gly	Phe	Asp	Asn	Ile	Glu	Ser	
			20						25					30			
	Gly	Ala	Val	Trp	Lys	Gln	Val	Tyr	Gln	Asp	Leu	Gly	Ile	Pro	Val	Leu	
			35					40					45				
	Asn	Ser	Ala	Ala	Gly	Tyr	Asn	Val	Lys	Cys	Ala	Tyr	Lys	Lys	Tyr	Leu	

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 Tyr Gly Phe Glu Glu Tyr Cys Arg Ser Ala Asn Ile Glu Phe Gln Met  
 65 70 75 80  
 Ala Leu Pro Glu Lys Val Val Asn Lys Gln Cys Lys Glu Cys Glu Asn  
 5 Val Lys Glu Ile Lys Val Lys Glu Glu Asn Glu Thr Glu Ile Lys Glu  
 85 90 95  
 Ile Lys Met Glu Glu Glu Arg Asn Ile Ile Pro Arg Glu Glu Lys Pro  
 100 105 110  
 Ile Lys Met Glu Glu Glu Arg Asn Ile Ile Pro Arg Glu Glu Lys Pro  
 115 120 125  
 10 Ile Glu Asp Glu Ile Glu Arg Lys Glu Asn Ile Lys Pro Ser Leu Gly  
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 Ser Lys Lys Asn Leu Leu Glu Ser Ile Pro Thr His Ser Asp Gln Glu  
 145 150 155 160  
 Lys Glu Val Asn Ile Lys Lys Pro Glu Asp Asn Glu Asn Leu Asp Asp  
 15 165 170 175  
 Lys Asp Asp Asp Thr Thr Arg Val Asp Glu Ser Leu Asn Ile Lys Val  
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 Glu Ala Glu Glu Glu Lys Ala Lys Ser Gly Asp Glu Thr Asn Lys Glu  
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 35 Leu Val Gly His His His Leu His Pro Leu Leu Xaa Ser Ser Ser Ser  
 35 40 45  
 Ser Ser Ser Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Leu Phe Val  
 50 55 60  
 Ser Ser Pro Asp Phe Ala Phe Ser Ser Ser Ala Ser Thr Phe Met Leu  
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 Arg Asp Ser Ser Thr Leu Val Val Ser Ser Ser Leu Ser Ser Arg Phe  
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 55 Leu Leu Phe Leu Xaa Xaa Gly Ile Ile Phe Ile Xaa Phe Phe Phe  
 35 40 45  
 Phe Leu Leu Leu Leu Xaa Phe Cys Phe Phe Ile Ile Phe Ile Phe Phe  
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 60 Phe Ile Arg Xaa Ile Ser Xaa Phe Cys Phe Phe Phe Leu Ser Phe Tyr  
 65 70 75 80  
 Leu Tyr Xaa Glu Gly Phe Ile Tyr Pro Ser Xaa Val Ile Ile Phe Gly  
 85 90 95



Ala Gln Ile Phe Ile Gly Phe Trp Phe Xaa Asn Xaa Asn Phe Phe Phe  
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 20 25 30  
 Lys Pro Xaa Xaa Gly Ser Lys Lys Asn Leu Leu Glu Xaa Xaa Pro Thr  
 35 40 45  
 His Xaa Xaa Gln Glu Lys Glu Val Xaa Ile Xaa Lys Pro Glu Ala Asn  
 50 55 60  
 20 Glu Asn Leu Gly Ala Lys Asp Asp Asp Xaa Thr Arg Val Asp Glu Ser  
 65 70 75 80  
 Leu Xaa Ile Lys Val Glu Ala Glu Glu Glu Lys Ala Lys Xaa Gly Asp  
 85 90 95  
 Xaa Thr Asn Lys Glu Glu Asp Glu Asp Asp Glu Glu Ala Glu Xaa Glu  
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 Val Lys Lys Asp Asn Ile Leu Val Arg Ser Phe Lys Asp Gly Lys Phe  
 20 25 30  
 45 Thr Ser Val Pro Arg Lys Asp Val His Glu Ile Thr Ser Asp Thr Ala  
 35 40 45  
 Pro Lys Pro Asp Ala Val Leu Lys Gln Ala Phe Glu Gln Ala Leu Glu  
 50 55 60  
 Phe His Lys Ser Arg Thr Ile Pro Ala Asn Trp Lys Thr Glu Leu Lys  
 65 70 75 80  
 50 Glu Asp Ser Ser Ser Ser Glu Ala Glu Glu Glu Glu Glu Glu Asp  
 85 90 95  
 Asp Glu Lys Glu Lys Glu Asp Asn Ser Ser Glu Glu Glu Glu Glu Ile  
 100 105 110  
 55 Glu Pro Phe Pro Glu Glu Arg Glu Asn Phe Leu Gln Gln Leu Tyr Lys  
 115 120 125  
 Phe Met Glu Asp Arg Gly Thr Pro Ile Asn Lys Arg Pro Val Leu Gly  
 130 135 140  
 Tyr Arg Asn Leu Asn Leu Phe Lys Leu Phe Arg Leu Val His Lys Leu  
 145 150 155 160  
 60 Gly Gly Phe Asp Asn Ile Glu Ser Gly Ala Val Trp Lys Gln Val Tyr  
 165 170 175  
 Gln Asp Leu Gly Ile Pro Val Leu Asn Ser Ala Ala Gly Tyr Asn Val

180 185 190  
 Lys Cys Ala Tyr Lys Lys Tyr Leu Tyr Gly Phe Glu Gly Val Leu  
 195 200 205

5 <210> 728  
 <211> 221  
 <212> PRT  
 <213> Homo sapiens

10 <400> 728  
 Met Leu Phe Ala Pro Cys Cys His Gln Cys Gly Glu Phe Ile Ile Gly  
 1 5 10 15  
 Arg Val Ile Lys Ala Met Asn Asn Ser Trp His Pro Glu Cys Phe Arg  
 20 25 30  
 15 Cys Asp Leu Cys Gln Glu Val Leu Ala Asp Ile Gly Phe Val Lys Asn  
 35 40 45  
 Ala Gly Arg His Leu Cys Arg Pro Cys His Asn Arg Glu Lys Ala Arg  
 50 55 60  
 Gly Leu Gly Lys Tyr Ile Cys Gln Lys Cys His Ala Ile Ile Asp Glu  
 65 70 75 80  
 20 Gln Pro Leu Ile Phe Lys Asn Asp Pro Tyr His Pro Asp His Phe Asn  
 85 90 95  
 Cys Ala Asn Cys Gly Lys Glu Leu Thr Ala Asp Ala Arg Glu Leu Lys  
 100 105 110  
 25 Gly Glu Leu Tyr Cys Leu Pro Cys His Asp Lys Met Gly Val Pro Ile  
 115 120 125  
 Cys Gly Ala Cys Arg Arg Pro Ile Glu Gly Arg Val Val Asn Ala Met  
 130 135 140  
 Gly Lys Gln Trp His Val Glu His Phe Val Cys Ala Lys Cys Glu Lys  
 145 150 155 160  
 30 Pro Phe Leu Gly His Arg His Tyr Glu Arg Lys Gly Leu Ala Tyr Cys  
 165 170 175  
 Glu Thr His Tyr Asn Gln Leu Phe Gly Asp Val Cys Phe His Cys Asn  
 180 185 190  
 35 Arg Val Ile Glu Xaa Asp Val Val Ser Ala Leu Asn Lys Ala Trp Cys  
 195 200 205  
 Val Asn Cys Phe Ala Cys Ser Thr Leu Gln His Leu Asn  
 210 215 220

40 <210> 729  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

45 <400> 729  
 Leu Pro Phe Gln Leu Pro Cys Ile Gly Ser Gln Leu Leu Pro Ala Val  
 1 5 10 15  
 Gly Ala Val Glu Met Val Trp Met Val Gly Val Val Leu Glu Tyr Gln  
 20 25 30  
 50 Arg Leu Leu Ile Asp Asp Ser Met Ala Phe Leu Ala Asp Val Phe Pro  
 35 40 45  
 Lys Ala Ser Gly Phe Leu Thr Ile Met Thr Gly Ala Thr Gln Val Ser  
 50 55 60  
 Pro Ser Ile Leu Asp Lys Pro Asp Ile Cys Gln Asn Phe Leu Ala Glu  
 65 70 75 80  
 55 Val Thr Ala Glu Ala Leu Arg Met Pro Ala Val Ile His Gly Phe Asp  
 85 90 95  
 Asn Ser Ala Asn Asp Glu Phe Thr Thr Leu Met Thr Ala Arg Gly Lys  
 100 105 110  
 60 Glu His

<210> 730

<211> 191  
 <212> PRT  
 <213> Homo sapiens

5           <400> 730  
 Arg Arg Pro Ala Ala Gly Leu Arg Asp Xaa Val Xaa Ser Ala Pro Arg  
   1                  5                  10                  15  
 Gly Met Ala Ser Glu Gly Pro Xaa Glu Pro Glu Ser Glu Gly Ile Lys  
           20                  25                  30  
 10 Leu Ser Gly Ile Cys Gln Thr Ile Cys Pro Gln Ile Cys Arg Ala Gln  
           35                  40                  45  
 Cys Gly Met Val Arg Val Leu Arg Ser Met Cys Leu Pro Gln Leu Cys  
   50                  55                  60  
 Ser His Ile Leu Ser Val Cys Ser Gly Thr Thr Ser Asp Arg Asn Xaa  
 15 65                  70                  75                  80  
 Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro Ser Cys Tyr  
           85                  90  
 Arg Gly Phe Gln Thr Xaa Lys His Arg Asn Glu Asn Thr Cys Pro Leu  
           100                  105                  110  
 20 Pro Gln Glu Met Lys Ala Leu Phe Lys Lys Lys Thr Xaa Asp Glu Lys  
           115                  120                  125  
 Lys Thr Tyr Asp Gln Gln Lys Phe Asp Ser Glu Arg Ala Asp Gly Thr  
   130                  135                  140  
 Ile Ser Ser Glu Ile Lys Ser Ala Arg Gly Ser His His Leu Ser Ile  
 25 145                  150                  155                  160  
 Tyr Ala Glu Asn Ser Leu Lys Ser Asp Gly Tyr His Lys Arg Thr Asp  
           165                  170                  175  
 Arg Lys Ser Arg Ile Ile Cys Lys Lys Trp Ile Tyr Leu Gln Thr  
           180                  185                  190

30           <210> 731  
           <211> 115  
           <212> PRT  
           <213> Homo sapiens

35           <400> 731  
 Asp Gly Pro Leu Leu Ala Ser Val Thr Xaa Ser Xaa Pro Arg Leu Ala  
   1                  5                  10                  15  
 Ala Trp Arg Arg Gly Xaa Gly Ser Pro Lys Ala Arg Ala Ser Ser  
 40           20                  25                  30  
 Tyr Gln Ala Tyr Val Lys Pro Phe Val Pro Arg Phe Ala Gly Leu Asn  
           35                  40                  45  
 Val Ala Trp Leu Glu Ser Ser Glu Ala Cys Val Phe Pro Ser Ser Ala  
   50                  55                  60  
 45 Ala Thr Tyr Tyr Pro Phe Val Gln Glu Pro Pro Val Thr Glu Met Xaa  
   65                  70                  75                  80  
 Thr Gln Cys Leu Ala Pro Ser Ile Phe Ile Thr Asn Pro Val Val Thr  
           85                  90                  95  
 Glu Val Phe Lys Gln Xaa Ser Ile Glu Met Arg Thr His Ala Leu Ser  
 50           100                  105                  110  
 His Lys Lys  
           115

55           <210> 732  
           <211> 139  
           <212> PRT  
           <213> Homo sapiens

60           <400> 732  
 Ser Ile Ser Arg Phe Asn Ser Tyr Thr Asn Tyr Ile Val Met Lys Asn  
   1                  5                  10                  15  
 Arg Arg Lys Ser Pro Lys Val Phe Phe Arg Pro Pro Leu Leu Thr Gln  
           20                  25                  30

Asn Thr Asp Thr Gln Ala Arg Thr Leu Ile Asn Ser Asn Ser Ser Phe  
                   35                  40                  45  
 Glu Arg Leu Lys Pro Pro Arg Ile Leu Leu Ala Pro Gly Tyr Ile His  
                   50                  55                  60  
 5 Cys Met Leu Pro Asp Val Phe Ser Arg Phe Gln Cys Ser Val Ala Leu  
    65                  70                  75                  80  
 Leu Phe Leu Ser Gly Leu Gly Gly His Leu Leu Gln Gly Ser Trp Gly  
                   85                  90                  95  
 Pro Val Trp Val Gly Trp Glu Val Pro Glu Ala Trp Ala Leu Pro Pro  
                   100                  105                  110  
 10 Ala Pro Ala Ala His Ser Pro Ala Trp Leu Asp Trp Ile Phe Leu Val  
                   115                  120                  125  
 His Thr Xaa Leu Glu Thr Asp Xaa Phe Phe Glu  
           130                  135  
 15  
       <210> 733  
       <211> 155  
       <212> PRT  
       <213> Homo sapiens  
 20  
       <400> 733  
 Gly Gln Ser Leu Lys Lys Xaa Pro Gly Pro Arg Ala Pro Lys Glu Xaa  
    1                  5                  10                  15  
 Arg Gly Leu Pro Pro Leu Xaa Pro Ile Thr Pro Pro Phe Pro Lys Ile  
                   20                  25                  30  
 25 His Gln Pro Gln Ile Gln Gly Xaa Leu Gln Pro Asp Ala Leu Val Lys  
                   35                  40                  45  
 Lys Val Asp Ala Cys Val Thr Asp Pro Thr Gln Arg Xaa Gly Pro Phe  
                   50                  55                  60  
 30 Pro Xaa Pro Tyr Val Pro Glu Arg Ser Ser Gln Ala Met Leu Glu Asn  
    65                  70                  75                  80  
 Val Gln Gln Glu Leu Val Gly Glu Pro Arg Pro Gln Ala Pro Pro Ser  
                   85                  90                  95  
 35 Leu Pro Thr Gln Gly Pro Ser Cys Pro Ala Glu Asp Gly Pro Pro Ala  
                   100                  105                  110  
 Leu Lys Glu Lys Glu Glu Pro His Tyr Ile Glu Ile Trp Lys Lys His  
                   115                  120                  125  
 Leu Glu Ala Tyr Ser Gly Cys Thr Leu Glu Leu Glu Glu Ser Leu Glu  
                   130                  135                  140  
 40 Ala Ser Thr Ser Gln Met Met Asn Leu Asn Leu  
    145                  150                  155  
       <210> 734  
       <211> 126  
       <212> PRT  
       <213> Homo sapiens  
 45  
       <400> 734  
 Gly Glu Ala Gly His Trp Ala Gly Arg Ile Ser Arg Tyr Leu Asp Leu  
    1                  5                  10                  15  
 Tyr Arg Trp Pro Gly Leu Ile Val His Gly Arg Leu Leu Gly Cys Ser  
                   20                  25                  30  
 Glu Cys Lys Gly Ser Leu Ser Lys Pro Phe Ser Leu Val Leu Ser Gly  
                   35                  40                  45  
 55 Val Arg Leu Phe Pro Phe Ser Phe Thr Ser Arg Ser Ser Ser Glu Glu  
                   50                  55                  60  
 Ser Thr Gly Glu Val Val Leu Ala Ser Arg Ser Ser Cys Ser Cys Trp  
    65                  70                  75                  80  
 Ala Arg Tyr Trp Ala Gly Phe Cys Leu Ala Ser Leu Ala Gln Trp Arg  
                   85                  90                  95  
 60 Ser Ser Arg Cys Ser Arg Gly Lys Leu Ala Phe Lys Asn Gly Met Thr  
                   100                  105                  110  
 Lys Gly Leu Ser Gly Lys Leu Val Ala Ser Cys Ser Leu Glu  
                                   115  
                                   120  
                                   125  
                                   130  
                                   135  
                                   140  
                                   145  
                                   150  
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                                   265  
                                   270

115 120 125

5 <210> 735  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 735  
 10 Thr Lys Thr Gly Arg Gly Glu Leu Gln Thr Glu Pro Lys Lys Met Ala  
 1 5 10 15  
 Leu Thr Glu Ser Leu Cys Thr Gln Asn Ile Gln Ala Ser Asp His Ala  
 20 25 30  
 Leu Leu Ala Gln Ala Ser Gly Thr Ser Pro Asn Asn Gly Leu Ser Tyr  
 35 40 45  
 15 Gln Pro Asn Gly Leu Pro His Pro Thr Pro Pro Pro Xaa His Tyr  
 50 55 60  
 Arg Leu Asp Asp Met Ala Ile Ala His His Tyr Arg Asp Ser Tyr Arg  
 65 70 75 80  
 His Pro Ser His Arg Gly Pro Xaa Gly Gln Lys Xaa Thr Tyr Gly Val  
 20 85 90 95  
 Ala Trp His Thr Ser Arg Arg Asn Asp  
 100 105

25 <210> 736  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 736  
 30 Val Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu  
 1 5 10 15  
 Ala Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala  
 20 25 30  
 Asn Leu Pro Leu Leu Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala  
 35 35 40 45  
 Lys Gln Asn Pro Ala Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu  
 50 55 60  
 Asp Ala Ser Thr Thr Ser Pro Val Asp Ser Ser Glu Leu Leu Leu Asp  
 65 70 75 80  
 40 Val Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg Thr Lys Glu Asn  
 85 90 95  
 Gly Phe Asp Arg Glu Pro Leu His Ser Glu His Pro Ser Lys Arg Pro  
 100 105 110  
 Cys Thr Ile Ser Pro Gly Gln Arg Tyr Lys Ser Lys  
 45 115 120

50 <210> 737  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 737  
 55 Leu Gln Val Cys Leu Pro Ala Gly Gly Pro Cys Xaa Val Cys Pro Gln  
 1 5 10 15  
 Lys Val Met Xaa Leu Leu Pro Ile Phe Xaa Leu Xaa Lys Met Xaa Pro  
 20 25 30  
 Pro Val Xaa Arg Ala Val Val Thr Ser Pro Trp Xaa Gly Phe Thr Ser  
 35 40 45  
 Leu Leu Xaa Xaa Xaa Asn Phe Gln Thr Asn Xaa Xaa Leu Gly Asn Pro  
 60 50 55 60  
 Pro Gly Gly Leu Glu Lys Pro Xaa Gln Val Ala Val Pro Pro Pro Pro  
 65 70 75 80  
 Leu Pro Phe Xaa Ala Xaa Gly Glu Pro Xaa Pro Ser Ile Phe Trp Ala  
 271

85 90 95  
 Pro Phe Xaa Trp Gly Asn Xaa Val Gly Gly Leu Phe Xaa Ser Pro Leu  
 100 105 110  
 5 Lys Lys Xaa Gly Phe Leu Glu Xaa Pro Xaa Ile Xaa Xaa Xaa Pro Leu  
 115 120 125  
 Xaa Phe Leu Asp Gly Pro Pro Lys Phe Phe Phe Gln Xaa Phe Phe Gly  
 130 135 140  
 Pro Phe Phe Lys Xaa  
 145  
 10 <210> 738  
 <211> 202  
 <212> PRT  
 <213> Homo sapiens  
 15 <400> 738  
 Val Asn Ser Thr Leu Thr Ile Glu Glu Phe His Ser Lys Leu Gln Glu  
 1 5 10 15  
 20 Ala Thr Asn Phe Pro Leu Arg Pro Phe Val Ile Pro Phe Leu Lys Ala  
 20 25 30  
 Asn Leu Pro Leu Leu Gln Arg Glu Leu Leu His Cys Ala Arg Leu Ala  
 35 40 45  
 Lys Gln Asn Pro Ala Gln Tyr Leu Ala Gln His Glu Gln Leu Leu Leu  
 50 55 60  
 25 Asp Ala Ser Thr Thr Ser Pro Val Asp Ser Ser Glu Leu Leu Leu Asp  
 65 70 75 80  
 Val Asn Glu Asn Gly Lys Arg Arg Thr Pro Asp Arg Thr Lys Glu Asn  
 85 90 95  
 Gly Phe Asp Arg Glu Pro Leu His Ser Glu His Pro Ser Lys Arg Pro  
 100 105 110  
 30 Cys Thr Ile Ser Pro Gly Gln Arg Tyr Ser Pro Asn Asn Gly Leu Ser  
 115 120 125  
 Tyr Gln Pro Asn Gly Leu Pro His Pro Thr Pro Pro Pro Gln His  
 130 135 140  
 35 Tyr Arg Leu Asp Asp Met Ala Ile Ala His His Tyr Arg Asp Ser Tyr  
 145 150 155 160  
 Arg His Pro Ser His Arg Asp Leu Arg Asp Arg Asn Arg Pro Met Gly  
 165 170 175  
 40 Leu His Gly Thr Arg Gln Glu Glu Met Ile Asp His Arg Leu Thr Asp  
 180 185 190  
 Arg Glu Trp Gly Arg Arg Val Glu Thr Ser  
 195 200  
 45 <210> 739  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens  
 50 <400> 739  
 Arg Gly Val Val Ser Met Val Glu Gly Val Pro Gly Val Val Asp Leu  
 1 5 10 15  
 Gly Val Ala Ala Gly Gly Val Ser Ile Gly Leu Pro Ala Pro Leu Leu  
 20 25 30  
 Gly Val Thr Lys Glu Leu Thr Ala Gly Val Ser Pro Cys Cys Trp Ala  
 35 40 45  
 55 Cys Xaa Val Cys Pro Gln Met Trp Met Gly Leu Xaa Pro Ser Phe Xaa  
 50 55 60  
 Ala Gly Gln Met Ser Pro  
 65 70  
 60 <210> 740  
 <211> 105  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 740

5 Trp Ala His Leu Pro Ser Xaa Lys Ala Gly Xaa Lys Pro His Pro His  
 1 5 10 15  
 Leu Trp Thr Asp Xaa Ala Gly Pro Ala Ala Gly Arg His Pro Cys Ser  
 20 25 30  
 Gln Leu Phe Cys His Ala Gln Gln Arg Gly Trp Glu Pro Asp Gly His  
 35 40 45  
 10 Thr Thr Ser Ser His Ser Glu Val Asn His Pro Gly Asn Pro Phe His  
 50 55 60  
 His Arg Asp Asn Pro Ser Leu Asp Val Asn Ser Glu Leu Ser Glu Glu  
 65 70 75 80  
 Arg Gln His Asn Gln Arg Glu Thr Asn Ser Ser Ser Ser Asp Ala Gln  
 15 85 90 95  
 Ser Cys Phe Phe Cys Leu Phe Val Tyr  
 100 105

&lt;210&gt; 741

20 &lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 741

25 Met Met Leu Pro Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu  
 1 5 10 15  
 Met His Leu Asp Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu  
 20 25 30  
 Leu Gln Leu Ala Met Thr His Pro Ser His His Leu Asn Phe Gly Met  
 30 35 40 45  
 Asn Pro Asp His Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln  
 50 55 60  
 Pro Lys Tyr Gly Asp Arg Lys Val His His Met His Met Arg Lys Lys  
 65 70 75 80  
 35 Gly Ile Asn Thr Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp  
 85 90 95  
 Pro Thr Pro Ser Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly  
 100 105 110  
 Asp Ala Val Val Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe  
 40 115 120 125  
 Pro Ser Leu Glu Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val  
 130 135 140  
 Gln Asn Gln His Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Arg  
 145 150 155 160  
 45 Phe Met Leu Tyr Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu  
 165 170 175  
 Arg His Ala Met Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr  
 180 185 190  
 Leu Glu Gly Ser Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu  
 50 195 200 205  
 Phe Asn Asp Pro Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His  
 210 215 220  
 Pro Leu Gln Leu Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Gly Asn  
 225 230 235 240  
 55 Phe Phe Gln Phe Tyr Lys Lys Leu Thr Glu Phe Glu Arg Asn Gln Leu  
 245 250 255  
 Gly Val Asn Phe Leu Leu Ile Gly Ser Asp Phe  
 260 265

60 &lt;210&gt; 742

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

<400> 742  
 Asn Pro Gly Pro Arg Tyr Gly Arg Thr Trp Ala Ser Arg Ser Xaa Pro  
 1 5 10 15  
 5 Ile Pro Thr Pro Ser Gln Lys Ala Leu Gly Val Ser Pro Gln Ala Xaa  
 20 25 30  
 Xaa Xaa Leu Leu Glu Ser Phe Ile Ala Ala Leu Xaa Ile Asp Lys Asp  
 35 40 45  
 10 Leu Xaa Tyr Val His Thr Phe His Glu Cys Leu Phe Leu Ser Xaa Ile  
 50 55 60  
 Lys Arg Val His Phe Glu Ser Gly Leu Glu Cys Pro Lys Ser Gln Leu  
 65 70 75 80  
 Gln Gln Cys Cys Leu Pro Leu Gly Arg Arg Lys Arg Ala Arg His Ser  
 85 90 95  
 15 Phe Val Gln Asp Ser Ala Asp Ser Gly Pro Ile Pro Cys Pro Asn Leu  
 100 105 110  
 His Cys Gly Cys Leu Phe Gln Gly Arg Lys Asn Arg Leu Trp Glu Arg  
 115 120 125  
 20 Thr Lys Tyr Ser Ala Ser Gly Asn Gly Ser Ser Asn Gly Cys Ala  
 130 135 140

<210> 743  
 <211> 87  
 <212> PRT  
 25 <213> Homo sapiens

<400> 743  
 Lys Thr Gln Ala Gln Gly Thr Glu Glu Leu Gly His Pro Gly Val Xaa  
 1 5 10 15  
 30 Gln Tyr Pro Arg Gln Ala Lys Arg Pro Trp Gly Phe Arg Pro Lys Xaa  
 20 25 30  
 Trp Xaa Xaa Phe Trp Asn His Leu Leu Gln Arg Cys Xaa Leu Ile Arg  
 35 40 45  
 Ile Xaa Asn Met Phe Ile Leu Phe Met Asn Val Cys Phe Phe Xaa Arg  
 50 55 60  
 35 Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Ala Pro Asn Pro Ser  
 65 70 75 80  
 Phe Ser Ser Val Ala Cys Pro  
 85

<210> 744  
 <211> 101  
 <212> PRT  
 40 <213> Homo sapiens

<400> 744  
 Leu Leu Ser Val Leu Pro Phe Asp Glu Pro Leu Leu Met Gly His Leu  
 1 5 10 15  
 50 Gly Lys Ile Ile Phe Phe Lys Arg Ile His Cys Cys Ser His Phe Arg  
 20 25 30  
 Leu Leu Asn Thr Trp Ser Phe Pro Thr Ala Tyr Ser Phe Ser Leu Glu  
 35 40 45  
 Ile Asn Ser His Ser Val Gly Ser Gly Met Gly Trp Ala His Cys Leu  
 50 55 60  
 55 Gln Ser Leu Val Gln Arg Asn Val Trp Leu Phe Ser Phe Cys Leu Arg  
 65 70 75 80  
 Ala Ser Asn Thr Ala Glu Ala Gly Ile Trp Gly Ile Pro Ile Leu Ile  
 85 90 95  
 60 Gln Asn Glu Leu Phe  
 100

<210> 745  
 <211> 277



&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 745

5 Ile Asn Thr Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro  
 1 5 10 15  
 Thr Pro Ser Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp  
 20 25 30  
 Ala Val Val Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro  
 35 40 45  
 10 Ser Leu Glu Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln  
 50 55 60  
 Asn Gln His Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Arg Phe  
 65 70 75 80  
 15 Met Leu Tyr Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg  
 85 90 95  
 His Ala Met Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr Leu  
 100 105 110  
 Glu Gly Ser Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu Phe  
 115 120 125  
 20 Asn Asp Pro Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His Pro  
 130 135 140  
 Leu Gln Leu Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser  
 145 150 155 160  
 25 Pro Val Leu Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile  
 165 170 175  
 Phe Thr His Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val  
 180 185 190  
 Gly Phe Asn His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu  
 195 200 205  
 30 Gly Asp Ser Ile Met Gln Leu Val Pro Gln Ser Thr Tyr Ser Phe Ile  
 210 215 220  
 Ser Gln Ile Ile Ile Glu Gly His Leu Thr Phe Val Ala Lys Ala Ser  
 225 230 235 240  
 35 Leu Gly Glu Ile Asn Lys Asn Phe Arg Pro Lys Gly Asn Arg Lys Glu  
 245 250 255  
 Ala Trp Ala Leu Gln Gly Ser Thr Pro Ile Thr Gln Pro Asp Gln Glu  
 260 265 270  
 Pro Lys Lys Ala Cys  
 275  
 40

&lt;210&gt; 746

&lt;211&gt; 187

&lt;212&gt; PRT

45 <213> Homo sapiens

&lt;400&gt; 746

Arg Thr Lys Ala Lys Lys Asp Lys Ala Gln Arg Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 50 Xaa Xaa Gly Xaa Ala Pro His Ser Glu Ser Asp Leu Pro Glu Gln Glu  
 20 25 30  
 Glu Glu Ile Leu Gly Ser Asp Asp Asp Glu Gln Glu Asp Pro Asn Asp  
 35 40 45  
 Tyr Cys Lys Gly Gly Tyr His Leu Val Lys Ile Gly Asp Leu Phe Asn  
 50 55 60  
 55 Gly Arg Tyr His Val Ile Arg Lys Leu Gly Trp Gly His Phe Ser Thr  
 65 70 75 80  
 Val Trp Leu Ser Trp Asp Ile Gln Gly Lys Lys Phe Val Ala Met Lys  
 85 90 95  
 60 Xaa Val Lys Ser Ala Glu His Tyr Thr Glu Thr Ala Leu Asp Glu Ile  
 100 105 110  
 Xaa Leu Leu Lys Ser Val Arg Asn Ser Asp Pro Asn Asp Pro Asn Arg  
 115 120 125

Glu Met Val Val Gln Leu Leu Asp Asp Phe Lys Ile Ser Gly Val Asn  
 130 135 140  
 Gly Thr His Ile Cys Met Val Phe Glu Val Leu Gly His His Leu Leu  
 145 150 155 160  
 5 Lys Trp Ile Ile Lys Ser Asn Tyr Xaa Gly Leu Pro Leu Pro Cys Xaa  
 165 170 175  
 Lys Lys Ile Ile Xaa Xaa Val Phe Thr Gly Xaa  
 180 185  
  
 10 <210> 747  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens  
  
 15 <400> 747  
 Ile Asp Pro Pro Pro Phe Pro Phe Lys His Phe Pro Leu Pro Phe Ser  
 1 5 10 15  
 Gly Glu Ala Xaa Pro Ser Lys Val Xaa Arg Ser Cys Phe Phe Asn  
 20 20 25 30  
 Pro Thr Cys Ser Phe Gly Phe Ala Tyr Leu Thr Leu Xaa Xaa Ser Pro  
 35 40 45  
 Gln Pro Leu Gly Ile Leu Gly Glu Phe Gly Leu Gly Trp Ala Xaa Pro  
 50 55 60  
 Lys Thr Asn Gly Xaa Lys Cys Glu Thr Ala Ser Cys Xaa Xaa Pro Phe  
 25 65 70 75 80  
 Leu Pro Ile Arg Thr Ser Phe Lys Leu  
 85  
  
 30 <210> 748  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens  
  
 35 <400> 748  
 Xaa Leu Xaa Ser Met Asn Lys Arg Met Gly Ser Tyr Thr Phe Ile Ala  
 1 5 10 15  
 Xaa Phe Lys Lys Asp Ala Tyr Asn Leu Lys Asp Val Leu Met Gly Arg  
 20 25 30  
 Lys Gly Xaa Gly Gln Glu Ala Val Ser His Phe Xaa Pro Leu Val Phe  
 40 35 40 45  
 Gly Xaa Ala Gln Pro Arg Pro Asn Ser Pro Arg Met Pro Asn Gly Cys  
 50 55 60  
 Gly Asp Xaa Xaa Arg Val Lys  
 65 70  
  
 45 <210> 749  
 <211> 254  
 <212> PRT  
 <213> Homo sapiens  
  
 50 <400> 749  
 Val Cys Lys Gly Ile Leu Glu Tyr Leu Thr Val Ala Glu Val Val Glu  
 1 5 10 15  
 Thr Met Glu Asp Leu Val Thr Tyr Thr Lys Asn Leu Gly Pro Gly Met  
 55 20 25 30  
 Thr Lys Met Ala Lys Met Ile Asp Glu Arg Gln Gln Glu Leu Thr His  
 35 40 45  
 Gln Glu His Arg Val Met Leu Val Asn Ser Met Asn Thr Val Lys Glu  
 50 55 60  
 60 Leu Leu Pro Val Leu Ile Ser Ala Met Lys Ile Phe Val Thr Thr Lys  
 65 70 75 80  
 Asn Ser Lys Asn Gln Gly Ile Glu Glu Ala Leu Lys Asn Arg Asn Phe  
 85 90 95

Thr Val Glu Lys Met Ser Ala Glu Ile Asn Glu Ile Ile Arg Val Leu  
 100 105 110  
 Gln Leu Thr Ser Trp Asp Glu Asp Ala Trp Ala Ser Lys Asp Thr Glu  
 115 120 125  
 5 Ala Met Lys Arg Ala Leu Ala Ser Ile Asp Ser Lys Leu Asn Gln Ala  
 130 135 140  
 Lys Gly Trp Leu Arg Asp Pro Ser Ala Ser Pro Gly Asp Ala Gly Glu  
 145 150 155 160  
 Gln Ala Ile Arg Gln Ile Leu Asp Glu Ala Gly Lys Val Gly Glu Leu  
 165 170 175  
 10 Cys Ala Gly Lys Lys Arg Arg Glu Xaa Leu Gly Asn Leu Gln Asn Ala  
 180 185 190  
 Xaa Ala Asp Asp Cys Gln Ser Gly Leu Thr Ser Val Pro Arg Gly Gln  
 195 200 205  
 15 Gly Ser Leu Pro Xaa Gly Pro Cys Xaa Lys Ser Xaa Thr Xaa Tyr Xaa  
 210 215 220  
 Gln Gly Leu Gly Xaa Cys Ser Pro Ala Lys Xaa Glu Lys Ala Ser Phe  
 225 230 235 240  
 Gln Ser Trp Glu Ser Leu Ala His Xaa Lys Pro Lys His Leu  
 245 250  
 20

&lt;210&gt; 750

&lt;211&gt; 82

&lt;212&gt; PRT

25 <213> Homo sapiens

&lt;400&gt; 750

Leu Phe Ser Arg Pro Ser Ala Tyr Leu Tyr Ser Cys Leu Pro Asp Ile  
 1 5 10 15  
 30 Asn Ala Ile Leu Met Pro Leu Lys Tyr Glu Ser Met Pro Lys Ile Thr  
 20 25 30  
 Cys Cys Phe Thr Lys Glu Arg Leu Arg Gly Asn Lys Lys Asn His  
 35 35 40 45  
 Val Cys Ser Pro Gly Ser Ser Ser Gly Leu Arg His Trp Phe Thr Leu  
 50 55 60  
 35 Tyr Ala Gly Cys Ala Phe Leu Gln Tyr Gln Cys Ser Arg His Ser Glu  
 65 70 75 80  
 Ala Asn

40

&lt;210&gt; 751

&lt;211&gt; 162

&lt;212&gt; PRT

45 <213> Homo sapiens

&lt;400&gt; 751

Gln Lys Leu Val Ile Glu Asn Phe Asp Asp Glu Gln Ile Trp Gln Gln  
 1 5 10 15  
 50 Leu Glu Leu Gln Asn Glu Pro Ile Leu Gln Tyr Phe Gln Asn Ala Val  
 20 25 30  
 Ser Glu Thr Ile Asn Asp Glu Asp Ile Ser Leu Leu Pro Glu Ser Glu  
 35 40 45  
 Glu Gln Glu Arg Glu Glu Asp Gly Ser Glu Ile Glu Ala Asp Asp Lys  
 50 55 60  
 55 Glu Asp Leu Glu Asp Leu Glu Glu Glu Val Ser Asp Met Gly Asn  
 65 70 75 80  
 Asp Asp Pro Glu Met Gly Glu Arg Ala Glu Asn Ser Ser Lys Ser Asp  
 85 90 95  
 60 Leu Arg Lys Ser Pro Val Phe Ser Asp Glu Asp Ser Asp Leu Asp Phe  
 100 105 110  
 Asp Ile Ser Lys Leu Glu Gln Gln Ser Lys Val Gln Asn Lys Gly Gln  
 115 120 125  
 Gly Lys Pro Arg Glu Lys Ser Ile Val Asp Asp Lys Phe Phe Lys Leu

130 135 140  
 Ser Glu Met Glu Ala Tyr Leu Glu Asn Ile Glu Lys Glu Glu Glu Pro  
 145 150 155 160  
 Lys Arg

5  
 <210> 752  
 <211> 120  
 <212> PRT  
 10 <213> Homo sapiens

<400> 752  
 Ala Ser Ile Ser Glu Ser Leu Lys Asn Leu Ser Ser Thr Met Asp Phe  
 1 5 10 15  
 15 Ser Leu Gly Phe Pro Cys Pro Leu Phe Cys Thr Leu Leu Cys Cys Ser  
 20 25 30  
 Asn Leu Leu Ile Ser Lys Ser Arg Ser Glu Ser Ser Ser Leu Lys Thr  
 35 40 45  
 20 Gly Leu Phe Leu Arg Ser Asp Leu Leu Glu Phe Ser Ala Leu Ser Pro  
 50 55 60  
 Ile Ser Gly Ser Ser Leu Pro Met Ser Asp Thr Ser Ser Ser Ser Lys  
 65 70 75 80  
 Ser Ser Arg Ser Ser Leu Ser Ser Ala Ser Ile Ser Glu Pro Ser Ser  
 85 90 95  
 25 Ser Arg Ser Cys Ser Ser Leu Ser Gly Arg Arg Leu Ile Ser Ser Ser  
 100 105 110  
 Leu Ile Val Ser Leu Thr Ala Phe  
 115 120

30  
 <210> 753  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

35  
 <400> 753  
 Xaa Ala Cys Pro Xaa Ile Lys Val Xaa Ser Asn Phe Pro Xaa Ile Xaa  
 1 5 10 15  
 Met Xaa Glu Xaa Ala Pro Val Xaa Val Ser Xaa Ala Ala Phe Xaa Ala  
 20 25 30  
 40 Xaa Xaa Xaa Xaa Xaa Lys Asn Lys Xaa Xaa Xaa Ile Lys Xaa Xaa  
 35 40 45  
 Ala Glu Lys Xaa Ala Pro Ala Lys Asn Xaa Xaa Xaa Xaa Lys Lys Lys  
 50 55 60  
 Xaa Gln Xaa Xaa Xaa Lys Ile Lys Xaa Lys Glu Lys Xaa Arg Xaa Xaa  
 65 70 75 80  
 Xaa Xaa Xaa Thr Xaa Val Xaa Gln Ala Gly Lys Ser Ser Lys Xaa Xaa  
 85 90 95  
 Xaa Trp Xaa Lys Leu Lys Gln Xaa Xaa Lys Xaa Gly Lys Ala Ser Xaa  
 100 105 110  
 50 Ile Lys Asp Glu Gly Lys Xaa Xaa Xaa Leu Lys Xaa Xaa Gln Ala Phe  
 115 120 125  
 Phe Phe Xaa Phe Gln Asp Gln Val Lys Met Gln Ile Asn Xaa Ala  
 130 135 140

55  
 <210> 754  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

60  
 <400> 754  
 Asn Gln Arg His Leu Glu Lys His Met Ile Asp Phe Phe Ala Ser Arg  
 1 5 10 15  
 Met Pro Glu Thr Leu His Leu Pro His Gly Thr Met Arg Gln Ser Pro

20 25 30  
 Asn Pro Met Ser Ala Leu Glu Arg Tyr Ser Tyr Tyr Tyr Ser Cys Lys  
 35 40 45  
 Thr Ile Asn Gln Leu Ile His Ile Cys Thr Ala Gly Ser Pro Arg Asp  
 5 50 55 60  
 Lys Ile  
 65  
  
 <210> 755  
 10 <211> 69  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 755  
 15 Asn Thr Ser Asn Ile Pro Phe Ile Ala Tyr Val Thr Tyr Ser Asn Glu  
 1 5 10 15  
 Tyr Asn Lys Leu Leu Phe Lys Lys Val Arg His Met Lys Ser Leu Leu  
 20 20 25 30  
 Cys Lys Phe His Val Ile Leu Lys Phe Leu Leu Ala Asn Lys Ser Ile  
 35 40 45  
 Cys Thr Ile Glu Pro Glu Thr Ser Arg Lys Ala His Asp Arg Phe Phe  
 50 55 60  
 Cys Lys Gln Asn Ala  
 65  
 25  
 <210> 756  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens  
 30  
 <400> 756  
 Trp Phe Cys Asn Cys Asn Ser Ser Cys Ile Val Leu Met Gln Thr Leu  
 1 5 10 15  
 Asp Leu Val Thr Val Ser Leu Cys His Glu Val Asn Val Met Phe Gln  
 35 20 25 30  
 Ala Phe Cys Leu Gln Lys Asn Leu Ser Cys Ala Phe Leu Asp Val Ser  
 35 40 45  
 Gly Ser Ile Val Gln Met Leu Leu Ala Asn Arg Asn Phe Lys Ile  
 50 55 60  
 40 Thr Trp Asn Leu His Lys Arg Leu Phe Met Cys Leu Thr Phe Leu Lys  
 65 70 75 80  
 Arg Ser Leu Leu Tyr Ser Leu Glu Tyr Val Thr  
 85 90  
 45  
 <210> 757  
 <211> 63  
 <212> PRT  
 <213> Homo sapiens  
 50  
 <400> 757  
 Asn Ser Tyr Xaa Leu Ile Lys Xaa Phe Ala Leu Xaa Asn Xaa Xaa His  
 1 5 10 15  
 Xaa Xaa Lys Xaa Met Xaa Asp Phe Phe Ala Ser Xaa Met Pro Glu Thr  
 20 25 30  
 55 Leu His Leu Pro Tyr Gly Thr Met Arg Gln Xaa Pro Asn Pro Met Xaa  
 35 40 45  
 Ala Leu Xaa Arg Tyr Ser Tyr Phe Tyr Xaa Xaa Glu Thr Ile Asn  
 50 55 60  
 60  
 <210> 758  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

<400> 758  
 Asp Ser Xaa Gln Ile Gln Cys Xaa His Xaa Asn Asp Thr Ala Thr Phe  
 1 5 10 15  
 5 Thr Xaa Ala Lys Pro Leu Ile Xaa Leu Ser Xaa Tyr Val Gln Xaa Gly  
 20 25 30  
 Pro His Val Thr Lys Ser Xaa Ala Glu Xaa Phe Gly Ser Xaa Asn Val  
 35 40 45  
 10 Asp Pro Ala Gly Xaa Arg Xaa Ser Lys Leu Leu Xaa Pro Phe  
 50 55 60

<210> 759  
 <211> 68  
 <212> PRT  
 15 <213> Homo sapiens

<400> 759  
 Thr Xaa Asn Ile Pro Phe Ile Ala Tyr Val Xaa Tyr Ser Asn Glu Tyr  
 1 5 10 15  
 20 Asn Lys Leu Leu Phe Lys Lys Val Arg Xaa Met Lys Ser Leu Leu Xaa  
 20 25 30  
 Lys Phe His Val Ile Leu Lys Phe Leu Xaa Ala Asn Lys Ser Xaa Cys  
 35 40 45  
 25 Thr Ile Xaa Xaa Xaa Thr Xaa Xaa Lys Xaa His Asp Xaa Phe Phe Cys  
 50 55 60  
 Lys Xaa Asn Ala  
 65

<210> 760  
 <211> 91  
 <212> PRT  
 30 <213> Homo sapiens

<400> 760  
 35 Trp Phe Arg Xaa Cys Lys Ser Ser Cys Ile Val Xaa Met Xaa Thr Leu  
 1 5 10 15  
 Asp Leu Xaa Thr Val Ser Leu Cys His Lys Val Asn Val Met Phe Gln  
 20 25 30  
 40 Ala Xaa Cys Leu Gln Lys Asn Xaa Ser Xaa Ala Phe Xaa Xaa Xaa  
 35 40 45  
 Gly Xaa Ile Val Gln Xaa Leu Leu Leu Ala Xaa Arg Asn Phe Lys Ile  
 50 55 60  
 Thr Trp Asn Leu Xaa Lys Arg Leu Phe Met Xaa Leu Thr Phe Leu Lys  
 65 70 75 80  
 45 Arg Ser Leu Leu Tyr Ser Leu Glu Tyr Xaa Thr  
 85 90

<210> 761  
 <211> 46  
 <212> PRT  
 50 <213> Homo sapiens

<400> 761  
 55 His Phe Ser Leu Leu Met Pro Leu Gly Leu Gly Arg Arg Lys Lys Ala  
 1 5 10 15  
 Pro Pro Leu Val Glu Asn Glu Glu Ala Glu Pro Gly Arg Gly Gly Leu  
 20 25 30  
 Gly Val Gly Glu Pro Gly Pro Leu Gly Gly Gly Gly Ser Gly  
 35 40 45  
 60

<210> 762  
 <211> 46  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 762

5 Pro Asp Pro Pro Pro Pro Arg Gly Pro Gly Ser Pro Thr Pro Ser Pro  
 1 5 10 15  
 Pro Arg Pro Gly Ser Ala Ser Ser Phe Ser Thr Arg Gly Gly Ala Phe  
 20 25 30  
 Phe Arg Arg Pro Ser Pro Ser Gly Met Ser Ser Glu Lys Trp  
 35 40 45

10

&lt;210&gt; 763

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

15

&lt;400&gt; 763

Ala Ala Gln Gly Gln Trp Xaa Gly Gly Gly Pro Gly Pro Leu Pro Arg  
 1 5 10 15  
 Ser Asn Gly Thr Ile Pro Ser Leu Val Pro Ser Leu Ala Gly Val Pro  
 20 25 30  
 Gly Pro Pro Val Pro Cys Ser Pro Pro Thr Ser Val Gly Ser Gly Thr  
 35 40 45  
 Gly Arg Gly Gly Ile Ser Gln Ile Gly Gly Pro Pro Pro Pro Pro  
 50 55 60  
 25 Leu Ser Thr Ile Ser Cys Gln Thr Gly Pro Ser Val Ser Leu Gly Pro  
 65 70 75 80  
 Trp Val Leu Phe Gly Gly His Xaa Leu Pro Ser Phe Leu Thr Gln Gly  
 85 90 95  
 Ile Gln Gly Arg Gly Leu Ser Phe Pro Pro Ala Asn Ala Ile Met Pro  
 100 105 110  
 30 Ser Pro Leu Leu Arg Gly Ala Pro Ser Leu Xaa Ser Leu Leu Pro Pro  
 115 120 125  
 His Leu Thr Xaa Val Cys Cys Glu Pro Arg Asn Leu Leu Pro Thr Ser  
 130 135 140  
 35 Asn Phe Ser Phe Gln Ala His Pro Trp Pro Arg Ala Gly Gly Arg Glu  
 145 150 155 160  
 Gly Arg Trp Arg Trp Val Phe Val Ser Glu Phe Ala Val Leu Asn Ile  
 165 170 175  
 Lys Asn Gln Ser Ala  
 40 180

40

&lt;210&gt; 764

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

45

&lt;400&gt; 764

Pro Pro Asn Arg Thr Gln Gly Pro Arg Glu Thr Glu Gly Pro Val Trp  
 1 5 10 15  
 50 Gln Leu Met Val Glu Ser Gly Gly Gly Gly Gly Gly Pro Pro Ile Trp  
 20 25 30  
 Leu Ile Pro Pro Leu Pro Val Pro Asp Pro Thr Glu Val Gly Gly Glu  
 35 40 45  
 Gln Gly Thr Gly Gly Pro Gly Thr Pro Ala Arg Leu Gly Thr Arg Glu  
 50 55 60  
 55 Gly Met Val Pro Leu Glu Arg Gly Lys Gly Pro Gly Pro Pro Pro Xaa  
 65 70 75 80  
 His Cys Pro Trp Ala Ala Xaa Leu Ala Gln Leu Glu Ala Xaa Val Leu  
 85 90 95  
 60 Xaa Xaa Xaa Pro Cys Trp Gly Pro Pro Gln Val  
 100 105

60

&lt;210&gt; 765

<211> 114  
 <212> PRT  
 <213> Homo sapiens

5           <400> 765  
 Ala Pro Gly Gly Ala Pro Ser Arg Asp Xaa Xaa Ser Gly Xaa Glu Pro  
   1                           5                           10                           15  
 Pro Ala Glu Leu Xaa Lys Gln Pro Lys Asp Asn Xaa Arg Glu Val Gly  
                  20                           25                           30  
 10 Gln Ala Pro Cys Pro Ala Pro Met Gly Pro Ser Pro Pro Trp Phe Pro  
                  35                           40                           45  
 Val Trp Pro Gly Ser Pro Ala Pro Leu Cys Pro Val Pro His Leu Pro  
   50                           55                           60  
 Gln Leu Gly Gln Ala Gln Gly Gly Glu Gly Ser Ala Lys Leu Gly Gly  
 15 65                           70                           75                           80  
 His Pro Arg Leu His His Phe Pro Pro Ser Ala Ala Lys Leu Val Pro  
                  85                           90                           95  
 Leu Ser Pro Trp Gly Leu Gly Phe Cys Leu Gly Val Met Xaa Phe Leu  
                  100                           105                           110  
 20 Val Ser

<210> 766  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

25           <400> 766  
 Ser Ser Ser Asn Leu Arg Leu Ser Phe Leu Ile Asn Glu Asn Ile Leu  
   1                           5                           10                           15  
 Gly Lys Cys Phe Arg Ser Gly Pro Ser Cys Ala Gly Pro Arg Ile Ser  
                  20                           25                           30  
 Pro Leu Ala Ala Gln Tyr Glu Cys Pro Arg Pro Ser Leu Leu Ile Met  
                  35                           40                           45  
 35 Ala Ser Val Pro Lys Thr Asn Lys Ile Glu Pro Arg Ser Tyr Ser Ile  
   50                           55                           60  
 Ile Pro Ser Cys Gly Ile Gln Ala Ala Arg Ala Cys Phe Glu His Ser  
 65                           70                           75                           80  
 Asn Phe Phe Lys Val Asn Ala Ser Gly Pro Ala Gly His Ser Ala Lys  
                  85                           90                           95  
 40 Ser Ile Glu Gly Ala Pro Arg Gly Lys Gly Arg Gly Arg Ala Val Ala  
                  100                           105                           110  
 Arg Leu Ala Ala Asp Arg Pro Pro Ala Pro Lys Ile Gln Leu Arg Ala  
                  115                           120                           125  
 45 Phe

<210> 767  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

50           <400> 767  
 Lys Met Ala Ala Gly Phe Lys Thr Val Glu Pro Xaa Glu Tyr Tyr Arg  
   1                           5                           10                           15  
 Arg Phe Leu Lys Glu Asn Cys Arg Pro Asp Gly Arg Glu Leu Gly Glu  
                  20                           25                           30  
 Phe Arg Thr Thr Thr Val Asn Ile Gly Ser Ile Ser Thr Ala Asp Gly  
                  35                           40                           45  
 60 Ser Ala Leu Val Lys Leu Gly Asn Xaa Thr Xaa Ile Cys Gly Val Lys  
   50                           55                           60  
 Ala Glu Phe Ala Ala Pro Ser Thr Asp Ala Pro Asp Lys Gly Tyr Val  
 65                           70                           75                           80



Val Pro Asn Val Asp Leu Pro Pro Leu Cys Ser Ser Arg Phe Arg Ser  
                                     85                                    90                                    95  
 Gly Pro Pro Gly Glu Glu Ala Gln Val Ala Ser Gln Phe Ile Ala Asp  
                                     100                                    105                                    110  
 5 Val Ile Glu Asn Ser Gln Ile Ile Gln Lys Glu Asp Leu Cys Ile Ser  
                                     115                                    120                                    125  
 Pro Gly Lys Leu Val Trp Val Leu Tyr Cys Asp Leu Ile Cys Leu Asp  
                                     130                                    135                                    140  
 Tyr Asp Gly Asn Ile Leu Asp Ala Cys Thr Phe Ala Leu  
 10 145                                    150                                    155

&lt;210&gt; 768

&lt;211&gt; 171

&lt;212&gt; PRT

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 768

Lys Met Ala Ala Gly Phe Lys Thr Val Glu Pro Xaa Glu Tyr Tyr Arg  
   1                                    5                                    10                                    15  
 20 Arg Phe Leu Lys Glu Asn Cys Arg Pro Asp Gly Arg Glu Leu Gly Glu  
                                     20                                    25                                    30  
 Phe Arg Thr Thr Thr Val Asn Ile Gly Ser Ile Ser Thr Ala Asp Gly  
                                     35                                    40                                    45  
 Ser Ala Leu Val Lys Leu Gly Asn Xaa Thr Xaa Ile Cys Gly Val Lys  
 25 50                                    55                                    60  
 Ala Glu Phe Ala Ala Pro Ser Thr Asp Ala Pro Asp Lys Gly Tyr Val  
   65                                    70                                    75                                    80  
 Val Pro Asn Val Asp Leu Pro Pro Leu Cys Ser Ser Arg Phe Arg Ser  
                                     85                                    90                                    95  
 30 Gly Pro Pro Gly Glu Glu Ala Gln Val Ala Ser Gln Phe Ile Ala Asp  
                                     100                                    105                                    110  
 Val Ile Glu Asn Ser Gln Ile Ile Gln Lys Glu Asp Leu Cys Ile Ser  
                                     115                                    120                                    125  
 Pro Gly Lys Leu Val Trp Val Leu Tyr Cys Asp Leu Ile Cys Leu Asp  
 35 130                                    135                                    140  
 Tyr Asp Gly Asn Ile Leu Asp Ala Cys Thr Phe Xaa Leu Leu Ala Ala  
   145                                    150                                    155                                    160  
 Leu Lys Asn Val Gln Val Ala Leu Lys Leu Leu  
                                     165                                    170

40

&lt;210&gt; 769

&lt;211&gt; 112

&lt;212&gt; PRT

45 &lt;213&gt; Homo sapiens

&lt;400&gt; 769

Gln Leu Pro Glu Val Thr Ile Asn Glu Glu Thr Ala Leu Ala Glu Val  
   1                                    5                                    10                                    15  
 50 Asn Leu Lys Lys Lys Ser Tyr Leu Asn Ile Arg Thr His Pro Val Ala  
                                     20                                    25                                    30  
 Thr Ser Phe Ala Val Phe Asp Asp Thr Leu Leu Ile Val Asp Pro Thr  
                                     35                                    40                                    45  
 Gly Glu Glu Glu His Leu Ala Thr Gly Thr Leu Thr Ile Val Met Asp  
   50                                    55                                    60  
 55 Glu Glu Gly Lys Xaa Cys Xaa His Lys Pro Gly Gly Ser Gly Leu  
   65                                    70                                    75                                    80  
 Thr Gly Ala Lys Leu Gln Asp Cys Met Ser Arg Ala Val Thr Arg His  
                                     85                                    90                                    95  
 Lys Glu Val Lys Lys Leu Met Asp Glu Val Ile Lys Ser Met Lys Pro  
 60 100                                    105                                    110

&lt;210&gt; 770

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 770

5 Gln His Ala Gly Gly Ser Met Ser Gln Xaa Leu Gln Ala Lys Val Glu  
 1 5 10 15  
 Ile Phe Xaa Lys Met Phe Ile Ser Ala Gly Xaa Glu Gly Thr Glu Arg  
 20 25 30  
 Cys Thr Xaa Xaa Xaa Xaa Leu Gly Xaa Xaa Xaa Gly His Ala Ala Pro  
 35 40 45  
 10 Tyr Asn Arg Trp Ile Leu Xaa Glu Phe Xaa Xaa Asn Xaa Lys Val Xaa  
 50 55 60  
 Thr Glu Leu Ile Ser Tyr Phe Ser Xaa Thr Xaa Gly Thr Pro Ser Ala  
 65 70 75 80  
 15 Ser Gly Phe Thr Asn Glu Thr  
 85

&lt;210&gt; 771

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 771

25 Phe Phe Ile Phe Cys Arg Tyr Glu Val Ser Pro Cys Cys Ser Gly Trp  
 1 5 10 15  
 Ser Gln Ala Pro Glu Leu Lys Gln Pro Ala Cys Leu Arg Leu Pro Lys  
 20 25 30  
 Cys Trp Asp His Lys His Glu Pro Leu Cys Pro Ala Trp His Leu Ile  
 35 40 45  
 30 Cys Glu Ser His Thr Ile Ser Asn Arg Asn Ile Lys Ile Pro Gly His  
 50 55 60  
 Phe Xaa Ser Pro Arg Leu Gly Gln Leu His Ser Leu Thr Cys Ser Val  
 65 70 75 80  
 Leu Pro Gln Ser Gln Cys Gly Thr Arg Leu Gln Ala Gln His Trp Gly  
 85 90 95  
 35 Cys Ala Asp Arg Ser Trp Phe Lys Ser Gln Leu Pro Ala Leu Glu Pro  
 100 105 110  
 Tyr Ser Asp Leu Ser Ala Pro Arg Leu Pro Gln Arg Val Leu Leu Gln  
 115 120 125  
 40 Pro Val Ser Gln Cys Thr Cys Pro Ala His Glu Leu Thr Glu Leu Met  
 130 135 140  
 Ala Ser Glu Ser Glu Cys Leu  
 145 150

&lt;210&gt; 772

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 772

50 Glu Leu Pro Glu Lys Lys Lys Met Lys Tyr Ile Gln Asp Phe Gln Arg  
 1 5 10 15  
 Glu Lys Gln Glu Phe Glu Arg Asn Leu Ala Arg Phe Arg Glu Asp His  
 20 25 30  
 55 Pro Asp Leu Ile Gln Asn Ala Lys Lys Ser Asp Ile Pro Glu Lys Pro  
 35 40 45  
 Lys Thr Pro Gln Gln Leu Trp Tyr Thr His Glu Lys Lys Val Tyr Leu  
 50 55 60  
 Lys Val Arg Pro Asp Glu Ile Met Arg Asp Tyr Ile Gln Lys His Pro  
 65 70 75 80  
 60 Glu Leu Asn Ile Ser Glu Glu Gly Ile Thr Lys Ser Thr Leu Thr Lys  
 85 90 95  
 Ala Glu Arg Gln Leu Lys Asp Lys Phe Asp Gly Arg Pro Thr Lys Pro

100 105 110  
 Pro Pro Asn Ser Tyr Ser Leu Tyr Cys Ala Glu Leu Met Ala Asn Met  
 115 120 125  
 Lys Asp Val Pro Ser Thr Glu Ala His Gly Ala Val Gln Pro Ala Val  
 130 135 140  
 5 Glu Ala Ala Val Pro Glu Gly Glu Gly Arg Leu Xaa Gln Glu Val  
 145 150 155  
  
 <210> 773  
 10 <211> 151  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 773  
 15 Lys Lys Glu Arg Lys Trp Gly Arg Pro Gly Gly Gln Gly Thr Glu His  
 1 5 10 15  
 Gly Gly Glu Thr Lys Val Val Ser Trp Gly Gly Glu Leu Leu Gly Ser  
 20 20 25 30  
 Pro Trp Leu Pro Trp Gly Gly Ala Glu Pro Gln Leu Glu Ser Glu Ser  
 35 40 45  
 Glu Glu Ser Pro Glu Glu Glu Glu Leu Glu Leu Leu Pro Ser Asp Ser  
 50 55 60  
 Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser  
 65 70 75 80  
 25 Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Leu Asp Cys Arg  
 85 90 95  
 Val Val Arg Leu Asp Leu Gly Phe Gly Pro Arg Ser Leu Val Met Leu  
 100 105 110  
 Leu Arg Leu Leu Glu Met Tyr Ser Leu Tyr Ala Ala Arg Ser Trp Gly  
 115 120 125  
 30 Asp Arg Leu Leu Thr Gln Arg Ser Arg Cys Thr Leu Tyr Cys Phe Cys  
 130 135 140  
 Cys Ser Ser Ala Ser Phe Leu  
 145 150  
 35  
 <210> 774  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens  
 40  
 <400> 774  
 Gly Gly Gly Ala Gly Ala Ala Ala Leu Gly Leu Ile Ile Phe Ile Leu  
 1 5 10 15  
 Ile Val Ile Leu Val Val Val Phe Val Leu Val Ile Leu Ile Leu Phe  
 20 25 30  
 45 Ile Ile Leu Leu Gly Leu Arg Leu Gly Leu Gln Ser Ser Pro Ala Gly  
 35 40 45  
 Phe Gly Val Trp Ala Ser Gln Leu Gly His Ala Leu Thr Phe Ile Gly  
 50 55 60  
 Asp Val Leu Phe Ile Cys Cys Thr Val Leu Gly Arg Gln Ala Leu Asn  
 65 70 75 80  
 Pro Glu Val Gln Val His Leu Val Leu Leu Leu Leu Leu Gly Gln  
 85 90 95  
 50 Leu Phe Val Ser Ala Pro Ser Gly Ser Gly Arg Cys Ala Ala Ser Asp  
 100 105 110  
 55 Cys Arg Ser Pro Pro Cys Ala Pro Ser Ala Ala Gly Gly Ser Xaa Pro  
 115 120 125  
 His Trp Asn Ser Ser Ser Trp Glu Glu Leu Xaa Xaa  
 130 135 140  
 60  
 <210> 775  
 <211> 130  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 775

5 Arg Ser Ala Trp Trp Arg Ser Ala Val Ala Gly Ser Ala Ser Pro Arg  
 1 5 10 15  
 Ala Arg Arg Ser Thr Tyr Lys Lys Leu Ala Glu Glu Gln Gln Lys Gln  
 20 25 30  
 Tyr Lys Val His Leu Asp Leu Trp Val Lys Ser Leu Ser Pro Gln Asp  
 35 40 45  
 10 Arg Ala Ala Tyr Lys Glu Tyr Ile Ser Asn Lys Arg Lys Ser Met Thr  
 50 55 60  
 Lys Leu Arg Gly Pro Asn Pro Lys Ser Ser Arg Thr Thr Leu Gln Ser  
 65 70 75 80  
 Lys Ser Glu Ser Glu Glu Asp Asp Glu Glu Asp Glu Asp Asp Glu Asp  
 85 90 95  
 15 Glu Asp Asp Asp Glu Asp Asp Asp Glu Asp Glu Asp Asn Glu Ser Glu  
 100 105 110  
 Gly Ser Ser Ser Ser Ser Ser Ser Gly Asp Ser Ser Asp Ser Asp  
 115 120 125  
 20 Ser Asn  
 130

&lt;210&gt; 776

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 776

30 Pro Pro Ala Leu Pro Leu Pro Val Pro Arg Ser Ala Arg His Glu Ile  
 1 5 10 15  
 Pro Arg Arg Gly Ala Thr Arg Gly Arg Val Gly Glu Ala Gln Arg Gln  
 20 25 30  
 Pro Leu Pro Ala Met Glu Glu Glu Ala Arg Gly Ala His Leu Arg Pro  
 35 40 45  
 35 Pro Glu Pro Val Pro Arg Gln Pro Pro Arg Ala Pro Gln Gly Ala Ala  
 50 55 60  
 Leu Pro Leu His Pro Gln Gly Gly Leu Arg Gly Ala His Gly Gln Val  
 65 70 75 80  
 Arg Val Leu His His Arg His His Arg Pro Gln Gly Asp Arg Leu Pro  
 85 90 95  
 40 Leu Arg Gly Arg Glu Leu Leu Glu Arg Gly His Arg Ala Gly Ala His  
 100 105 110  
 Arg Phe Pro Glu Pro Pro Arg Pro Ala Gly Leu Ser Gln Pro Pro Gly  
 115 120 125  
 45 Thr His Arg Pro Ala Ala Pro Ala Glu Asp Ala Val Ala Ala Ala Ala  
 130 135 140  
 Ala Ala Pro Ser Glu Pro Ser Glu Pro Ser Arg Pro Ser Pro Gln Pro  
 145 150 155 160  
 50 Lys Pro Arg Thr Pro  
 165

&lt;210&gt; 777

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 777

60 Ala Cys Ser Pro Pro Ala Pro Ala Arg Ala Pro Arg Ser Cys Ala Ser  
 1 5 10 15  
 Thr Pro Ser Ser Arg Trp Thr Ala Trp Ser Ala Arg Ala Ser Thr Cys  
 20 25 30  
 Thr Ser Pro Ser Ser Pro Pro Thr Thr Arg Arg Ser Thr Ser Ala Ala  
 35 40 45

Arg Ala Arg Ala Ala Gly Thr Arg Pro Ser Arg Trp Arg Ser Ser Ile  
 50 55 60  
 Ser Arg Thr Ala Ala Pro Cys Arg Thr Phe Ala Ala Ala Arg Asn Ala  
 65 70 75 80  
 5 Pro Thr Arg Arg Thr Arg Arg Gly Arg Arg Gly Cys Arg Gly Arg Arg  
 85 90 95  
 Thr Leu Arg Ala Leu Gly Ala Leu Gln Ala Ile Pro Ala Ala Gln Thr  
 100 105 110  
 10 Pro His Ala Met Ser Pro Pro Arg Ala Ile Arg Trp Thr Ser Arg Thr  
 115 120 125  
 Glu Ala Arg Thr Trp Pro Ala Leu Leu Gln Pro Cys Ser Xaa Lys Asn  
 130 135 140  
 Xaa Pro Cys Ala Arg Ile Leu Ala Ser Val Gln Arg Ala Pro  
 145 150 155

15

<210> 778  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens

20

<400> 778  
 Arg Pro His Cys Arg Ser Gln Ser Arg Ala Arg His Asp Met Lys Ser  
 1 5 10 15  
 25 Pro Asp Glu Val Leu Arg Glu Gly Glu Leu Glu Lys Arg Ser Asp Ser  
 20 25 30  
 Leu Phe Gln Leu Trp Lys Lys Lys Arg Gly Val Leu Thr Ser Asp Arg  
 35 40 45  
 Leu Ser Leu Phe Pro Ala Ser Pro Arg Ala Arg Pro Lys Glu Leu Arg  
 50 55 60  
 30 Phe His Ser Ile Leu Lys Val Asp Cys Val Glu Arg Thr Gly Lys Tyr  
 65 70 75 80  
 Val Tyr Phe Thr Ile Val Thr Thr Asp His Lys Glu Ile Asp Phe Arg  
 85 90 95  
 Cys Ala Gly Glu Ser Cys Trp Asn Ala Ala Ile Ala Leu Ala Leu Ile  
 100 105 110  
 35 Asp Phe Gln Asn Arg Arg Ala Leu Gln Asp Phe Arg Ser Arg Gln Glu  
 115 120 125  
 Arg Thr Asp Pro Pro His Pro Pro Arg Thr Pro Trp Leu Pro Arg Pro  
 130 135 140  
 40 Pro His Pro Pro Ser Pro Arg Ser Pro Pro Gly His Pro Arg Ser Pro  
 145 150 155 160  
 Asn Pro Ala Arg His Glu Pro Ala Ala Gly His Thr Leu Asp Glu Ser  
 165 170 175  
 Asp Arg Gly

45

<210> 779  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens

50

<400> 779  
 Pro Arg Ser Asp Ser Ser Val Trp Pro Ala Ala Gly Ser Trp Arg  
 1 5 10 15  
 55 Ala Gly Phe Gly Leu Arg Gly Trp Pro Gly Gly Leu Arg Gly Leu Gly  
 20 25 30  
 Gly Cys Gly Gly Arg Gly Ser His Gly Val Leu Gly Gly Cys Gly Gly  
 35 40 45  
 Ser Val Arg Ser Trp Arg Leu Arg Lys Ser Cys Arg Ala Arg Arg Phe  
 50 55 60  
 60 Trp Lys Ser Met Ser Ala Ser Ala Met Ala Ala Phe Gln Gln Leu Ser  
 65 70 75 80  
 Pro Ala Gln Arg Lys Ser Ile Ser Leu Trp Ser Val Val Thr Met Val

85 90 95  
 Lys Tyr Thr Tyr Leu Pro Val Arg Ser Thr Gln Ser Thr Leu Arg Met  
 100 105 110  
 Glu Trp Lys Arg Ser Ser Leu Gly Arg Ala Arg Gly Leu Ala Gly Asn  
 115 120 125  
 5 Arg Leu Arg Arg Ser Glu Val Ser Thr Pro Arg Phe Phe Phe His Ser  
 130 135 140  
 Trp Lys Arg Leu Ser Leu Arg Phe Ser Asn Ser Pro Ser Arg Ser Thr  
 145 150 155 160  
 10 Ser Ser Gly Asp Phe Met Ser Cys Arg Ala Arg Asp Trp Glu Arg Gln  
 165 170 175  
 Cys Gly Arg

15 <210> 780  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

20 <400> 780  
 Ala Trp Arg Cys Thr Arg Val Ser Glu Ala Leu Leu Leu Ser Ala Arg  
 1 5 10 15  
 Gln Glu Asp Val Cys Arg Arg Arg Ser Ala Gly Pro Val Ala Phe Thr  
 20 25 30  
 25 Val Leu Cys Leu Ser Arg Pro Ser Arg Leu Pro Thr Ala Ala Ile Pro  
 35 40 45  
 Pro Tyr Ser Pro Ser Gly Thr Trp Arg Trp Ser Val Gln Ala Leu Ala  
 50 55 60  
 Cys Asn Gln His Xaa Ser Leu Gly Leu Val Gln Glu Gly Ser Ser Gly  
 65 70 75 80  
 30 Lys Ala Pro Ser Ser Phe Pro Ala Arg Leu Gly Pro Ala Thr Val Arg  
 85 90 95  
 Leu Arg Xaa Gly Leu Lys Glu Xaa Ala Gly Pro Glu Phe Pro Leu Ala  
 100 105 110  
 35 Arg Xaa Glu Leu Xaa Thr Lys Gly Arg Arg Xaa Pro Pro Gly Arg Xaa  
 115 120 125  
 Xaa Val Pro Pro Leu Ala  
 130

40 <210> 781  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

45 <400> 781  
 Gly Gly Met Ala Ala Val Gly Ser Leu Leu Gly Arg Leu Arg Gln Ser  
 1 5 10 15  
 Thr Val Lys Ala Thr Gly Pro Ala Leu Arg Arg Leu His Thr Ser Ser  
 20 25 30  
 50 Trp Arg Ala Asp Ser Ser Arg Ala Ser Leu Thr Arg Val His Arg Gln  
 35 40 45  
 Ala Tyr Ala Arg Leu Tyr Pro Val Leu Leu Val Lys Gln Asp Gly Ser  
 50 55 60  
 Thr Ile His Ile Arg Tyr Arg Glu Pro Arg Arg Met Leu Ala Met Pro  
 65 70 75 80  
 55 Ile Asp Leu Asp Thr Leu Ser Pro Glu Glu Arg Arg Ala Arg Leu Arg  
 85 90 95  
 Lys Arg Glu Ala Gln Leu Gln Ser Arg Lys Glu Tyr Glu Gln Glu Leu  
 100 105 110  
 60 Ser Asp Asp Leu His Val Glu Arg Tyr Arg Gln Xaa Trp Thr Arg Thr  
 115 120 125  
 Lys Lys  
 130

<210> 782  
 <211> 56  
 <212> PRT  
 5 <213> Homo sapiens  
  
 <400> 782  
 Asn Asp Val Pro Asn Gln Phe Leu Val Tyr Ser Phe Pro Lys Ser Lys  
 1 5 10 15  
 10 Ile Thr Lys Val Leu Lys Val His Lys Thr Asp Leu His Leu Cys Ile  
 20 25 30  
 Pro Phe Gln Ile Asn Pro Lys Ser Met Tyr Ser Met Phe Asn Ser Met  
 35 40 45  
 Gln Tyr Ala Lys Ala Leu Cys Cys  
 15 50 55  
  
 <210> 783  
 <211> 55  
 <212> PRT  
 20 <213> Homo sapiens  
  
 <400> 783  
 Asn Asp Val Pro Asn Gln Phe Leu Val Tyr Ser Phe Pro Lys Ser Lys  
 1 5 10 15  
 25 Ile Thr Lys Val Leu Lys Val His Lys Thr Asp Leu His Leu Cys Ile  
 20 25 30  
 Pro Phe Gln Ile Asn Pro Lys Ser Met Tyr Ser Met Phe Asn Ser Met  
 35 40 45  
 Gln Tyr Ala Lys Ala Leu Cys  
 30 50 55  
  
 <210> 784  
 <211> 259  
 <212> PRT  
 35 <213> Homo sapiens  
  
 <400> 784  
 Lys Leu Ser Ala Leu Phe Ile Asn Leu Ile Ser Asp Pro Ser Arg Trp  
 1 5 10 15  
 40 Val Arg Gln Ala Ala Phe Gln Ser Leu Gly Pro Phe Ile Ser Thr Phe  
 20 25 30  
 Ala Asn Pro Ser Ser Ser Gly Gln Tyr Phe Lys Glu Glu Ser Lys Ser  
 35 40 45  
 Ser Glu Glu Met Ser Val Glu Asn Lys Asn Arg Thr Arg Asp Gln Glu  
 45 50 55 60  
 Ala Pro Glu Asp Val Gln Val Arg Pro Glu Asp Thr Pro Ser Asp Leu  
 65 70 75 80  
 Ser Val Ser Asn Ser Ser Val Ile Leu Glu Asn Thr Met Glu Asp His  
 85 90 95  
 50 Ala Ala Glu Ala Ser Gly Lys Pro Leu Gly Glu Ile Ser Val Pro Leu  
 100 105 110  
 Asp Ser Ser Leu Leu Cys Thr Leu Ser Ser Glu Ser His Gln Glu Ala  
 115 120 125  
 Ala Ser Asn Glu Asn Asp Lys Lys Pro Gly Asn Tyr Lys Ser Met Leu  
 55 130 135 140  
 Arg Pro Glu Val Gly Thr Ser Gln Asp Ser Ala Leu Leu Asp Gln  
 145 150 155 160  
 Glu Leu Tyr Asn Ser Phe His Phe Trp Arg Thr Pro Leu Pro Glu Ile  
 165 170 175  
 60 Asp Leu Asp Ile Glu Leu Glu Gln Asn Ser Gly Gly Lys Pro Ser Pro  
 180 185 190  
 Glu Gly Pro Glu Glu Glu Ser Glu Gly Pro Val Pro Ser Ser Pro Asn  
 195 200 205

Ile Thr Met Ala Thr Arg Lys Glu Leu Glu Glu Met Ile Glu Asn Leu  
 210 215 220  
 Glu Pro Pro Ile Asp Asp Pro Asp Gly Xaa Ala Gln Val Gly Ser Ala  
 225 230 235 240  
 5 Val Arg Cys Thr Thr Cys Phe Gln Xaa Trp Asp Xaa His Glu Glu Xaa  
 245 250 255  
 His Arg Phe

10 <210> 785  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

15 <400> 785  
 Ile Leu Phe Gly Gln Glu Asn Leu Xaa His Asn Ser Leu Asn Ser Met  
 1 5 10 15  
 Ile Lys Asp Cys Ser Thr Pro Lys Ser Gly His Arg Tyr Val Gln Tyr  
 20 20 25 30  
 Val Lys Lys Leu His Leu Arg Ala Asp His Asp Gln Val Lys Asn Thr  
 35 40 45  
 Arg His Thr Leu Tyr Arg Leu Ile Asn Phe Leu Gln Val Met Thr Ser  
 50 55 60  
 Met Lys Lys Ser Asp Thr Asp Thr Gln Gln Pro Phe Cys Lys Cys Val  
 25 65 70 75 80  
 Gln Gln Tyr Ala Ala Leu Lys Ser Leu Ser Gln Ser Tyr Leu Xaa Trp  
 85 90 95  
 His Gln Xaa Leu Xaa Glu Met  
 100

30 <210> 786  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

35 <400> 786  
 Glu Leu Glu Asp Lys Val Ala Ala Cys Gln Lys Glu Gln Ala Asp Phe  
 1 5 10 15  
 Leu Pro Arg Ile Glu Glu Thr Lys Trp Glu Val Cys Gln Lys Ala Gly  
 40 20 25 30  
 Glu Ile Ser Leu Leu Lys Gln Gln Leu Lys Asp Ser Gln Ala Asp Val  
 35 40 45  
 Ser Gln Lys Leu Ser Glu Ile Val Gly Leu Arg Ser Gln Leu Arg Glu  
 50 55 60  
 Gly Arg Ala Ser Leu Arg Glu Lys Glu Glu Gln Leu Leu Ser Leu Arg  
 45 65 70 75 80  
 Asp Ser Phe Ser Ser Lys Gln Ala Ser Leu Glu Leu Gly Glu Gly Glu  
 85 90 95  
 Leu Pro Ala Ala Cys Leu Lys Pro Ala Leu Thr Pro Val Asp Pro Ala  
 50 100 105 110  
 Glu Pro Gln Asp Ala Leu Ala Thr Cys Glu Ser Asp Glu Ala Lys Met  
 115 120 125  
 Arg Arg Gln Ala Gly Val Ala Ala Ala Ser Leu Val Ser Val Asp  
 130 135 140  
 55 Gly Glu Ala Glu Ala Gly Gly Glu Ser Gly Thr Arg Ala Leu Arg Arg  
 145 150 155 160  
 Glu Val Gly Arg Leu Gln Ala Glu Leu Ala Ala Glu Arg Arg Ala Arg  
 165 170 175  
 Glu Arg Gln Gly Ala Ser Phe Ala Glu Glu Arg Arg Val Trp Leu Glu  
 180 185 190  
 60 Glu Lys Glu Lys Val Ile Glu Tyr Pro Glu Ser Ser Leu Gln Leu Xaa  
 195 200 205  
 Leu Arg Xaa Arg Cys Thr Asn Arg Asn Pro  
 290



210 215

<210> 787  
 <211> 208  
 <212> PRT  
 <213> Homo sapiens

<400> 787

Xaa Gln Leu Gln Ala Ala Phe Trp Val Leu Asp His Leu Leu Leu Phe  
 1 5 10 15  
 Leu Lys Pro Asn Ala Ala Leu Leu Gly Glu Ala Gly Thr Leu Ala Leu  
 20 25 30  
 Pro Gly Pro Pro Leu Ser Arg Gln Leu Gly Leu Gln Pro Pro His Leu  
 35 40 45  
 Pro Pro Gln Gly Pro Arg Pro Ala Leu Pro Ala Ser Leu Arg Leu Pro  
 50 55 60  
 Val His Gly Asn Gln Gly Gly Ser Gly His Pro Gly Leu Thr Ala  
 65 70 75 80  
 His Leu Ser Leu Val Ala Leu Ala Gly Gly Gln Ser Ile Leu Trp Leu  
 85 90 95  
 Gly Arg Val His Gly Gly Gln Arg Arg Leu Glu Ala Gly Gly Arg Gln  
 100 105 110  
 Leu Ala Phe Ala Gln Leu Gln Ala Gly Leu Leu Ala Ala Glu Gly Val  
 115 120 125  
 Pro Gln Ala Glu Gln Leu Leu Leu Leu Pro Gln Arg Ser Pro Ala  
 130 135 140  
 Leu Pro Gln Leu Arg Ala Gln Ser His Asp Leu Thr Gln Leu Leu Arg  
 145 150 155 160  
 His Ile Arg Leu Arg Val Leu Gln Leu Leu Leu Gln Glu Gly Asp Leu  
 165 170 175  
 Ala Ser Leu Leu Ala His Leu Pro Leu Ser Phe Leu Tyr Pro Gly Gln  
 180 185 190  
 Glu Val Gly Leu Leu Leu Leu Ala Gly Gly His Leu Val Leu Gln Leu  
 195 200 205

<210> 788  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 788

Arg Arg Ile Leu Ala Ser Ser Leu Ser Gln Val Ala Arg Ala Ser Cys  
 1 5 10 15  
 Gly Ser Ala Gly Ser Thr Gly Val Ser Ala Gly Leu Arg Gln Ala Ala  
 20 25 30  
 Gly Ser Ser Pro Ser Pro Ser Ser Arg Leu Ala Cys Leu Leu Lys  
 35 40 45  
 Glu Ser Arg Arg Leu Ser Ser Cys Ser Ser Phe Ser Arg Ser Glu Ala  
 50 55 60  
 Arg Pro Ser Arg Ser Cys Glu Arg Ser Pro Thr Ile Ser Leu Asn Phe  
 65 70 75 80  
 Cys Asp Thr Ser Ala Cys Glu Ser Phe Ser Cys Cys Phe Arg Arg Glu  
 85 90 95  
 Ile Ser Pro Ala Phe Trp His Thr Ser His Leu Val Ser Ser Ile Arg  
 100 105 110  
 Gly Arg Lys Ser Ala Cys Ser Phe Trp Gln Ala Ala Thr Leu Ser Ser  
 115 120 125  
 Ser Ser  
 130

<210> 789  
 <211> 252  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 789

5 Val Pro Gln Gly Tyr Pro Gly Gly Val Pro Thr Phe Phe Arg Asp Met  
 1 5 10 15  
 Lys Gln Gly Leu Leu Ser Val Gly Ile Gly Gly Arg Glu Ser Arg Asn  
 20 25 30  
 Gly Cys Leu Asp Val Glu Lys Asp Cys Ser Ile Thr Lys Phe Leu Asn  
 35 40 45  
 10 Arg Ile Leu Gly Leu Glu Val His Lys Gln Asn Ala Leu Phe Gln Tyr  
 50 55 60  
 Phe Ser Asp Thr Phe Asp His Leu Ile Glu Met Asp Lys Arg Glu Gly  
 65 70 75 80  
 Lys Tyr Asp Met Gly Ile Leu Asp Leu Ala Pro Gly Ile Glu Glu Ile  
 15 85 90 95  
 Tyr Glu Glu Ser Gln Gln Val Phe Leu Ala Pro Gly His Pro Gln Asp  
 100 105 110  
 Gly Gln Val Val Phe Tyr Lys Ile Ser Val Asp Arg Gly Leu Lys Trp  
 115 120 125  
 20 Glu Asp Ala Phe Ala Lys Ser Leu Ala Leu Thr Gly Pro Tyr Asp Gly  
 130 135 140  
 Phe Tyr Leu Ser Tyr Lys Val Arg Gly Asn Lys Pro Ser Cys Leu Leu  
 145 150 155 160  
 Ala Glu Gln Asn Arg Gly Gln Phe Phe Thr Val Tyr Lys Pro Asn Ile  
 25 165 170 175  
 Gly Arg Gln Ser Gln Leu Glu Ala Leu Asp Ser Leu Arg Arg Lys Phe  
 180 185 190  
 His Arg Val Thr Ala Glu Glu Ala Lys Gly Ala Leu Gly Glu Trp Leu  
 195 200 205  
 30 Arg Phe Val Ala Asp Ala Leu Gln Ala Thr Ala Pro Gly Thr Gly Thr  
 210 215 220  
 Cys Arg Leu Ala Gln Glu Gly Xaa Gly Leu Xaa Ala Gly Ala Cys Gly  
 225 230 235 240  
 Leu Arg His Gln Leu His Ala Cys Xaa Ala Pro Leu  
 35 245 250

&lt;210&gt; 790

&lt;211&gt; 94

&lt;212&gt; PRT

40 &lt;213&gt; Homo sapiens

&lt;400&gt; 790

Arg Gly Gln Gly Arg Ala Gly Gly Gly Arg Ile Ala Tyr Ile Ser Arg  
 1 5 10 15  
 45 Gly Leu Pro His Gly Ala Pro Glu Thr Arg Gly Pro Glu His Leu Gly  
 20 25 30  
 Phe Pro Glu Phe Leu Ala Leu Gly Thr Thr Arg Phe His Gly Phe Gln  
 35 40 45  
 Gly Phe Gly Pro Thr Glu Pro Leu Trp Val Pro Ser Pro Arg Ala Ala  
 50 50 55 60  
 Thr Arg Ser Pro Phe Leu Leu Gly Arg Arg Gly Thr Glu Arg Ala Leu  
 65 70 75 80  
 Pro Arg Pro Gly Pro Gln Leu Ser Xaa Trp Ala Pro Gln Gly  
 85 90

55

&lt;210&gt; 791

&lt;211&gt; 225

&lt;212&gt; PRT

60 &lt;213&gt; Homo sapiens

&lt;400&gt; 791

Leu Lys Ala Lys Asp Gln Gly Lys Pro Glu Val Gly Glu Tyr Ala Lys  
 1 5 10 15

Leu Glu Lys Ile Asn Ala Glu Gln Gln Leu Lys Ile Gln Glu Leu Gln  
 20 25 30  
 Glu Lys Leu Glu Lys Ala Val Lys Ala Ser Thr Glu Ala Thr Glu Leu  
 35 40 45  
 5 Leu Gln Asn Ile Arg Gln Ala Lys Glu Arg Ala Glu Arg Glu Leu Glu  
 50 55 60  
 Lys Leu Gln Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys Lys Leu  
 65 70 75 80  
 Val Glu Ala Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val Lys Arg  
 85 90 95  
 10 Leu Glu Thr Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp Ile Gln  
 100 105 110  
 Thr Lys Ser Gln Gln Ile Gln Gln Met Ala Asp Lys Ile Leu Glu Leu  
 115 120 125  
 15 Glu Glu Lys His Arg Glu Ala Gln Val Ser Ala Gln His Leu Glu Val  
 130 135 140  
 His Leu Lys Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys Val Leu  
 145 150 155 160  
 Asp Asn Gln Ile Lys Lys Asp Leu Ala Asp Lys Glu Thr Leu Glu Asn  
 165 170 175  
 20 Met Met Gln Arg His Glu Glu Glu Ala His Glu Lys Gly Lys Ile Leu  
 180 185 190  
 Ser Glu Gln Lys Ala Met Ile Asn Ala Met Asp Ser Lys Ile Arg Ser  
 195 200 205  
 25 Leu Glu Gln Xaa Ile Val Glu Leu Ser Glu Ala Asn Lys Leu Ala Ala  
 210 215 220  
 Lys  
 225  
 30 <210> 792  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens  
 35 <400> 792  
 Asn Ala Lys Thr Glu Arg Pro Ile Phe Xaa Asp Leu Ser Lys Tyr Trp  
 1 5 10 15  
 Gly Pro Arg Xaa Lys Thr Ser Ala Asn Ile Gln Ser Asn Leu Pro Trp  
 20 25 30  
 40 Gly Arg Glu Gly Arg Glu Tyr Asp Pro Thr Asp Ser Lys Gln His Ile  
 35 40 45  
 Lys Arg His Ser Arg Thr Phe Ala Lys Gly Ala Thr Thr Trp Arg Phe  
 50 55 60  
 Val Gly Val Ser Asn Lys Lys Ala Leu Arg Leu Lys His Xaa Xaa Glu  
 65 70 75 80  
 45 Gly Ala Gly Met Gln Ala Arg Leu Gln Ser Gly Lys Gly Ser Glu Leu  
 85 90 95  
 Xaa Thr Gln Leu Lys Thr Arg Ser Cys Ser Pro Ala Xaa Gly Glu Thr  
 100 105 110  
 50 Gly Leu Pro Leu Ser Leu Pro Lys Arg Cys Leu Gly Leu Leu Arg Arg  
 115 120 125  
 Ala  
 55 <210> 793  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens  
 60 <400> 793  
 Glu Tyr Lys Val Ser Cys Lys Tyr Val Gln Ser Phe Glu Leu Val Leu  
 1 5 10 15  
 Xaa Ser Arg Lys Gln Phe Thr Asp Xaa Thr His Asn Ile His Phe Gln

20 25 30  
 Gly Ser Arg Ser Pro Phe Leu Met Glu Ile Leu Asn Glu Met Pro Arg  
 35 40 45  
 Leu Lys Asp Pro Phe Ser Xaa Thr Phe Pro Asn Thr Gly Asp Gln Xaa  
 5 50 55 60  
 Thr Lys Leu Gln Gln Thr Phe Asn Gln Ile Cys Pro Gly Asp Gly Arg  
 65 70 75 80  
 Gly Gly Ser Thr Thr Pro Gln Thr Pro Ser Asn Thr  
 85 90  
 10  
 <210> 794  
 <211> 219  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 794  
 Ser Ala Met Ser Ser Asp Arg Met Asp Cys Gly Arg Lys Val Arg Val  
 1 5 10 15  
 Glu Ser Gly Tyr Phe Ser Leu Glu Lys Thr Lys Gln Asp Leu Lys Ala  
 20 20 25 30  
 Glu Glu Gln Gln Leu Pro Pro Pro Leu Ser Pro Pro Ser Pro Ser Thr  
 35 40 45  
 Pro Asn His Arg Arg Ser Gln Val Ile Glu Lys Phe Glu Ala Leu Asp  
 50 55 60  
 25 Ile Glu Lys Ala Glu His Met Glu Thr Asn Ala Val Gly Pro Ser Gln  
 65 70 75 80  
 Ser Ser Asp Thr Arg Gln Gly Arg Ser Glu Lys Arg Ala Phe Pro Arg  
 85 90 95  
 Lys Arg Asp Phe Thr Asn Glu Ala Pro Pro Ala Pro Leu Pro Asp Ala  
 100 105 110  
 30 Ser Ala Ser Pro Leu Ser Pro His Arg Arg Ala Lys Ser Leu Asp Arg  
 115 120 125  
 Arg Ser Thr Glu Pro Ser Val Thr Pro Asp Leu Leu Asn Phe Lys Lys  
 130 135 140  
 35 Gly Trp Leu Thr Lys Gln Tyr Glu Asp Gly Gln Trp Lys Lys His Trp  
 145 150 155 160  
 Phe Val Leu Ala Asp Gln Ser Leu Arg Tyr Tyr Arg Asp Ser Val Ala  
 165 170 175  
 Glu Glu Ala Ala Asp Leu Asp Gly Glu Ile Asp Leu Ser Ala Cys Tyr  
 180 185 190  
 40 Asp Val Thr Glu Tyr Pro Val Gln Xaa Lys Leu Trp Leu Pro Asp Thr  
 195 200 205  
 Tyr Lys Gly Gly Arg Ser Leu Pro Leu Ser Pro  
 210 215  
 45  
 <210> 795  
 <211> 77  
 <212> PRT  
 <213> Homo sapiens  
 50  
 <400> 795  
 Arg Gln Gln Glu Val Asn Thr Ala Glu Ser Gly Val Asp Asn Pro Xaa  
 1 5 10 15  
 Ala Ser Xaa Thr His Xaa Met Pro Thr Val Asn Asp Asp His Asn Arg  
 20 25 30  
 Asn Xaa Asn Asn Asn Lys Thr Lys Val Gln Val Lys Asn Xaa Ala  
 35 40 45  
 Trp Gly Val Leu Leu Gln Xaa Trp Gly Lys Arg Val Leu Asn Phe Gly  
 50 55 60  
 60 Trp Asp Thr Pro Ser Leu Ser Ser Ser Pro Trp Ile Lys  
 65 70 75  
 <210> 796

<211> 99  
 <212> PRT  
 <213> Homo sapiens

5           <400> 796  
 Leu Ile Gln Gly Leu Glu Glu Arg Leu Gly Val Ser His Pro Lys Leu  
   1                  5                  10                  15  
 Ser Thr Arg Phe Pro Gln Xaa Cys Ser Ser Thr Pro Gln Ala Xaa Phe  
                   20                  25                  30  
 10 Phe Thr Trp Thr Phe Val Leu Leu Leu Leu Xaa Leu Arg Leu Trp  
                   35                  40                  45  
 Ser Ser Leu Thr Val Gly Met Xaa Cys Xaa Arg Leu Ala Xaa Gly Leu  
                   50                  55                  60  
 Ser Thr Pro Leu Ser Ala Val Leu Thr Ser Cys Cys Leu His Gln Ser  
 15 65                  70                  75                  80  
 Phe Phe Pro Trp Tyr Ser Lys Ile Arg Pro Xaa Val Gly Val Gly Gly  
                   85                  90                  95  
 His Leu Cys

20  
           <210> 797  
           <211> 138  
           <212> PRT  
           <213> Homo sapiens

25           <400> 797  
 Ile His Thr Tyr Ile His Thr Tyr Ile His Thr Tyr Ile His Thr Ser  
   1                  5                  10                  15  
 Ile His Ala Tyr Arg Tyr Thr Arg Lys Lys Lys Arg Lys Glu Lys Lys  
 30                   20                  25                  30  
 Glu Lys Met Lys Glu Lys Ala Leu Tyr Cys Tyr Trp Ala Arg Ala Phe  
                   35                  40                  45  
 Ser Leu Ser Val Ser Leu Cys Ser Ser Leu Ser Phe Ser Leu Cys Leu  
                   50                  55                  60  
 35 Phe Leu Cys Leu Ser Val Ser Phe Phe Leu Ser Val Ser Val Ser Val  
   65                  70                  75                  80  
 Phe Val Ser Leu Ser Pro Ser Leu Pro Val Ser Leu Cys Leu Ser Ser  
                   85                  90                  95  
 Val Ser Leu Cys Leu Ser Met Ser Phe Ser Val Cys Leu Phe Leu Cys  
 40                   100                  105                  110  
 Leu Ser Ala Ser Leu Phe Leu Phe Leu Cys Leu Ser Val Gly Leu Ser  
                   115                  120                  125  
 Leu Ser Val Cys Leu Ser Val Ser Leu Ser  
                   130                  135

45  
           <210> 798  
           <211> 103  
           <212> PRT  
           <213> Homo sapiens

50           <400> 798  
 Lys Lys Arg His Cys Ile Ala Thr Gly Leu Gly Pro Ser Leu Cys Leu  
   1                  5                  10                  15  
 Phe Leu Ser Val Arg Leu Cys Leu Ser Leu Cys Val Ser Phe Ser Val  
 55                   20                  25                  30  
 Cys Leu Ser Leu Ser Phe Ser Leu Ser Leu Ser Leu Ser Leu Ser Leu  
                   35                  40                  45  
 Ser Leu Pro Leu Cys Leu Ser His Cys Val Cys Leu Leu Ser Leu Ser  
                   50                  55                  60  
 60 Val Cys Leu Cys Leu Ser Leu Ser Val Ser Phe Ser Val Cys Leu Pro  
   65                  70                  75                  80  
 Leu Ser Phe Phe Phe Cys Val Ser Leu Ser Val Ser Leu Ser Leu Ser  
                   85                  90                  95

Val Cys Leu Ser Leu Ser Leu  
100

5           <210> 799  
            <211> 95  
            <212> PRT  
            <213> Homo sapiens

            <400> 799

10   Glu Arg Glu Thr Asp Arg Gln Thr Glu Arg Glu Arg Pro Thr Glu Arg  
      1                   5                   10                   15  
     His Arg Lys Arg Lys Arg Glu Ala Asp Arg Gln Arg Lys Arg Gln Thr  
          20                   25                   30  
15   Glu Lys Asp Ile Asp Arg Gln Arg Glu Thr Glu Asp Arg His Ser Glu  
      35                   40                   45  
     Thr Gly Arg Glu Gly Glu Arg Glu Thr Lys Thr Glu Thr Glu Thr Glu  
      50                   55                   60  
     Arg Lys Lys Glu Thr Asp Arg Gln Arg Lys Arg His Arg Glu Lys Asp  
     65                   70                   75                   80  
20   Arg Asp Glu Gln Arg Glu Thr Asp Arg Glu Lys Ala Leu Ala Gln  
          85                   90                   95

            <210> 800  
            <211> 100  
25         <212> PRT  
            <213> Homo sapiens

            <400> 800

30   Asp Arg Gln Arg Gly Arg Glu Arg Asp Lys Asp Arg Asp Arg Asp Arg  
      1                   5                   10                   15  
     Glu Lys Glu Arg Asp Arg Gln Thr Glu Lys Glu Thr Gln Arg Glu Arg  
          20                   25                   30  
     Gln Arg Arg Thr Glu Arg Asn Arg Gln Arg Glu Gly Pro Ser Pro Val  
          35                   40                   45  
35   Ala Ile Gln Cys Leu Phe Phe His Phe Leu Phe Leu Phe Phe Ser Phe  
      50                   55                   60  
     Phe Leu Ser Cys Ile Ser Val Cys Met Asp Gly Cys Met Tyr Val Cys  
     65                   70                   75                   80  
     Met Tyr Val Cys Met Tyr Val Cys Val Tyr Leu Phe Met Tyr Val Phe  
     85                   90                   95  
40   Ile Trp Arg Pro  
      100

            <210> 801  
45         <211> 185  
            <212> PRT  
            <213> Homo sapiens

            <400> 801

50   Thr Val Gly Thr Ala Met Ala Pro Val Leu Ser Lys Asp Ser Ala Asp  
      1                   5                   10                   15  
     Ile Glu Ser Ile Leu Ala Leu Asn Pro Arg Thr Gln Thr His Ala Thr  
          20                   25                   30  
     Leu Cys Ser Thr Ser Ala Lys Lys Leu Asp Lys Lys His Trp Lys Arg  
      35                   40                   45  
55   Asn Pro Asp Lys Asn Cys Phe Asn Cys Glu Lys Leu Glu Asn Asn Phe  
      50                   55                   60  
     Asp Asp Ile Lys His Thr Thr Leu Gly Glu Arg Gly Ala Leu Arg Glu  
     65                   70                   75                   80  
60   Ala Met Arg Cys Leu Lys Cys Ala Asp Ala Pro Cys Gln Lys Ser Cys  
          85                   90                   95  
     Pro Thr Asn Leu Asp Ile Lys Ser Phe Ile Thr Ser Ile Ala Asn Lys  
         100                   105                   110

Asn Tyr Tyr Gly Ala Ala Lys Met Ile Phe Ser Asp Asn Pro Leu Gly  
           115                  120          125  
 Leu Thr Cys Gly Met Val Cys Pro Thr Ser Asp Leu Cys Val Gly Gly  
           130                  135          140  
 5 Cys Asn Leu Tyr Ala Thr Glu Glu Gly Pro Ile Asn Ile Gly Gly Leu  
    145                  150          155          160  
 Gln Gln Phe Ala Thr Glu Val Cys Met Ile Tyr Thr Val Thr Ser Pro  
                   165                  170          175  
 10 His Tyr His His His Ala Gln Ile Ser  
                   180                  185

&lt;210&gt; 802

&lt;211&gt; 155

&lt;212&gt; PRT

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 802

Asp Tyr Arg Xaa Ile Glu Ile Thr Ile Cys Lys Asn Asp Glu Cys Val  
    1          5          10          15  
 20 Leu Glu Asp Asn Ser Gln Arg Thr Lys Trp Lys Val Ile Ser Pro Thr  
           20          25          30  
 Gly Asn Glu Ala Xaa Val Pro Xaa Val Cys Phe Leu Ile Pro Pro Pro  
           35          40          45  
 25 Asn Lys Asp Ala Ile Xaa Met Ala Ser Arg Val Glu Gln Ser Tyr Xaa  
    50          55          60  
 Lys Val Met Ala Leu Trp His Gln Leu His Val Asn Thr Lys Ser Leu  
    65          70          75          80  
 Xaa Ser Trp Asn Tyr Leu Arg Lys Asp Leu Asp Leu Val Gln Thr Trp  
           85          90          95  
 30 Asn Leu Glu Lys Leu Arg Ser Ser Ala Pro Gly Glu Cys His Gln Ile  
           100          105          110  
 Met Xaa Asn Leu Gln Ala His Tyr Glu Asp Phe Xaa Gln Asp Ser Arg  
           115          120          125  
 35 Asp Ser Val Leu Val Ser Val Ala Asp Arg Leu Arg Leu Glu Glu Glu  
    130          135          140  
 Xaa Glu Ala Cys Lys Ala Arg Phe Gln His Leu  
    145          150          155

&lt;210&gt; 803

40 &lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 803

Arg Gly Asn Xaa Gln Gly Lys Ala Xaa Ser Ser Glu Thr Lys Glu Ser  
    1          5          10          15  
 Thr Asp Ile Glu Lys Ala Ile Leu Glu Gln Gln Val Leu Ser Glu Glu  
           20          25          30  
 50 Leu Thr Thr Lys Lys Glu Gln Val Phe Glu Ala Ile Lys Thr Ser Gln  
    35          40          45  
 Ile Phe Leu Ala Lys His Gly His Lys Leu Ser Glu Lys Glu Lys Lys  
    50          55          60  
 Gln Ile Ser Glu Gln Leu Asn Ala Leu Asn Lys Ala Tyr His Asp Leu  
    65          70          75          80  
 55 Cys Asp Gly Ser Ala Asn Gln Leu Gln Gln Leu Gln Ser Gln Leu Ala  
           85          90          95  
 His Gln Thr Glu Gln Lys Glu Cys Arg Ala Val Ala Gly Val Ile Asp  
           100          105          110  
 60 Leu Gly Thr Val Glu Ile Phe Pro Ile Phe Lys Ala Met Gln Lys Gly  
           115          120          125  
 Leu Leu Asp Gln Asp Thr Gly Leu Val Leu Leu Glu Ser Gln Val Ile  
    130          135          140  
 Met Ser Gly Leu Ile Ala Pro Glu Thr Gly Glu Asn Leu Ser Leu Glu

145                      150                      155                      160  
 Glu Gly Val Ala Arg Asn Leu Ile Asn Pro Gln Met Tyr Gln Gln Leu  
                                  165                      170                      175  
 Arg Glu Leu Gln Asp Ala Leu Ala Leu Ile Ser Arg Leu Thr Glu Ser  
 5                      180                      185                      190  
 Arg Gly Pro Leu Ser Val Val Glu  
                                  195                      200  
  
 <210> 804  
 10                      <211> 204  
                                  <212> PRT  
                                  <213> Homo sapiens  
  
                                  <400> 804  
 15    Ala Val Glu Gly Arg Arg Val Gln Ala Leu Glu Glu Val Leu Gly Asp  
       1                      5                      10                      15  
 Leu Arg Ala Glu Ser Arg Glu Gln Glu Lys Ala Leu Leu Ala Leu Gln  
                                  20                      25                      30  
 Gln Gln Cys Ala Glu Gln Ala Gln Glu His Glu Val Glu Thr Arg Ala  
 20                      35                      40                      45  
 Leu Gln Asp Ser Trp Leu Gln Ala Gln Ala Val Leu Lys Glu Arg Asp  
       50                      55                      60  
 Gln Glu Leu Glu Ala Leu Arg Ala Glu Ser Gln Ser Ser Arg His Gln  
       65                      70                      75                      80  
 25    Glu Glu Ala Ala Arg Ala Arg Ala Glu Ala Leu Gln Glu Ala Leu Gly  
                                  85                      90                      95  
 Lys Ala His Ala Ala Leu Gln Gly Lys Glu Gln His Leu Leu Glu Gln  
                                  100                      105                      110  
 Ala Glu Leu Ser Arg Ser Leu Glu Ala Ser Thr Ala Thr Leu Gln Ala  
 30                      115                      120                      125  
 Ser Leu Asp Ala Cys Gln Ala His Ser Arg Gln Leu Glu Glu Ala Leu  
       130                      135                      140  
 Arg Ile Gln Glu Gly Glu Ile Gln Asp Gln Asp Leu Arg Tyr Gln Glu  
       145                      150                      155                      160  
 35    Asp Val Gln Gln Leu Gln Gln Ala Leu Ala Gln Arg Asp Glu Glu Leu  
                                  165                      170                      175  
 Arg His Gln Xaa Gly Thr Gly Ala Ser Cys Trp Lys Lys Ser Phe Gly  
                                  180                      185                      190  
 Pro Lys Gly Xaa Lys Lys Asn Met Ile Gln Glu Glu  
 40                      195                      200  
  
 <210> 805  
 <211> 187  
 <212> PRT  
 45                      <213> Homo sapiens  
  
                                  <400> 805  
 Phe Phe Leu Asp His Ile Leu Leu Xaa Pro Phe Trp Ala Lys Arg Leu  
       1                      5                      10                      15  
 50    Phe Pro Ala Ala Cys Ser Arg Ser Xaa Leu Met Ser Gln Leu Phe Ile  
                                  20                      25                      30  
 Pro Leu Gly Lys Cys Leu Leu Gln Leu Leu His Ile Leu Leu Val Ser  
       35                      40                      45  
 Glu Ile Leu Val Leu Asp Leu Thr Phe Leu Tyr Pro Gln Ser Leu Leu  
 55                      50                      55                      60  
 Gln Leu Pro Thr Val Cys Leu Ala Gly Ile Gln Gly Gly Leu Gln Gly  
       65                      70                      75                      80  
 Cys Ser Ala Gly Leu Gln Thr Ala Ala Gln Phe Cys Leu Leu Glu Glu  
                                  85                      90                      95  
 60    Met Leu Leu Phe Pro Leu Gln Gly Ser Met Ser Leu Ala Lys Gly Leu  
                                  100                      105                      110  
 Leu Gln Ser Leu Ser Pro Gly Pro Gly Ser Leu Leu Leu Met Pro Gly  
                                  115                      120                      125



Gly Leu Thr Phe Cys Pro Gln Ser Phe Gln Leu Leu Val Pro Phe Leu  
 130 135 140  
 Glu His Cys Leu Gly Leu Gln Pro Ala Val Leu Gln Gly Pro Gly Leu  
 145 150 155 160  
 5 His Leu Met Leu Leu Cys Leu Leu Ser Thr Leu Leu Leu Glu Gly Gln  
 165 170 175  
 Gln Ser Phe Leu Leu Leu Pro Arg Leu Ser Pro  
 180 185  
  
 10 <210> 806  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens  
  
 15 <400> 806  
 Asp Lys Lys Asn Ser Arg Trp Pro Ser Val Gly Leu Lys Leu Gln Lys  
 1 5 10 15  
 Xaa Arg Trp Ser Cys Cys Lys Ala Gln Leu Thr Leu Glu Arg Lys Gln  
 20 25 30  
 20 Lys Gln Asp Tyr Ile Thr Arg Ser Ala Gln Thr Ser Arg Glu Leu Ala  
 35 40 45  
 Gly Leu His His Ser Leu Ser His Ser Leu Leu Ala Val Ala Gln Ala  
 50 55 60  
 Pro Glu Ala Thr Val Leu Glu Ala Glu Thr Arg Arg Leu Asp Glu Ser  
 25 65 70 75 80  
 Leu Thr Gln Ser Leu Thr Ser Pro Gly Pro Val Leu Leu His Pro Ser  
 85 90 95  
 Pro Ser Thr Thr Gln Ala Ala Ser Arg  
 100 105  
  
 30 <210> 807  
 <211> 256  
 <212> PRT  
 <213> Homo sapiens  
  
 35 <400> 807  
 Phe Glu Lys Asp Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg  
 1 5 10 15  
 Trp Gly Leu Val Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu  
 40 20 25 30  
 Gln Phe Asn Thr Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg  
 35 40 45  
 Ser Phe Lys Val Pro Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala  
 50 55 60  
 45 Asp Gly Phe Tyr Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln  
 65 70 75 80  
 Pro Tyr Phe Ile Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser  
 85 90 95  
 Ile Gly Ala Ala Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn  
 50 100 105 110  
 Trp Arg Leu Leu Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro  
 115 120 125  
 Glu Gly Gly Asp Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser  
 130 135 140  
 55 Cys Lys Gly Leu Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp  
 145 150 155 160  
 Gly Glu Glu Ala Val Ser Lys Trp Leu Asp Phe Gly Glu Val Ser Thr  
 165 170 175  
 Xaa Glu Ala Leu Lys Leu Ile His Pro Thr Glu Asn Ile Thr Phe His  
 60 180 185 190  
 Ala Val Ser Ser Val Xaa Asn Asn Ser Arg Asn Asn Thr Ser Glu Cys  
 195 200 205  
 Leu Ala Xaa Val Asp Leu Val Val Lys Xaa Glu Leu Lys Ala Ser Gly

210                      215                      220  
 Asn Xaa Pro Lys Asp Val Ala Met Gly Trp Xaa Gln Ser Xaa Pro Lys  
 225                      230                      235                      240  
 Lys Glu Asp Ser Lys Thr Leu Gln Lys Glu Lys Val Arg Cys Xaa Pro  
 5                      245                      250                      255  
  
 <210> 808  
 <211> 88  
 <212> PRT  
 10                      <213> Homo sapiens  
  
 <400> 808  
 Lys Ser Glu Arg Ala Gln Trp Leu Ser Arg Lys Gln Leu Thr Thr Arg  
 1                      5                      10                      15  
 15 Ser Thr Arg Ser Gly Gln Arg Leu Pro Ser Trp Val Arg His Ala Leu  
                     20                      25                      30  
 Arg Glu Asp Ser Thr Ser Pro Ala Arg Lys Gly Gln Gln Ala Gln Cys  
                     35                      40                      45  
 20 Pro Tyr Gly Ala His Met Ala Gly Asn Ser Ser Arg Thr Pro Leu Pro  
                     50                      55                      60  
 Lys Leu Ser Thr Ser Pro Thr Arg Gly Ser Tyr Ser Trp Gln Lys Arg  
 65                      70                      75                      80  
 Leu His Glu Pro Thr Thr Val Asn  
                     85  
 25  
 <210> 809  
 <211> 96  
 <212> PRT  
 30                      <213> Homo sapiens  
  
 <400> 809  
 Gly Lys Thr Pro Pro Ala Leu Pro Gly Lys Gly Ser Arg Arg Ser Ala  
 1                      5                      10                      15  
 35 Pro Met Gly Pro Thr Trp Leu Val Thr Ala Ala Gly His Leu Phe Gln  
                     20                      25                      30  
 Ser Cys Pro Pro Ala Pro Leu Gly Ala Pro Thr His Gly Lys Lys Asp  
                     35                      40                      45  
 Tyr Met Ser Pro Gln Leu Ser Thr Asn Thr Val Pro Pro Pro Pro Lys  
                     50                      55                      60  
 40 Ala Asn Thr Tyr Thr Tyr Asn Val Lys Asn Leu Ser Glu Gln Gln  
                     65                      70                      75                      80  
 Cys Ser Arg Pro Trp Pro Trp Ser Leu Lys Val Leu Cys His Trp Leu  
                     85                      90                      95  
 45  
 <210> 810  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens  
  
 50                      <400> 810  
 Gln Ser Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp  
 1                      5                      10                      15  
 Ala Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val  
                     20                      25                      30  
 55 Pro Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr  
                     35                      40                      45  
 Thr Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val  
                     50                      55                      60  
 60 Pro Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr  
                     65                      70                      75                      80  
 Glu Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile  
                     85                      90                      95  
 Tyr Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala

100 105 110  
 Asp Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu  
 115 120 125  
 Thr Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp  
 5 130 135 140  
 Val Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu  
 145 150 155 160  
 Ser Asp Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala  
 165 170 175  
 10 Ser Phe

<210> 811  
 <211> 294  
 15 <212> PRT  
 <213> Homo sapiens

<400> 811  
 Arg Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr  
 20 1 5 10 15  
 Arg Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu  
 20 25 30  
 Trp Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln  
 35 40 45  
 25 Ser Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala  
 50 55 60  
 Asp Ser Ser Glu Arg Ile Ile Ala Pro Met Arg Trp Gly Leu Val Pro  
 65 70 75 80  
 Ser Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr  
 85 90 95  
 30 Asn Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro  
 100 105 110  
 Leu Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu  
 115 120 125  
 35 Trp Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr  
 130 135 140  
 Phe Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala Asp  
 145 150 155 160  
 Ser Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr  
 165 170 175  
 40 Met Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val  
 180 185 190  
 Leu Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser  
 195 200 205  
 45 Asp Ile His His Xaa Met Pro Ala His Ile Xaa Met Glu Lys Glu Ala  
 210 215 220  
 Val Ser Lys Met Ala Trp Thr Leu Val Lys Val Phe Asn Leu Arg Lys  
 225 230 235 240  
 Leu Leu Lys Phe Asn Pro Pro Asn Lys Arg Lys Phe Thr Phe Pro Cys  
 245 250 255  
 50 Gln Xaa Phe Xaa Gly Gly Thr Asn Leu Arg Lys Gln His Phe Pro Glu  
 260 265 270  
 Trp Phe Gly Phe Leu Ser Thr Leu Gly Gly Xaa Lys Xaa Asn Leu Xaa  
 275 280 285  
 55 Ala Lys Trp Glu Xaa Pro  
 290

<210> 812  
 <211> 96  
 60 <212> PRT  
 <213> Homo sapiens

<400> 812

Gly Lys Thr Pro Pro Ala Leu Pro Gly Lys Gly Ser Arg Arg Ser Ala  
 1 5 10 15  
 Pro Met Gly Pro Thr Trp Leu Val Thr Ala Ala Gly His Leu Phe Gln  
 20 25 30  
 5 Ser Cys Pro Pro Ala Pro Leu Gly Ala Pro Thr His Gly Lys Lys Asp  
 35 40 45  
 Tyr Met Ser Pro Gln Leu Ser Thr Asn Thr Xaa Pro Pro Pro Pro Lys  
 50 55 60  
 Ala Asn Thr Tyr Thr Tyr Asn Val Lys Asn Leu Ser Glu Gln Gln  
 65 70 75 80  
 10 Cys Ser Arg Pro Trp Pro Trp Ser Leu Lys Val Leu Cys His Trp Leu  
 85 90 95

15 <210> 813  
 <211> 235  
 <212> PRT  
 <213> Homo sapiens

<400> 813  
 20 Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu  
 1 5 10 15  
 Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu  
 20 25 30  
 Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Met  
 35 40 45  
 25 Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val  
 50 55 60  
 Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser Glu Cys  
 65 70 75 80  
 30 Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met Asp Phe  
 85 90 95  
 Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr Asp Thr  
 100 105 110  
 Lys Lys Ala Ser Ile Leu Leu Ile Arg Lys Ile Tyr Ile Leu Met Gln  
 115 120 125  
 35 Asn Leu Gly Pro Leu Pro Asn Asp Val Cys Leu Thr Met Lys Leu Phe  
 130 135 140  
 Tyr Tyr Asp Glu Val Thr Pro Pro Asp Tyr Gln Pro Pro Gly Phe Lys  
 145 150 155 160  
 40 Asp Gly Asp Cys Glu Gly Val Ile Phe Glu Gly Glu Pro Met Tyr Leu  
 165 170 175  
 Asn Val Gly Glu Val Ser Thr Pro Phe His Ile Phe Lys Val Lys Val  
 180 185 190  
 Thr Thr Glu Arg Glu Arg Met Glu Asn Ile Asp Ser Thr Xaa Leu Ser  
 195 200 205  
 45 Pro Lys Gln Ile Lys Thr Pro Phe Gln Lys Ile Leu Arg Asp Lys Asp  
 210 215 220  
 Val Xaa Xaa Glu Gln Asp Xaa Tyr Ile Ser Gly  
 225 230 235

50 <210> 814  
 <211> 59  
 <212> PRT  
 <213> Homo sapiens

<400> 814  
 55 Leu Asn Asn Ile Leu Phe Met Leu Gln Lys Met Pro Tyr Phe Lys Asn  
 1 5 10 15  
 Gln Ser Phe Cys Pro Val Lys Lys Ser Ile Val Lys Val Lys His Gln  
 20 25 30  
 60 Phe Leu Asn Cys Thr Leu Tyr Ile Lys Met Leu Ile His Tyr Val Lys  
 35 40 45  
 Ile Leu Lys Asn Ile Val Leu Ile Thr Ala Gln

50  
5  
10  
15  
20  
25  
30  
35  
40  
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55  
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<210> 815  
<211> 148  
<212> PRT  
<213> Homo sapiens  
  
<400> 815  
Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp Arg  
1 5 10 15  
Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg Cys  
20 25 30  
Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu Asn  
35 40 45  
His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp Glu  
50 55 60  
Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser Glu  
65 70 75 80  
Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr Ala  
85 90 95  
Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser Asp  
100 105 110  
Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu Pro  
115 120 125  
Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys Arg  
130 135 140  
Arg Asn Xaa Arg  
145  
  
<210> 816  
<211> 77  
<212> PRT  
<213> Homo sapiens  
  
<400> 816  
Asn Val Thr His Leu Phe Ile Tyr Leu Phe Met Met Glu Ser His Ser  
1 5 10 15  
Val Thr Gln Ala Gly Val Gln Trp His Asp Leu Ser Ser Leu Gln Pro  
20 25 30  
Leu Pro Pro Trp Phe Gln Leu Val Ser Cys Leu Ser Leu Pro Ser Ser  
35 40 45  
Trp Asp Tyr Arg Cys Pro Pro Pro Arg Ser Ser Asn Phe Cys Ile Phe  
50 55 60  
Ser Lys Asp Gly Val Ser Pro Cys Trp Pro Gly Arg Ser  
65 70 75  
  
<210> 817  
<211> 83  
<212> PRT  
<213> Homo sapiens  
  
<400> 817  
Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Thr Gly Val His His  
1 5 10 15  
His Ala Arg Leu Ile Phe Val Phe Leu Val Lys Thr Gly Phe His His  
20 25 30  
Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Leu Pro Ala  
35 40 45  
Ser Ala Ser Gln Ser Ala Gly Ile Tyr Arg Tyr Glu Pro Pro His Pro  
50 55 60  
Ala Asn Val Thr His Tyr Leu Thr Val Leu Tyr Ile Arg Ser Pro Ala  
65 70 75 80  
Gln Asn Arg

5 <210> 818  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens

<400> 818  
 10 Lys Glu Gln Arg Lys Glu Asn Glu Pro Glu Ala Glu Lys Thr His Leu  
 1 5 10 15  
 Phe Ala Lys Gln Glu Lys Ala Phe Tyr Pro Lys Ser Phe Lys Ser Lys  
 20 25 30  
 Lys Gln Lys Pro Ser Arg Val Leu Tyr Ser Ser Thr Glu Ser Ser Asp  
 35 40 45  
 15 Glu Glu Ala Leu Gln Asn Lys Lys Ile Ser Thr Ser Cys Ser Val Ile  
 50 55 60  
 Pro Glu Thr Ser Asn Ser Asp Met Gln Thr Lys Lys Glu Tyr Val Val  
 65 70 75 80  
 20 Ser Gly Glu His Lys Gln Lys Gly Lys Val Lys Arg Lys Leu Lys Asn  
 85 90 95  
 Gln Asn Lys Asn Lys Glu Asn Gln Glu Leu Lys Gln Glu Lys Glu Gly  
 100 105 110  
 Lys Glu Asn Thr Arg Ile Thr Asn Leu Thr Val Asn Thr Gly Leu Asp  
 115 120 125  
 25 Cys Ser Glu Lys Thr Arg Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser  
 130 135 140  
 Pro Lys Asp Asp Thr Ser Leu His Leu Phe His Ile Ser Thr Gly Lys  
 145 150 155 160  
 30 Ser Pro Lys His Ser Cys Gly Leu Lys  
 165

35 <210> 819  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 819  
 40 Ala Phe Leu Phe Pro Ser Xaa Tyr Ala Ser Ile Tyr Val Phe Leu Met  
 1 5 10 15  
 Xaa Tyr Leu Xaa Tyr Pro Phe Phe Ser Xaa Gly Asn Leu Asn Phe Gln  
 20 25 30  
 Met Xaa Asp Tyr Asp Leu His Pro Leu Phe Trp His Leu Ile Phe His  
 35 40 45  
 45 Gln Ile Leu Xaa Gly Asn Leu Ser Asp Val Xaa Phe Phe Pro Tyr Ala  
 50 55 60  
 Tyr Xaa Ile Leu Xaa Leu Asn Phe Xaa Ala Xaa Ile Gln Ile Leu Xaa  
 65 70 75 80  
 Tyr His Xaa Xaa Gln Xaa Gln Ala Val Met Thr Phe Gln Asn Phe Leu  
 85 90 95  
 50 Gly Ile Asn Met Phe Xaa Tyr Val Leu Xaa Leu Gly Gly Xaa Thr Xaa  
 100 105 110  
 Phe His Leu Ile Xaa Xaa Asn Val Trp Xaa Ile Tyr Xaa Xaa Lys Tyr  
 115 120 125  
 55 Glu Ile Asn Val Met Lys Xaa His Xaa Leu Gly  
 130 135

60 <210> 820  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 820  
 Pro Arg Xaa Pro Thr Leu Pro Val Asn Thr Xaa Xaa Asp Cys Ser Glu

1 5 10 15  
 Lys Thr Arg Glu Glu Gly Asn Phe Arg Lys Xaa Phe Ser Pro Lys Xaa  
 20 25 30  
 Xaa Thr Ser Leu His Leu Phe His Ile Ser Xaa Gly Lys Xaa Pro Lys  
 35 40 45  
 5 His Xaa Xaa Gly Leu Ser Glu Xaa Gln Ser Xaa Pro Leu Xaa Gln Glu  
 50 55 60  
 His Xaa Lys Thr Cys Leu Ser Pro Gly Ser Phe Glu Met Ser Leu Gln  
 65 70 75 80  
 10 Pro Asp Xaa Val Xaa Xaa Asp Xaa Thr Glu Phe Glu Xaa Leu Pro Xaa  
 85 90 95  
 Ser Ser Xaa Val Lys Xaa Cys Lys His Lys Glu Lys Ser Xaa His Gln  
 100 105 110  
 Lys Asp Phe Xaa Leu Glu Phe Gly Glu Lys Ser Asn Ala Lys Ile Lys  
 115 120 125  
 15 Asp Glu Asp His Ser Pro Xaa Phe Glu Asn Ser Asp Cys Xaa Leu Lys  
 130 135 140  
 Lys Met Asp Lys Xaa Gly Lys Xaa Leu Lys Lys His Lys Leu Lys His  
 145 150 155 160  
 20 Lys Xaa Arg Glu Lys Glu Lys His  
 165

&lt;210&gt; 821

&lt;211&gt; 176

25 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 821

30 Leu Ser Phe Val Lys Glu Ile Lys Glu Cys Arg Arg Ile Glu Asn Leu  
 1 5 10 15  
 Trp Lys Asn Arg Met His Glu Lys Ala Arg Lys Ala Glu Glu Met Arg  
 20 25 30  
 Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val Glu Gln Tyr Arg Glu  
 35 35 40 45  
 Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys Glu Leu Gln Glu Met  
 50 55 60  
 Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly Ser Asp Glu Asn Glu  
 65 70 75 80  
 Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp Gly Lys Asp Ser Asp  
 85 90 95  
 40 Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu Tyr Cys Pro Ala Cys  
 100 105 110  
 Asp Lys Ser Phe Lys Thr Glu Xaa Ala Met Lys Asn His Glu Lys Ser  
 115 120 125  
 45 Lys Lys His Arg Glu Met Val Ala Leu Leu Lys Gln Gln Leu Glu Glu  
 130 135 140  
 Glu Glu Xaa Asn Phe Ser Xaa Pro Gln Ile Asp Glu Asn Pro Leu Asp  
 145 150 155 160  
 Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro Lys Gln Lys Leu Ser  
 165 170 175  
 50

&lt;210&gt; 822

&lt;211&gt; 193

55 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 822

60 Ile Arg Xaa Lys Ala Arg Lys Glu Lys Asn Glu Leu Val Arg Gln Leu  
 1 5 10 15  
 Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln Ala His Arg Lys  
 20 25 30  
 Leu Val Glu Gln Asn Ala Glu Lys Ala Arg Lys Ala Glu Glu Met  
 35 40 45

Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val Glu Gln Tyr Arg  
 50 55 60  
 Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys Glu Leu Gln Glu  
 65 70 75 80  
 5 Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly Ser Asp Glu Asn  
 85 90 95  
 Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp Gly Lys Asp Ser  
 100 105 110  
 10 Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu Tyr Cys Pro Ala  
 115 120 125  
 Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys Asn His Glu Lys  
 130 135 140  
 Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys Gln Gln Leu Glu  
 145 150 155 160  
 15 Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp Glu Asn Pro Leu  
 165 170 175  
 Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro Lys Gln Lys Leu  
 180 185 190  
 Ser  
 20  
 <210> 823  
 <211> 253  
 <212> PRT  
 25 <213> Homo sapiens  
 <400> 823  
 Ala Val Gln Ala Ser Ser Gly Ser Pro Lys Ala Arg Thr Thr Glu Gly  
 1 5 10 15  
 30 Pro Val Asp Ser Met Pro Cys Leu Asp Arg Met Pro Leu Leu Ala Lys  
 20 25 30  
 Gly Lys Gln Ala Thr Gly Glu Glu Lys Ala Ala Thr Ala Pro Gly Ala  
 35 35 40 45  
 Gly Ala Lys Ala Ser Gly Glu Gly Met Ala Gly Asp Ala Ala Gly Glu  
 50 55 60  
 35 Thr Glu Gly Ser Met Glu Arg Met Gly Glu Pro Ser Gln Asp Pro Lys  
 65 70 75 80  
 Gln Gly Thr Ser Gly Gly Val Asp Thr Ser Ser Glu Gln Ile Ala Thr  
 85 90 95  
 40 Leu Thr Gly Phe Pro Asp Phe Arg Glu His Ile Ala Lys Ile Phe Glu  
 100 105 110  
 Lys Pro Val Leu Gly Ala Leu Ala Thr Pro Gly Glu Lys Ala Gly Ala  
 115 120 125  
 45 Gly Arg Ser Ala Val Gly Lys Asp Leu Thr Arg Pro Leu Gly Pro Glu  
 130 135 140  
 Lys Leu Leu Asp Gly Pro Pro Gly Val Asp Val Thr Leu Leu Pro Ala  
 145 150 155 160  
 Pro Pro Ala Arg Leu Gln Val Glu Lys Lys Gln Gln Leu Ala Gly Glu  
 165 170 175  
 50 Ala Glu Ile Ser His Leu Ala Leu Gln Asp Pro Ala Ser Asp Lys Leu  
 180 185 190  
 Leu Gly Pro Ala Gly Leu Thr Trp Glu Arg Asn Leu Pro Gly Ala Gly  
 195 200 205  
 55 Val Gly Lys Glu Met Ala Gly Cys Pro Thr His Thr Glu Gly Arg Xaa  
 210 215 220  
 Xaa Gly Gln Lys Gly Leu Gly Gln Pro Gly Gln Ala Trp Lys Ala Arg  
 225 230 235 240  
 Leu Thr Tyr Ser Leu Glu Lys Asn Xaa Gln Glu Leu Leu  
 245 250  
 60  
 <210> 824  
 <211> 242  
 <212> PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 824

5 Val Ser Leu Ala Phe Gln Ala Trp Pro Gly Cys Pro Arg Pro Phe Trp  
 1 5 10 15  
 Pro Xaa Xaa Leu Pro Ser Val Trp Val Gly Gln Pro Ala Ile Ser Phe  
 20 25 30  
 Pro Thr Pro Ala Pro Gly Lys Phe Arg Ser Gln Val Ser Pro Ala Gly  
 35 40 45  
 10 Pro Arg Ser Leu Ser Glu Ala Gly Ser Cys Arg Ala Arg Trp Glu Ile  
 50 55 60  
 Ser Ala Ser Pro Ala Asn Cys Cys Phe Phe Ser Thr Trp Ser Arg Ala  
 65 70 75 80  
 Gly Gly Ala Gly Arg Arg Val Thr Ser Thr Pro Gly Gly Pro Ser Arg  
 15 85 90 95  
 Ser Phe Ser Gly Pro Asn Gly Leu Val Arg Ser Leu Pro Thr Ala Leu  
 100 105 110  
 Leu Pro Ala Pro Ala Phe Ser Pro Gly Val Ala Arg Ala Pro Ser Thr  
 115 120 125  
 20 Gly Phe Ser Lys Ile Leu Ala Met Cys Ser Leu Lys Ser Gly Lys Pro  
 130 135 140  
 Val Arg Val Ala Ile Cys Ser Glu Leu Val Ser Thr Pro Pro Asp Val  
 145 150 155 160  
 Pro Cys Phe Gly Ser Trp Glu Gly Ser Pro Ile Leu Ser Met Leu Pro  
 25 165 170 175  
 Ser Val Ser Pro Ala Ala Ser Pro Ala Met Pro Ser Pro Leu Ala Leu  
 180 185 190  
 Ala Pro Ala Pro Gly Ala Val Ala Ala Phe Ser Ser Pro Val Ala Cys  
 195 200 205  
 30 Leu Pro Leu Ala Arg Ser Gly Ile Arg Ser Arg His Gly Met Glu Ser  
 210 215 220  
 Thr Gly Pro Ser Val Val Leu Ala Leu Gly Leu Pro Leu Leu Ala Cys  
 225 230 235 240  
 Thr Ala

35

&lt;210&gt; 825

&lt;211&gt; 82

&lt;212&gt; PRT

40 &lt;213&gt; Homo sapiens

&lt;400&gt; 825

45 Phe Tyr Asn Leu Lys Xaa Leu Lys Gln Gln Val Met Lys Tyr Leu Leu  
 1 5 10 15  
 Tyr Tyr Tyr Thr Ser Gly Pro Ala Phe Ser Lys Lys Xaa Leu Thr Cys  
 20 25 30  
 Leu Arg Thr Leu Lys Lys Lys Ala Leu Ile Trp Ser Phe Leu Gly Trp  
 35 40 45  
 Gly Arg Leu Phe Gln Ala Arg Gln Ile Phe Leu Leu Pro Leu Asn Trp  
 50 50 55 60  
 Glu Tyr Lys Lys Tyr Ile Thr Ala Lys Ala Ala Gly Asn Cys Ile Leu  
 65 70 75 80  
 Ser Gln

55

&lt;210&gt; 826

&lt;211&gt; 64

&lt;212&gt; PRT

60 &lt;213&gt; Homo sapiens

&lt;400&gt; 826

Pro Leu Val Leu Cys Xaa Ser Cys Xaa Pro Arg Phe His Pro Phe Gly  
 1 5 10 15

Lys Arg Gly Xaa Cys Ala Arg Thr Gln Thr His Arg Asn Lys Leu Ser  
                   20                  25                  30  
 Ala Ser Xaa Ala Phe Gly Cys Xaa Gly Ala Val Cys Ala His Ile Tyr  
                   35                  40                  45  
 5 Met His Thr Thr Leu Val Cys Met Ser Arg Gly Asn Gln Xaa Leu Asn  
                   50                  55                  60  
  
                   <210> 827  
                   <211> 157  
 10                <212> PRT  
                   <213> Homo sapiens  
  
                   <400> 827  
 15 Ala Trp Pro Ala Leu Ala Pro Gly Ser Pro Val Pro Ala Ala Arg Pro  
       1                  5                  10                  15  
       Pro Arg Ser Arg Ala Pro Phe Arg Pro Gly Arg Ser Pro Ala Gly Met  
                   20                  25                  30  
       Gln Xaa Ser Pro Xaa Gly Tyr Gly Ala Gln Asp Asp Pro Pro Ala Arg  
                   35                  40                  45  
 20 Arg Asp Cys Ala Trp Ala Pro Gly His Gly Ala Ala Ala Asp Thr Arg  
       50                  55                  60  
       Gly Leu Thr Ala Gly Pro Ala Ala Leu Ala Ala Pro Ala Xaa Pro Ala  
       65                  70                  75                  80  
       Xaa Xaa Pro Ser Pro Gln Arg Xaa Pro Pro Arg Asn Xaa Glu Pro Gly  
 25                   85                  90                  95  
       Arg Tyr Gly Leu Ser Pro Ala Gly Arg Gly Glu Arg Xaa Ala Xaa Tyr  
                   100                  105                  110  
       Glu Xaa Xaa Ile Pro Leu Ala His Glu Arg Leu Xaa Gly Val Gly Lys  
                   115                  120                  125  
 30 Xaa Thr Xaa Ser Lys Leu Xaa Gly Xaa Xaa Xaa Thr Arg Xaa Cys Xaa  
       130                  135                  140  
       Asn Ala Val Xaa Gln Xaa Arg Cys Trp Xaa Lys Ser Val  
       145                  150                  155  
  
 35                <210> 828  
                   <211> 138  
                   <212> PRT  
                   <213> Homo sapiens  
  
                   <400> 828  
 40 Pro Gly Leu Pro Leu Arg Pro Ala Pro Gln Cys Pro Pro Pro Ala Arg  
       1                  5                  10                  15  
       Arg Ala Pro Ala Leu Arg Ser Ala Gln Ala Ala Ala Gln Leu Glu Cys  
                   20                  25                  30  
 45 Lys Xaa Arg Xaa Pro Ala Thr Ala His Arg Thr Thr Arg Pro Pro Ala  
       35                  40                  45  
       Ala Thr Val His Gly Pro Arg Asp Thr Gly Pro Pro Leu Thr Arg Ala  
       50                  55                  60  
       Ala Ser Pro Pro Ala Pro Pro Ser Pro Arg Pro Xaa Xaa Pro Pro  
       65                  70                  75                  80  
       Xaa Arg Pro Ala Arg Ser Ala Xaa Pro Arg Ala Thr Xaa Ser Arg Gly  
                   85                  90                  95  
       Ala Met Ala Ser Ala Arg Pro Ala Ala Gly Asn Ala Xaa Arg Xaa Thr  
                   100                  105                  110  
 55 Ser Xaa Ala Ser Arg Trp Pro Met Asn Ala Xaa Met Gly Trp Ala Xaa  
       115                  120                  125  
       Gly Arg Xaa Ala Ser Xaa Leu Ala Xaa Xaa  
       130                  135  
  
 60                <210> 829  
                   <211> 164  
                   <212> PRT  
                   <213> Homo sapiens

<400> 829  
 Arg Xaa Val Xaa Ala Pro Ser His Ala Phe Xaa Pro Ala Ser Xaa Leu  
 1 5 10 15  
 5 Xaa His Arg Val Xaa Ala Xaa Pro Gly Xaa Xaa Xaa Ala Xaa Gln Leu  
 20 25 30  
 Ala Xaa Arg Xaa Phe Ala His Pro Xaa Lys Ala Phe Met Gly Gln Arg  
 35 40 45  
 Asp Xaa Xaa Leu Val Xaa Arg Xaa Ala Phe Pro Ala Ala Gly Arg Ala  
 50 55 60  
 10 Glu Ala Ile Ala Pro Arg Leu Xaa Val Ala Arg Gly Xaa Ala Leu Arg  
 65 70 75 80  
 Ala Gly Xaa Xaa Gly Gly Xaa Gly Gly Arg Gly Glu Gly Gly Gly Ala  
 85 90 95  
 15 Gly Gly Glu Ala Ala Arg Val Ser Gly Gly Pro Val Ser Arg Gly Pro  
 100 105 110  
 Cys Thr Val Ala Ala Gly Gly Arg Val Val Leu Cys Ala Val Ala Xaa  
 115 120 125  
 Arg Arg Xaa Leu His Ser Ser Trp Ala Ala Ala Trp Ala Glu Arg Ser  
 130 135 140  
 20 Ala Gly Ala Arg Arg Ala Gly Gly Gly His Trp Gly Ala Gly Arg Lys  
 145 150 155 160  
 Gly Arg Pro Gly

25  
 <210> 830  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens

30  
 <400> 830  
 Pro Ala Phe Ile Gly Glu Val Asn His Lys Glu Ile Lys Met Ser Lys  
 1 5 10 15  
 35 Ser Lys Asp Asp Ala Pro His Glu Leu Glu Ser Gln Phe Ile Leu Arg  
 20 25 30  
 Leu Pro Pro Glu Tyr Ala Ser Thr Val Arg Arg Ala Val Gln Ser Gly  
 35 40 45  
 His Val Asn Leu Lys Asp Arg Leu Thr Ile Glu Leu His Pro Asp Gly  
 50 55 60  
 40 Arg His Gly Ile Val Arg Val Asp Arg Val Pro Leu Ala Ser Lys Leu  
 65 70 75 80  
 Val Asp Leu Pro Cys Val Met Glu Ser Leu Lys Thr Ile Asp Lys Lys  
 85 90 95  
 Thr Phe Tyr Lys Thr Ala Asp Ile Cys Gln Met Leu Val Ser Thr Val  
 100 105 110  
 45 Asp Gly Asp Leu Tyr Pro Pro Val Glu Glu Pro Val Ala Ser Thr Asp  
 115 120 125  
 Pro Lys Ala Ser Lys Lys Lys Asp Lys Asp Lys Glu Lys Lys Phe Ile  
 130 135 140  
 50 Trp Asn His Gly Ile Thr Leu Pro Leu Lys Asn Val Arg Lys Lys Lys  
 145 150 155 160  
 Val Pro Glu Asp Ser Gln Arg Arg Asn Ile Leu Asn Leu Gln Met Leu  
 165 170 175  
 Lys Lys Lys

55  
 <210> 831  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

60  
 <400> 831  
 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly



Ser His Xaa Xaa Pro Xaa  
130

5 <210> 834  
<211> 128  
<212> PRT  
<213> Homo sapiens

<400> 834  
10 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly  
1 5 10 15  
Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn  
20 25 30  
15 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly  
35 40 45  
Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser  
50 55 60  
Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg  
65 70 75 80  
20 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro  
85 90 95  
Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu  
100 105 110  
Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu  
115 120 125  
25

<210> 835  
<211> 78  
<212> PRT  
30 <213> Homo sapiens

<400> 835  
Arg Ala Gly Glu Val Arg Gly Leu Val Met Arg Ala Ala Pro Leu Gly  
1 5 10 15  
35 Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu Ser Ser Val Ile Gly Ser  
20 25 30  
Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile Lys Glu Thr Thr Arg Arg  
35 40 45  
Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys Gly Leu Leu Phe Pro Ser  
50 55 60  
40 Leu Arg Pro Gly Glu Thr Glu Leu Ile Ile Val Thr Gly Leu  
65 70 75

<210> 836  
45 <211> 107  
<212> PRT  
<213> Homo sapiens

<400> 836  
50 Leu Leu Leu Gln Arg Ala Glu Leu Leu Leu Phe Ser Xaa Phe Leu Leu  
1 5 10 15  
Val Glu Leu Ile Gln Tyr Ser Leu Lys Ser Val Leu Glu Ser Gln Ile  
20 25 30  
Ser Thr Phe Met Met Arg Pro Leu Xaa Gly Leu Pro Cys Pro Gly Leu  
35 40 45  
55 Leu Gly Ala Trp Leu Tyr Gly Asn Leu Leu Xaa Lys Xaa His Asn  
50 55 60  
Xaa Leu Asp Xaa Val Leu Xaa Phe Pro Gly Ala Gly His Leu Asp Gln  
65 70 75 80  
60 Leu Thr Trp Xaa Gly Thr Xaa Phe Ser Lys Xaa Ser Ser Xaa Gln Arg  
85 90 95  
Arg Leu Tyr Leu Leu Xaa Leu Gly Gly Xaa Gly  
100 105

<210> 837  
 <211> 87  
 <212> PRT  
 5 <213> Homo sapiens  
  
 <400> 837  
 Leu Ile Gln Met Thr Ser Pro Arg Lys Xaa Lys Asp Xaa Ile Gln Xaa  
 1 5 10 15  
 10 Val Met Xaa Phe Xaa Lys Gln Ile Ala Thr Ile Lys Pro Ser Ser Gln  
 20 25 30  
 Glu Pro Arg Thr Gly Gln Thr Xaa Lys Arg Ser His His Glu Ser Gly  
 35 40 45  
 15 Asn Leu Ala Leu Lys Asn Arg Phe Gln Ala Val Leu Asp Glu Leu Asn  
 50 55 60  
 Gln Lys Glu Xaa Arg Glu Lys Glu Gln Leu Ser Ser Leu Gln Glu Glu  
 65 70 75 80  
 Leu Glu Ser Leu Leu Glu Lys  
 85  
 20  
 <210> 838  
 <211> 183  
 <212> PRT  
 25 <213> Homo sapiens  
  
 <400> 838  
 Pro Ala Phe Ile Gly Glu Val Asn His Lys Glu Ile Lys Met Ser Lys  
 1 5 10 15  
 30 Ser Lys Asp Asp Ala Pro His Glu Leu Glu Ser Gln Phe Ile Leu Arg  
 20 25 30  
 Leu Pro Pro Glu Tyr Ala Ser Thr Val Arg Arg Ala Val Gln Ser Gly  
 35 40 45  
 His Val Asn Leu Lys Asp Arg Leu Thr Ile Glu Leu His Pro Asp Gly  
 50 55 60  
 35 Arg His Gly Ile Val Arg Val Asp Arg Val Pro Leu Ala Ser Lys Leu  
 65 70 75 80  
 Val Asp Leu Pro Cys Val Met Glu Ser Leu Lys Thr Ile Asp Lys Lys  
 85 90 95  
 Thr Phe Tyr Lys Thr Ala Asp Ile Cys Gln Met Leu Val Ser Thr Val  
 100 105 110  
 40 Asp Gly Asp Leu Tyr Pro Pro Val Glu Glu Pro Val Ala Ser Thr Asp  
 115 120 125  
 Pro Lys Ala Ser Lys Lys Lys Asp Lys Asp Lys Glu Lys Lys Phe Ile  
 130 135 140  
 45 Trp Asn His Gly Ile Thr Leu Pro Leu Lys Asn Val Xaa Glu Glu Lys  
 145 150 155 160  
 Gly Ser Gly Arg Gln Pro Lys Lys Lys Xaa Xaa Glu Ser Xaa Asp Val  
 165 170 175  
 Glu Lys Glu Val Lys Arg Cys  
 180  
 50  
 <210> 839  
 <211> 64  
 <212> PRT  
 55 <213> Homo sapiens  
  
 <400> 839  
 Leu Leu Leu Gln Arg Ala Glu Leu Leu Leu Phe Ser Xaa Phe Leu Leu  
 1 5 10 15  
 60 Phe Glu Leu Ile Pro Val Gln Ala Trp Lys Xaa Val Leu Glu Lys Pro  
 20 25 30  
 Asp Phe Pro Leu Ser Trp Met Arg Xaa Leu Leu Ser Phe Leu Pro Cys  
 35 40 45

Pro Gly Ser Phe Gly Ala Leu Pro Phe His Gly Xaa Asn Leu Ala Ser  
50 55 60

5 <210> 840  
<211> 79  
<212> PRT  
<213> Homo sapiens

10 <400> 840  
Glu Ala Arg Phe Ser Thr Phe Met Asp Glu Xaa Pro Leu Val Val Phe  
1 5 10 15  
Ala Leu Ser Trp Val Phe Trp Ser Leu Ala Leu Ser Trp Xaa Gln Ser  
20 25 30  
Gly Phe Leu Asn Ser His Asn Pro Ala Xaa Xaa Gly Pro Phe Ile Phe  
15 35 40 45  
Xaa Gly Xaa Gly His Phe Gly Phe His Leu Asn Leu Xaa Pro Gly Xaa  
50 55 60  
Leu Ala Xaa Ser Xaa Xaa Phe Ser Ser Arg Xaa Xaa Lys Glu Gly  
65 70 75

20 <210> 841  
<211> 57  
<212> PRT  
<213> Homo sapiens

25 <400> 841  
Lys Gly Lys Ala Pro Lys Asp Pro Gly Gln Gly Lys Asn Asp Lys Arg  
1 5 10 15  
Xaa Leu Ile His Glu Ser Gly Lys Ser Gly Phe Ser Arg Thr Xaa Phe  
30 20 25 30  
Gln Ala Cys Thr Gly Met Ser Ser Asn Lys Arg Lys Xaa Glu Lys Arg  
35 40 45  
Ser Asn Ser Ala Leu Cys Lys Arg Ser  
50 55

35 <210> 842  
<211> 57  
<212> PRT  
<213> Homo sapiens

40 <400> 842  
Thr Pro Gly Thr Gly Gln Asn Arg Gln Glu Xaa Ser His His Glu Ser  
1 5 10 15  
Gly Asn Leu Ala Leu Lys Thr Asp Phe Gln Gly Leu Tyr Trp Asp Glu  
45 20 25 30  
Leu Lys Gln Lys Glu Xaa Arg Glu Lys Glu Gln Leu Ser Ser Leu Gln  
35 40 45  
Glu Glu Leu Glu Ser Leu Leu Glu Lys  
50 55

50 <210> 843  
<211> 50  
<212> PRT  
<213> Homo sapiens

55 <400> 843  
Pro Gln Gly Gln Gly Lys Thr Asp Lys Arg Xaa Leu Ile Met Lys Val  
1 5 10 15  
Glu Ile Trp Leu Ser Arg Gln Ile Phe Arg Ala Cys Thr Gly Met Ser  
60 20 25 30  
Ser Asn Lys Arg Lys Xaa Glu Lys Arg Ser Asn Ser Ala Leu Cys Lys  
35 40 45  
Arg Ser

50

5 <210> 844  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 844  
 10 Leu Gly Arg Arg Pro Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val  
 1 5 10 15  
 Met Arg Ala Ala Pro Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala  
 20 25 30  
 Leu Ser Ser Val Ile Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg  
 35 40 45  
 15 Ile Lys Glu Thr Thr Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro  
 50 55 60  
 Cys Gly Leu Leu Phe Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile  
 65 70 75 80  
 Ile Val Thr Gly Leu  
 20 85

25 <210> 845  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 845  
 30 Leu Ala Arg Glu Gln Glu Ser Lys Trp Arg Leu Pro Arg Asn Gly Phe  
 1 5 10 15  
 Arg Pro Arg Lys Pro Ser Arg Asp Thr Phe Asn Ser Gln Thr Leu Pro  
 20 25 30  
 Glu Gln Arg His Ser Lys Asn Gln Gly Ser Ala Ser Ser Leu Arg Leu  
 35 40 45  
 Gly Tyr Leu Gln Ser Ser Asp Tyr Lys Phe Ser Phe Thr Gly Pro  
 50 55 60  
 35 Glu Arg Arg Glu Glu Glu Ala Ala Arg Ser Gln Ala Gly Glu Ser Arg  
 65 70 75 80  
 Ala Ser Pro Cys Arg Phe Leu Asn Ser Ser Cys Arg Leu Ala Glu  
 85 90 95

40 <210> 846  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

45 <400> 846  
 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly  
 1 5 10 15  
 Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn  
 20 25 30  
 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly  
 35 40 45  
 Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser  
 50 55 60  
 55 Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg  
 65 70 75 80  
 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro  
 85 90 95  
 Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu  
 100 105 110  
 60 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu  
 115 120 125  
 Arg Pro Gly Arg Leu Pro Ser



130

135

5 <210> 847  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

<400> 847  
 10 Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly  
 1 5 10 15  
 Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn  
 20 25 30  
 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly  
 35 40 45  
 15 Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser  
 50 55 60  
 Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg  
 65 70 75 80  
 20 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro  
 85 90 95  
 Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu  
 100 105 110  
 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu  
 115 120 125  
 25 Arg Pro Gly Arg Leu  
 130

30 <210> 848  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<400> 848  
 35 Gly Arg Arg Pro Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val Met  
 1 5 10 15  
 Arg Ala Ala Pro Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu  
 20 25 30  
 Ser Ser Val Ile Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile  
 35 40 45  
 40 Lys Glu Thr Thr Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys  
 50 55 60  
 Gly Leu Leu Phe Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile Ile  
 65 70 75 80  
 Val Thr Gly Leu

45 <210> 849  
 <211> 73  
 <212> PRT  
 50 <213> Homo sapiens

<400> 849  
 55 Ala Gln Pro Met Lys Arg Ala Lys Gly Ser Xaa Lys Lys Thr Pro Xaa  
 1 5 10 15  
 Gly Pro Gly Ala Lys Asn Arg Pro Xaa Arg Xaa Phe Ser Phe His Glu  
 20 25 30  
 Lys Xaa Lys Ile Trp Ala Xaa Gln Glu Xaa Ile Ser Gly Xaa Tyr Leu  
 35 40 45  
 60 Asp Glu Leu Asn Gln Lys Glu Ala Arg Xaa Lys Glu Gln Leu Ser Xaa  
 50 55 60  
 Leu Gln Glu Glu Leu Glu Ile Pro Pro  
 65 70

<210> 850  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

5

<400> 850

Leu Gly Asn Arg Lys Ala Asn Gly Gly Ser Pro Gly Thr Val Phe Gly  
 1 5 10 15  
 Pro Glu Ser Pro Ala Glu Ile Leu Ser Thr His Lys Leu Ser Arg Asn  
 10 20 25 30  
 Lys Asp Thr Gln Lys Ile Arg Ala Gln Arg Ala Leu Phe Ala Ser Gly  
 35 40 45  
 Thr Tyr Asn Pro Val Thr Ile Ile Ser Ser Val Ser Pro Gly Arg Ser  
 50 55 60  
 Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu Arg Ala Glu Arg  
 15 65 70 75 80  
 Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp Gln Ser Asp Pro  
 85 90 95  
 Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln Arg Glu Ile Leu  
 20 100 105 110  
 Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr Ser Pro Ala Leu  
 115 120 125  
 Arg

25

<210> 851  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

30

<400> 851

Leu Ala Arg Glu Gln Glu Ser Lys Trp Arg Leu Pro Arg Asn Gly Phe  
 1 5 10 15  
 Arg Pro Arg Lys Pro Ser Arg Asp Thr Phe Asn Ser Gln Thr Leu Pro  
 35 20 25 30  
 Glu Gln Arg His Ser Lys Asn Gln Gly Ser Ala Ser Ser Leu Arg Leu  
 35 40 45  
 Gly Tyr Leu Gln Ser Ser Asp Asp Tyr Lys Phe Ser Phe Thr Gly Pro  
 50 55 60  
 Glu Arg Arg Glu Glu Glu Ala Ala Arg Ser Gln Ala Gly Glu Ser Arg  
 40 65 70 75 80  
 Ala Ser Pro Cys Arg Phe Leu Asn Ser Ser Cys Arg Leu Ala Glu  
 85 90 95

45

<210> 852  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

50

<400> 852

Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val Met Arg Ala Ala Pro  
 1 5 10 15  
 Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu Ser Ser Val Ile  
 20 25 30  
 Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile Lys Glu Thr Thr  
 55 35 40 45  
 Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys Gly Leu Leu Phe  
 50 55 60  
 Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile Ile Val Thr Gly Leu  
 60 65 70 75 80

<210> 853  
 <211> 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 853

5 Pro Gln Gly Phe Phe Pro Xaa Xaa Ser Phe Ile Asn Ser Asn Pro Met  
 1 5 10 15  
 Pro Val Pro Thr Phe Xaa Cys Arg Xaa Arg Thr Thr Arg Lys Lys Xaa  
 20 25 30  
 Xaa Xaa Xaa Val Arg Asn Xaa Lys Xaa Xaa Gly Xaa Phe Pro Gly Thr  
 10 35 40 45  
 Gly Phe Xaa Pro Xaa Lys Pro Xaa Xaa Xaa Thr Phe Xaa Xaa Gln Leu  
 50 55 60  
 Ser Arg Asn Lys Asp Thr Gln Lys Ile Arg Xaa Gln Xaa Ala Phe Phe  
 65 70 75 80  
 15 Arg Leu Arg Gly Leu Ser Ile Pro Val Thr Ile Ile Ser Ser Val Ser  
 85 90 95  
 Pro Gly Arg Ser Glu Gly Lys Arg Arg Pro Gln Gly Ala Lys Arg Glu  
 100 105 110  
 Arg Ala Glu Arg Leu Leu Val Val Ser Leu Ile Leu Pro Ala Ala Trp  
 115 120 125  
 20 Gln Ser Asp Pro Leu Pro Ile Thr Asp Glu Arg Ala Arg Asp Gly Gln  
 130 135 140  
 Arg Glu Ile Leu Pro Arg Gly Ala Ala Arg Ile Thr Arg Pro Arg Thr  
 145 150 155 160  
 25 Ser Pro Ala Leu Arg Pro  
 165

&lt;210&gt; 854

&lt;211&gt; 91

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 854

35 Pro Gly Arg Arg Ala Gly Glu Val Arg Gly Leu Val Met Arg Ala Ala  
 1 5 10 15  
 Pro Leu Gly Lys Ile Ser Arg Cys Pro Ser Arg Ala Leu Ser Ser Val  
 20 25 30  
 Ile Gly Ser Gly Ser Leu Cys Gln Ala Ala Gly Arg Ile Lys Glu Thr  
 35 40 45  
 40 Thr Arg Arg Arg Ser Ala Leu Ser Arg Leu Ala Pro Cys Gly Leu Leu  
 50 55 60  
 Phe Pro Ser Leu Arg Pro Gly Glu Thr Glu Leu Ile Ile Val Thr Gly  
 65 70 75 80  
 Met Glu Arg Pro Arg Arg Arg Lys Lys Ala Xaa  
 85 90  
 45

&lt;210&gt; 855

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 855

55 Ser Xaa Arg Xaa Ile Thr Xaa Ser Phe Xaa Pro Gly Xaa Lys Xaa Trp  
 1 5 10 15  
 Glu Lys Xaa Ser Xaa Gln Gly Pro Xaa Xaa Xaa Phe Gln Met Gly  
 20 25 30  
 Xaa Ala Pro Arg Xaa Asn Glu Gly Thr Xaa Ile Pro Xaa Xaa Val Xaa  
 35 40 45  
 60 Gly Ile Xaa Xaa Ser Gln Asp Cys Xaa Thr Xaa Lys Arg Ala Xaa Phe  
 50 55 60  
 Gln Lys Ala Xaa Arg Thr Gly Xaa Asn Gly Pro Lys Gly Xaa Ser Phe  
 65 70 75 80  
 Xaa Lys Gly Gly Lys Phe Xaa Xaa Ser Lys Asn Lys Phe Ser Gly Cys

85 90 95  
 Xaa Gly Xaa Ala Gln Xaa Lys Gly Ser Pro Arg Lys Gly Ala Thr Gln  
 100 105 110  
 Leu Phe Ala Arg Xaa Ala Arg Ile Thr Pro Arg Glu Val Lys Xaa Thr  
 115 120 125  
 5 Asp Ile  
 130  
 <210> 856  
 10 <211> 119  
 <212> PRT  
 <213> Homo sapiens  
 <400> 856  
 15 Pro Xaa Pro Xaa Xaa Pro Gly Xaa Xaa Phe Gly Lys Asn Xaa Val Xaa  
 1 5 10 15  
 Arg Ala Gln Xaa Xaa Xaa Tyr Ser Arg Trp Ala Xaa Pro Pro Xaa Lys  
 20 20 25 30  
 Met Lys Gly Pro Xaa Phe Xaa Xaa Gly Xaa Trp Glu Phe Xaa Xaa Ala  
 35 40 45  
 20 Arg Ile Ala Xaa Pro Xaa Lys Gly Gln Xaa Ser Lys Lys Pro Xaa Gly  
 50 55 60  
 Gln Xaa Lys Thr Asp Gln Arg Xaa Ser Leu Ser Xaa Lys Gly Glu Asn  
 65 70 75 80  
 25 Leu Xaa Phe Gln Arg Thr Asn Phe Gln Ala Val Xaa Xaa Glu Leu Asn  
 85 90 95  
 Xaa Lys Glu Ala Arg Glu Lys Glu Gln Leu Ser Ser Leu Gln Glu Xaa  
 100 105 110  
 Leu Glu Ser Leu Leu Glu Lys  
 115  
 30 <210> 857  
 <211> 79  
 <212> PRT  
 35 <213> Homo sapiens  
 <400> 857  
 Arg Asp Pro Xaa Ser Xaa Xaa Gly Xaa Gly Asn Phe Xaa Lys Pro Gly  
 1 5 10 15  
 40 Leu Pro Xaa His Xaa Lys Gly Lys Xaa Pro Lys Ser Pro Xaa Asp Arg  
 20 25 30  
 Xaa Lys Arg Thr Lys Gly Xaa Leu Phe Xaa Glu Arg Gly Lys Ile Trp  
 35 40 45  
 Xaa Phe Lys Glu Gln Ile Phe Arg Leu Xaa Trp Xaa Ser Ser Thr Xaa  
 50 55 60  
 45 Arg Lys Pro Glu Lys Arg Ser Asn Ser Ala Leu Cys Lys Xaa Ser  
 65 70 75  
 <210> 858  
 50 <211> 63  
 <212> PRT  
 <213> Homo sapiens  
 <400> 858  
 55 Xaa Leu Leu Gln Xaa Ala Glu Leu Pro Leu Phe Ser Gly Phe Leu Leu  
 1 5 10 15  
 Xaa Glu Leu Xaa Pro Val Gln Pro Trp Lys Xaa Val Xaa Glu Asn Xaa  
 20 25 30  
 Xaa Phe Pro Pro Phe Met Glu Arg Lys Thr Pro Trp Ala Val Phe Xaa  
 35 40 45  
 60 Pro Gly Xaa Gly Ala Phe Trp Glu Pro Gly Pro Phe Asn Gly Gly  
 50 55 60

<210> 859  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

5

<400> 859  
 Xaa Ser Gly Leu Phe Thr Ser Leu Gly Xaa Asp Xaa Ser Xaa Ser Cys  
 1 5 10 15  
 Lys Xaa Leu Ser Cys Pro Phe Ser Arg Ala Ser Phe Xaa Xaa Ser Ser  
 10 20 25 30  
 Xaa Gln Tyr Ser Pro Gly Asn Xaa Xaa Leu Lys Thr Xaa Xaa Phe Pro  
 35 40 45  
 Leu Ser Trp Lys Glu Lys Pro Leu Gly Arg Phe Leu Xaa Leu Ala Xaa  
 50 55 60  
 15 Gly Leu Phe Gly Asn Leu Ala Leu Leu Met Gly Gly  
 65 70 75

<210> 860  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

20

<400> 860  
 Ala Pro Pro Leu Lys Gly Pro Gly Ser Gln Lys Ala Xaa Gly Pro Gly  
 1 5 10 15  
 Xaa Lys Thr Ala Gln Gly Val Phe Leu Ser Met Lys Gly Gly Xaa Phe  
 20 25 30  
 Xaa Phe Ser Xaa Thr Xaa Phe Gln Gly Cys Thr Xaa Met Ser Xaa Xaa  
 35 40 45  
 30 Lys Arg Lys Pro Glu Lys Arg Gly Asn Ser Ala Xaa Cys Lys Arg Xaa  
 50 55 60  
 Xaa Asn Xaa Leu Leu Glu Lys  
 65 70

<210> 861  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens

35

<400> 861  
 Met Ala Gly Gly Asp Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe  
 1 5 10 15  
 Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met  
 20 25 30  
 45 Tyr Arg Cys Gly Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala  
 35 40 45  
 Phe Arg Glu Gly Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val  
 50 55 60  
 Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe  
 50 65 70 75 80  
 Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly  
 85 90 95  
 Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn  
 100 105 110  
 55 Thr Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser  
 115 120 125  
 Val Thr Ser Ser Thr Ala Thr Val Val Ser  
 130 135

<210> 862  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

60

<400> 862  
 Leu Trp Ser Glu Met Met Glu Ser Phe Ile Pro Pro Ala Leu Pro Leu  
 1 5 10 15  
 5 Pro Thr His Gln Asn Gln Gly Arg Gly His Ile Ala Val Gln Gln Glu  
 20 25 30  
 Gln Ser Phe Glu Pro Ile Gln Ala Arg Cys Pro Leu Thr Asn Gln Thr  
 35 40 45  
 Gln Thr Ala Arg Glu Val Thr Gln Thr Pro Ala Gln Ile Gln Pro Val  
 50 55 60  
 10 Ser His His Leu Gln Pro Gln Trp Tyr Pro Asn Tyr Arg Leu Phe Ala  
 65 70 75 80  
 Arg Thr  
 15  
 <210> 863  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens  
 20  
 <400> 863  
 Met Ile Pro Ser Phe Arg Thr Lys Val Thr Gly Thr Trp Thr Gly Cys  
 1 5 10 15  
 Arg Thr His Leu Gln Pro Ser Arg Asn Ala Glu Met Ser Gly Thr Thr  
 20 25 30  
 25 Gln Ser Ile Leu Ser Pro His Leu Tyr Ile Val Ser Ala Ser Thr Ser  
 35 40 45  
 Pro Asn His Thr Arg Lys Phe Gly Val Lys Phe Cys Pro Val Ser Ser  
 50 55 60  
 30 Ser Ile Ala Thr Ser Pro Pro Ala Ile Gln Leu Lys Ala Leu Tyr His  
 65 70 75 80  
 Xaa Xaa Gln Xaa  
 35  
 <210> 864  
 <211> 138  
 <212> PRT  
 <213> Homo sapiens  
 40  
 <400> 864  
 Met Ala Gly Gly Asp Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe  
 1 5 10 15  
 Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met  
 20 25 30  
 45 Tyr Arg Cys Gly Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala  
 35 40 45  
 Phe Arg Glu Gly Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val  
 50 55 60  
 Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe  
 50 65 70 75 80  
 Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly  
 85 90 95  
 Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn  
 100 105 110  
 55 Thr Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser  
 115 120 125  
 Val Thr Ser Ser Thr Ala Thr Val Val Ser  
 130 135  
 60  
 <210> 865  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 865  
 Phe Lys Gly Phe Pro Glu Lys Glu Asn Gly Ile Xaa Ala Leu Phe Ser  
 1 5 10 15  
 5 Lys Lys Lys Asn Ile Ser Asn Xaa Gln Ala His Ser His Val Gln Lys  
 20 25 30  
 Asp Pro Asn Lys Glu Met Ile Asn Asp Gly Arg Phe Leu Xaa Asn Ser  
 35 40 45  
 10 Leu Xaa Gln Ile Xaa Gln Glu Tyr Thr Phe Tyr Glu Gly Met Gly Pro  
 50 55 60  
 Val Leu Ala Pro Val Thr Pro Val Pro Val Glu Ser Leu Gln Leu  
 65 70 75 80  
 Asn Gly Gly Gly Asp Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe  
 85 90 95  
 15 Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met  
 100 105 110  
 Tyr Arg Cys Gly Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala  
 115 120 125  
 Phe Arg Glu Gly Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val  
 130 135 140  
 20 Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe  
 145 150 155 160  
 Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly  
 165 170 175  
 25 Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn  
 180 185 190  
 Thr Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser  
 195 200 205  
 Val Thr Ser Ser Thr Ala Thr Val Val Ser  
 210 215  
 30

<210> 866  
 <211> 109  
 <212> PRT  
 35 <213> Homo sapiens

<400> 866  
 Asn Tyr Val Gln Val Trp Xaa Lys Val Cys Xaa Cys Val Val Pro Xaa  
 1 5 10 15  
 40 Ile Phe Ala Phe Arg Xaa Gly Trp Xaa Trp Val Arg Gln Pro Val Gln  
 20 25 30  
 Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser  
 35 40 45  
 45 Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser  
 50 55 60  
 Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser Gln Xaa Pro Pro Asn  
 65 70 75 80  
 Glu Ser Asn Xaa Asn Ser Glu Gly Ser Tyr Xaa Asn Ala Ser Thr Asn  
 85 90 95  
 50 Ser Thr Xaa Val Thr Ser Xaa Thr Ala Xaa Xaa Val Ser  
 100 105

<210> 867  
 <211> 98  
 55 <212> PRT  
 <213> Homo sapiens

<400> 867  
 Gly Glu Asn Gly Ala Pro Trp Ser Phe Gly Pro Xaa Val His Phe Leu  
 1 5 10 15  
 Gly Ala Leu Gly Xaa Lys Xaa Pro Phe Lys Phe Lys Trp Arg Val Gly  
 20 25 30  
 Thr Xaa Gln Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu

35 40 45  
 Xaa Ser Val Val Trp Gly Xaa Xaa Ser Leu Lys Leu Cys Thr Gly Val  
 50 55 60  
 Xaa Lys Ser Met Xaa Leu Cys Arg Pro Xaa His Phe Cys Ile Pro Xaa  
 5 65 70 75 80  
 Arg Leu Xaa Met Gly Pro Ala Thr Ser Pro Gly Ser Ser Asn Phe Gly  
 85 90 95  
 Pro Lys  
 10  
 <210> 868  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 868  
 Phe His His Phe Gly Pro Lys Leu Leu Glu Pro Gly Leu Val Ala Gly  
 1 5 10 15  
 Pro Xaa Ser Asn Leu Xaa Gly Met Gln Lys Cys Xaa Gly Arg His Xaa  
 20 20 25 30  
 Ser Ile Leu Xaa Ser Thr Pro Val His Ser Phe Lys Leu Xaa His Pro  
 35 40 45  
 Gln Thr Thr Leu Xaa Lys Phe Gly Val Lys Phe Cys Pro Val Ser Ser  
 50 55 60  
 25 Ser Ile Xaa Tyr Val Pro Thr Arg His Leu Asn Leu Lys Xaa Phe Phe  
 65 70 75 80  
 Xaa Pro Lys Ala Pro Arg Lys Trp Thr Xaa Gly Pro Lys Asp Gln Gly  
 85 90 95  
 Ala Pro Phe Ser Pro Gln  
 30 100  
 <210> 869  
 <211> 115  
 <212> PRT  
 35 <213> Homo sapiens  
 <400> 869  
 Met Ile Pro Ser Phe Arg Thr Lys Val Thr Gly Thr Trp Thr Gly Cys  
 1 5 10 15  
 40 Arg Thr His Phe Gln Pro Xaa Arg Asn Ala Lys Met Ser Gly Thr Thr  
 20 25 30  
 Gln Ser Ile Xaa Xaa Pro His Leu Tyr Ile Val Ser Ala Xaa Thr Ser  
 35 40 45  
 Pro Asn His Thr Arg Lys Ile Xaa Ser Glu Asn Ser Val Leu Val Ser  
 45 50 55 60  
 Ser Ser Ile Ala Thr Ser Xaa Pro Ala Ile Xaa Thr Gly Arg Xaa Xaa  
 65 70 75 80  
 Leu Xaa Gln Gly Pro Xaa Asn Glu Leu Gly Gly Lys Gly Pro Xaa Ala  
 85 90 95  
 50 Pro Phe Pro Ser Xaa Lys Xaa Val Leu Pro Leu Gly Pro Tyr Phe Trp  
 100 105 110  
 Gly Pro Lys  
 115  
 55  
 <210> 870  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens  
 60  
 <400> 870  
 Gly Pro Arg Gly Asn Xaa Phe Xaa Ile Glu Gly Asn Gly Ala Xaa Gly  
 1 5 10 15  
 Pro Leu Pro Pro Ser Ser Phe Xaa Gly Pro Xaa Gly Lys Xaa Xaa Leu  
 322



20 25 30  
 Pro Val Xaa Met Ala Xaa Gly Asp Val Ala Met Leu Glu Leu Thr Arg  
 35 40 45  
 Thr Glu Phe Ser Leu Xaa Ile Leu Arg Val Trp Phe Gly Asp Val Xaa  
 5 50 55 60  
 Ala Glu Thr Met Tyr Arg Cys Gly Xaa Ser Met Leu Cys Val Val Pro  
 65 70 75 80  
 Asp Ile Phe Ala Phe Arg Xaa Gly Trp Lys Trp Val Arg Gln Pro Val  
 85 90 95  
 10 Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr  
 100 105 110  
 Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys  
 115 120 125  
 Ser Ala Ala Gly Ala Thr Leu Arg Ala Asn Ser Ser Gln Xaa Pro Pro  
 15 130 135 140  
 Asn Glu Ser Asn Xaa Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr  
 145 150 155 160  
 Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val Ser  
 165 170  
 20  
 <210> 871  
 <211> 237  
 <212> PRT  
 <213> Homo sapiens  
 25  
 <400> 871  
 Lys Thr Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu  
 1 5 10 15  
 Ser Val Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu  
 30 20 25 30  
 Ser Lys Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser  
 35 35 40 45  
 Leu Lys Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu  
 50 55 60  
 Phe Asn Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val  
 65 70 75 80  
 Glu Gly Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe  
 85 90 95  
 Ile His Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val  
 40 100 105 110  
 Arg Asp Gly Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser  
 115 120 125  
 Val Thr Gly Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys  
 130 135 140  
 45 Gln Thr Ala Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys  
 145 150 155 160  
 Cys Ala Phe Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser  
 165 170 175  
 Gln Glu Arg Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro  
 50 180 185 190  
 Asn Lys Glu Met Ile Asn Asp Gly Ala Xaa Trp Thr Ile Ile Ser Thr  
 195 200 205  
 Asp Lys Ala Glu Tyr Thr Phe Tyr Xaa Gly Met Gly Pro Val Leu Ala  
 210 215 220  
 55 Pro Ile Thr Pro Val Pro Val Lys Lys Ala Phe Xaa  
 225 230 235  
 60  
 <210> 872  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens  
 <400> 872

Leu Asn Asp Gly Ala Ser Trp Pro Phe Ile Ser Xaa Asp Lys Ala Glu  
 1 5 10 15  
 Tyr Thr Phe Tyr Glu Gly Met Gly Pro Val Xaa Ala Pro Val Thr Pro  
 20 25 30  
 5 Val Pro Val Val Glu Ser Leu Gln Leu Asn Gly Gly Gly Asp Val Ala  
 35 40 45  
 Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu Arg Val Trp  
 50 55 60  
 Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser Met  
 65 70 75 80  
 10 Leu Cys Val Val Pro Asp Ile Ser Ala Phe Arg Glu Gly Trp Arg Trp  
 85 90 95  
 Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly  
 100 105 110  
 15 Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly  
 115 120 125  
 Pro Arg Pro His Cys Ser Ala Glu Ala Ile Leu Arg Ala Asn Ser  
 130 135 140  
 Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr  
 145 150 155 160  
 20 Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala Thr  
 165 170 175  
 Val Val Ser

25

<210> 873  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

30

<400> 873  
 Pro Arg Ile Gly Gln Ser Xaa His Phe Tyr Glu Gly Met Gly Pro Cys  
 1 5 10 15  
 Pro Cys Pro Ser His Xaa Cys Ala Cys Gly Xaa Glu Pro Ser Val Glu  
 20 25 30  
 35 Trp Arg Val Gly Thr Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe  
 35 40 45  
 Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met  
 50 55 60  
 40 Tyr Arg Cys Gly Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala  
 65 70 75 80  
 Phe Arg Glu Gly Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val  
 85 90 95  
 Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe  
 100 105 110  
 45 Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly  
 115 120 125  
 Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn  
 130 135 140  
 50 Thr Asn Ser Glu Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser  
 145 150 155 160  
 Val Thr Ser Ser Thr Ala Thr Val Val Ser  
 165 170

55

<210> 874  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

60

<400> 874  
 Gln Cys Leu Asn Phe Thr Xaa Gln Asn Phe Thr Pro Asn Leu Arg Val  
 1 5 10 15  
 Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser

20 25 30  
 Met Leu Cys Val Val Pro Asp Ile Xaa Ala Phe Arg Glu Gly Trp Arg  
 35 40 45  
 Trp Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp  
 5 50 55 60  
 Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro  
 65 70 75 80  
 Gly Pro Arg Pro His Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn  
 85 90 95  
 10 Ser Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser  
 100 105 110  
 Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala  
 115 120 125  
 Thr Val Val Ser  
 15 130

&lt;210&gt; 875

&lt;211&gt; 160

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 875

Ile Gly Ser Lys Asp Cys Ser Cys Cys Thr Ala Met Trp Pro Arg Pro  
 1 5 10 15  
 25 Trp Phe Trp Cys Val Gly Lys Gly Lys Ala Gly Gly Ile Asn Asp Ser  
 20 25 30  
 Ile Ile Ser Asp Gln Ser Tyr Trp Asn Leu Asp Trp Leu Pro Asp Pro  
 35 40 45  
 Ser Pro Thr Xaa Ser Glu Cys Lys Asn Val Trp Asp Asp Thr Lys His  
 30 50 55 60  
 Thr Xaa Ser Thr Pro Xaa His Lys Phe Gln Ala Xaa Thr Ser Pro Asn  
 65 70 75 80  
 His Thr Arg Lys Phe Gly Val Lys Phe Cys Pro Val Ser Ser Lys His  
 85 90 95  
 35 Trp Tyr Val Pro Thr Ala Ile Gln Leu Xaa Xaa Xaa Phe His Xaa Pro  
 100 105 110  
 Xaa Xaa Asp Trp Gly Lys Asp Xaa Xaa His Ser Leu Xaa Lys Gly Tyr  
 115 120 125  
 Ser Gly Xaa Ser Gly Xaa Lys Xaa Gly Gln Xaa Xaa Pro His Leu Ser  
 40 130 135 140  
 Thr Xaa Tyr Leu Gly Leu Leu Glu Ile Gly Gly Ala Xaa Asn Xaa Ile  
 145 150 155 160

&lt;210&gt; 876

45 &lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 876

50 Thr Tyr Arg Thr Glu Phe His Ser Lys Phe Thr Ser Val Val Trp Gly  
 1 5 10 15  
 Cys Xaa Ser Leu Lys Leu Met Xaa Arg Cys Gly Xaa Ser Met Leu Cys  
 20 25 30  
 Val Val Pro Asp Ile Phe Ala Phe Arg Xaa Gly Trp Arg Trp Val Arg  
 55 35 40 45  
 Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile  
 50 55 60  
 Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro Arg  
 65 70 75 80  
 60 Pro His Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser Gln  
 85 90 95  
 Xaa Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr Xaa Asn  
 100 105 110

Ala Ser Xaa Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val  
 115 120 125  
 Ser

5  
 <210> 877  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

10  
 <400> 877  
 Xaa Asn Xaa Gly Pro Leu Gln Phe Pro Lys Asp Pro Asn Lys Xaa Leu  
 1 5 10 15  
 Ile Asn Glu Xaa Leu Xaa Gly Xaa Ser Xaa Ala Gln Ile Xaa Gln Ser  
 15 20 25 30  
 Ile Leu Xaa Ile Arg Asn Xaa Xaa Cys Pro Cys Pro Ser Xaa Xaa Trp  
 35 40 45  
 Xaa Cys Gly Lys Xaa Xaa Ser Val Glu Trp Arg Trp Gly Arg Thr Asn  
 50 55 60  
 20 Ala Leu Asn Leu Gln Asp Arg Ile Ser Leu Gln Ile Tyr Glu Cys Gly  
 65 70 75 80  
 Leu Gly Met Xaa Lys Leu Glu Thr Tyr Xaa Gln Val Trp Xaa Glu Tyr  
 85 90 95  
 Ala Leu Cys Arg Pro Arg His Phe Cys Ile Pro Xaa Arg Leu Glu Met  
 100 105 110  
 25 Gly Pro Ala Thr Ser Pro Gly Ser Ser Asn Phe Gly Pro Lys  
 115 120 125

30  
 <210> 878  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

35  
 <400> 878  
 Gly Lys Trp Ala Xaa Ser Xaa Ala Pro Val Ile Leu Val Pro Val Glu  
 1 5 10 15  
 Lys Xaa Xaa Gln Leu Asn Gly Gly Gly Asp Val Pro Met Leu Glu Leu  
 20 25 30  
 Thr Gly Xaa Asn Phe Thr Pro Asn Leu Arg Val Trp Phe Gly Asp Val  
 35 40 45  
 Xaa Ala Glu Thr Met Tyr Arg Cys Gly Xaa Ser Met Xaa Cys Val Val  
 50 55 60  
 Pro Asp Ile Xaa Ala Phe Arg Xaa Gly Trp Arg Trp Val Arg Gln Pro  
 65 70 75 80  
 45 Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser  
 85 90 95  
 Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro Arg Pro His  
 100 105 110  
 Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser Gln Val Pro  
 115 120 125  
 50 Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr Xaa Asn Ala Ser  
 130 135 140  
 Thr Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val Ser  
 145 150 155

55  
 <210> 879  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

60  
 <400> 879  
 Lys Leu Lys Leu Met Tyr Arg Cys Gly Xaa Ser Met Xaa Cys Val Val  
 1 5 10 15

Pro Xaa Ile Xaa Ala Phe Arg Xaa Gly Trp Arg Trp Val Arg Gln Pro  
                   20                  25                  30  
 Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile Ile Tyr Ser  
                   35                  40                  45  
 5 Xaa Ser Leu Thr Phe Thr Tyr Thr Pro Xaa Pro Gly Pro Arg Pro His  
       50                  55                  60  
 Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser Gln Xaa Pro  
   65                  70                  75                  80  
 10 Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr Xaa Asn Ala Ser  
                   85                  90                  95  
 Thr Asn Ser Thr Ser Val Thr Ser Xaa Thr Ala Xaa Val Val Ser  
                   100                  105                  110  
  
           <210> 880  
 15           <211> 96  
           <212> PRT  
           <213> Homo sapiens  
  
           <400> 880  
 20 Gly Gln Ser Ile Leu Xaa Ile Arg Xaa Trp Ala Xaa Xaa Leu Pro Gln  
       1                  5                  10                  15  
 Ser Phe Leu Gly Xaa Gly Lys Xaa Pro Ser Val Glu Trp Arg Gly Asp  
                   20                  25                  30  
 Val Xaa Met Phe Glu Leu Thr Xaa Gln Asn Phe Thr Pro Asn Leu Arg  
       35                  40                  45  
 25 Val Trp Phe Gly Asp Val Lys Ala Glu Thr Tyr Val Gln Val Trp Xaa  
       50                  55                  60  
 Glu Tyr Ala Xaa Cys Arg Pro Xaa His Xaa Cys Ile Pro Xaa Arg Leu  
   65                  70                  75                  80  
 30 Glu Met Gly Pro Ala Thr Ser Pro Gly Ser Ser Asn Phe Gly Pro Lys  
                   85                  90                  95  
  
           <210> 881  
           <211> 247  
 35           <212> PRT  
           <213> Homo sapiens  
  
           <400> 881  
 40 Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg Val Leu Ala Pro His  
       1                  5                  10                  15  
 Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly Ala Asp Ala Arg  
                   20                  25                  30  
 Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala Val  
                   35                  40                  45  
 45 Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile Glu Gln Ser Trp Gly  
       50                  55                  60  
 Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp  
   65                  70                  75                  80  
 Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val  
       85                  90                  95  
 50 Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr  
                   100                  105                  110  
 Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys  
                   115                  120                  125  
 55 Gly Ala Asn Pro Val Glu Ile Xaa Arg Gly Val Met Leu Ala Val Asp  
       130                  135                  140  
 Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr Pro  
   145                  150                  155                  160  
 Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys Glu  
                   165                  170                  175  
 60 Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Lys Gly  
                   180                  185                  190  
 Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn Asp Glu Leu Glu Ile

195 200 205  
 Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile Ser Pro Tyr Phe Ile  
 210 215 220  
 Asn Thr Ser Lys Gly Gln Lys Cys Glu Xaa Gln Asp Ala Tyr Val Leu  
 225 230 235 240  
 Val Ser Glu Lys Xaa Asn Xaa  
 245  
  
 <210> 882  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 882  
 15 Pro Arg Ser Asn Phe Met Pro Ser Ile Ile Ser Asn Ser Ser Phe Ser  
 1 5 10 15  
 Val Phe Pro Ser Phe Thr Val Met Thr Pro Phe Leu Pro Thr Phe Phe  
 20 25 30  
 Ile Ala Ser Glu Met Ile Leu Pro Ile Ser Leu Ser Pro Phe Ala Glu  
 35 40 45  
 Ile Val Ala Thr Cys Ala Ile Ser Ser Gly Val Val Thr Gly Leu Asp  
 50 55 60  
 Cys Phe Leu Ser Ser Ala Ile Thr Ala Ser Thr Ala Asn Ile Thr Pro  
 65 70 75 80  
 25 Leu Xaa Ile Ser Thr Gly Leu Ala Pro Leu Leu Ile Phe Ser Lys Pro  
 85 90 95  
 Ser Leu Ala Ile Glu Arg Ala Ser Thr Val Ala Val Val Val Pro Ser  
 100 105 110  
 Pro Ala Ser Ser Phe Val Leu Leu Ala Thr Ser  
 115 120  
 30  
  
 <210> 883  
 <211> 96  
 <212> PRT  
 35 <213> Homo sapiens  
  
 <400> 883  
 Lys Lys Cys Arg Val Leu Lys Asp Leu Leu Lys Ser Xaa Arg Lys Ile  
 1 5 10 15  
 40 Met Gln Lys Phe Leu Gln Lys Val Gly Tyr Asp Ala Lys Gly Xaa Arg  
 20 25 30  
 Phe Cys Glu Tyr Gly Glu Lys Gly Ser Phe Asp Pro Pro Lys Val Val  
 35 40 45  
 Arg Thr Ala Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr  
 50 55 60  
 45 Ala Xaa Val Val Val Thr Glu Ile Pro Lys Glu Lys Asp Pro Gly  
 65 70 75 80  
 Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe  
 85 90 95  
 50  
  
 <210> 884  
 <211> 212  
 <212> PRT  
 <213> Homo sapiens  
 55  
  
 <400> 884  
 Leu Ala Glu Arg Thr Pro Cys Arg Arg Pro Ala Glu Met Leu Arg Leu  
 1 5 10 15  
 Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg Val Leu Ala Pro  
 20 25 30  
 His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe Gly Ala Asp Ala  
 35 40 45  
 Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala  
 328

50 55 60  
 Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile Glu Gln Ser Trp  
 65 70 75 80  
 Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile  
 5 85 90 95  
 Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu Val Gln Asp  
 100 105 110  
 Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala  
 115 120 125  
 10 Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser  
 130 135 140  
 Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val Met Leu Ala Val  
 145 150 155 160  
 Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys Pro Val Thr Thr  
 15 165 170 175  
 Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala Asn Gly Asp Lys  
 180 185 190  
 Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys Val Gly Arg Xaa  
 195 200 205  
 20 Gly Val Ile Gln  
 210  
  
 <210> 885  
 <211> 123  
 25 <212> PRT  
 <213> Homo sapiens  
  
 <400> 885  
 Gly Ser Lys Phe Asn Ala Phe Lys Asn Phe Leu Ile His Pro Phe Arg  
 1 5 10 15  
 Val Xaa Pro Ser Phe Tyr Trp Met Thr Xaa Phe Leu Pro Thr Phe Phe  
 20 25 30  
 Ile Ala Ser Glu Met Ile Leu Pro Ile Ser Leu Ser Pro Phe Ala Glu  
 35 35 40 45  
 Ile Val Ala Thr Cys Ala Ile Ser Ser Gly Val Val Thr Gly Leu Asp  
 50 55 60  
 Cys Phe Leu Ser Ser Ala Ile Thr Ala Ser Thr Ala Asn Ile Thr Pro  
 65 70 75 80  
 Leu Leu Ile Ser Thr Gly Leu Ala Pro Leu Leu Ile Phe Ser Lys Pro  
 40 85 90 95  
 Ser Leu Ala Ile Glu Arg Ala Ser Thr Val Ala Val Val Val Pro Ser  
 100 105 110  
 Pro Ala Ser Ser Phe Val Leu Leu Ala Thr Ser  
 115 120  
 45  
 <210> 886  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens  
 50  
 <400> 886  
 Thr Val Thr Gly Ser Pro Arg Gln Cys Ser Ser Pro Ile Thr Ser Glu  
 1 5 10 15  
 Lys Ser Val Gly Glu Asn Glu Glu Lys Gly Trp Leu Lys Ile Thr Ile  
 55 20 25 30  
 Thr Ile Ser Tyr Trp Phe Gln Leu Thr Lys Tyr Ile Met Val Tyr Cys  
 35 40 45  
 Cys His Cys Pro Cys Leu Gln Ile Ile Tyr Phe Val Phe Leu Asn Lys  
 50 55 60  
 60 Lys His Leu Tyr Ile Pro Asp Thr Gly Tyr Lys Ser His Val Pro Val  
 65 70 75 80  
 Tyr Cys Phe Gln Leu Lys Ser Leu Arg His Phe Tyr Tyr Tyr Ser Val  
 85 90 95

Lys Ile Arg Ile Leu Val Leu Ala Thr Thr Arg  
 100 105  
 <210> 887  
 5 <211> 107  
 <212> PRT  
 <213> Homo sapiens  
 <400> 887  
 10 Thr Val Thr Gly Ser Pro Arg Gln Cys Ser Ser Pro Ile Thr Ser Glu  
 1 5 10 15  
 Lys Ser Val Gly Glu Asn Glu Glu Lys Gly Trp Leu Lys Ile Thr Ile  
 20 25 30  
 Thr Ile Ser Tyr Trp Phe Gln Leu Thr Lys Tyr Ile Met Val Tyr Cys  
 15 35 40 45  
 Cys His Cys Pro Cys Leu Gln Ile Ile Tyr Phe Val Phe Leu Asn Lys  
 50 55 60  
 Lys His Leu Tyr Ile Pro Asp Thr Gly Tyr Lys Ser His Val Pro Val  
 65 70 75 80  
 20 Tyr Cys Phe Gln Leu Lys Ser Leu Arg His Phe Tyr Tyr Tyr Ser Val  
 85 90 95  
 Lys Ile Arg Ile Leu Val Leu Ala Xaa Thr Arg  
 100 105  
 25 <210> 888  
 <211> 88  
 <212> PRT  
 <213> Homo sapiens  
 30 <400> 888  
 Asn Met Pro Pro Pro Ile Pro Pro Ser Ile Pro Pro Ile Ala Pro Ile  
 1 5 10 15  
 Pro Gly Ser Phe Ser Ser Leu Gly Ile Ser Val Thr Thr Thr Ser Ala  
 20 25 30  
 35 Val Val Asn Lys Arg Gly Pro Thr Gln Gln His Pro Ile Lys Ala Val  
 35 40 45  
 Leu Thr Thr Phe Gly Trp Gly Asn Asp Ser Phe Phe Xaa Pro Tyr Ser  
 50 55 60  
 Pro Lys Ile Xaa Pro Ala Xaa Ser Ile Ile Thr Xaa Leu Xaa Gly Gly  
 40 65 70 75 80  
 Lys Leu Cys Ile Asn Phe Leu Asn  
 85  
 45 <210> 889  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens  
 <400> 889  
 50 Thr Val Thr Gly Ser Pro Arg Gln Cys Ser Ser Pro Ile Thr Ser Glu  
 1 5 10 15  
 Lys Ser Val Gly Glu Asn Glu Glu Lys Gly Trp Leu Lys Ile Thr Ile  
 20 25 30  
 Thr Ile Ser Tyr Trp Phe Gln Leu Thr Lys Tyr Ile Met Val Tyr Cys  
 55 35 40 45  
 Cys His Cys Pro Cys Leu Gln Ile Ile Tyr Phe Val Phe Leu Asn Lys  
 50 55 60  
 Lys His Leu Tyr Ile Pro Asp Thr Gly Tyr Lys Ser His Val Pro Val  
 65 70 75 80  
 60 Tyr Cys Phe Gln Leu Lys Ser Leu Arg His Phe Tyr Tyr Tyr Ser Val  
 85 90 95  
 Lys Ile Arg Ile Leu Val Leu Ala Thr Thr Arg  
 100 105  
 330



<210> 890  
 <211> 68  
 <212> PRT  
 5 <213> Homo sapiens

<400> 890  
 Ser Thr Ser Leu Gly Val Arg Thr Cys His Leu Pro Tyr His Leu Pro  
 1 5 10 15  
 10 Phe His Pro Leu His Pro Phe Gln Gly Pro Phe Ser Ser Phe Xaa Asn  
 20 25 30  
 Phe Trp Gly Leu Gln Leu Leu Leu Val Val Asn Arg Glu Gly Pro His  
 35 40 45  
 Gln Ala Ala Phe Pro Ile Lys Pro Val Xaa His Gln Pro Phe Gly Trp  
 15 50 55 60  
 Gly Gln Arg Ile  
 65

<210> 891  
 20 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 891  
 25 Thr Val Thr Gly Ser Pro Arg Gln Cys Ser Ser Pro Ile Thr Ser Glu  
 1 5 10 15  
 Lys Ser Val Gly Glu Asn Glu Glu Lys Gly Trp Leu Lys Ile Thr Ile  
 20 25 30  
 Thr Ile Ser Tyr Trp Phe Gln Leu Thr Lys Tyr Ile Met Val Tyr Cys  
 30 35 40 45  
 Cys His Cys Pro Cys Leu Gln Ile Ile Tyr Phe Val Phe Leu Asn Lys  
 50 55 60  
 Lys His Leu Tyr Ile Pro Asp Thr Gly Tyr Lys Ser His Val Pro Val  
 65 70 75 80  
 35 Tyr Cys Phe Gln Leu Lys Ser Leu Arg His Phe Tyr Tyr Tyr Ser Val  
 85 90 95  
 Lys Ile Arg Ile Leu Val Leu Ala Thr Thr Arg  
 100 105

40 <210> 892  
 <211> 66  
 <212> PRT  
 <213> Homo sapiens

45 <400> 892  
 Asp Phe Gly Glu Tyr Gly Glu Lys Gly Ile Ile Asp Xaa Thr Lys Gly  
 1 5 10 15  
 Cys Glu Asn Cys Phe Tyr Trp Met Leu Leu Gly Val Xaa Ser Leu Leu  
 20 25 30  
 50 Thr Thr Ala Glu Val Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp  
 35 40 45  
 Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly  
 50 55 60  
 Met Phe  
 55 65

<210> 893  
 <211> 217  
 <212> PRT  
 60 <213> Homo sapiens

<400> 893  
 Met Ala Met Ala Tyr Leu Ala Trp Arg Leu Ala Arg Arg Ser Cys Pro

1                      5                      10                      15  
 Ser Ser Leu Gln Val Thr Ser Phe Pro Val Val Gln Leu His Met Asn  
                     20                      25                      30  
 Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn  
 5                      35                      40                      45  
 Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys  
                     50                      55                      60  
 Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn Met Pro  
 65                      70                      75                      80  
 10 Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp  
                     85                      90                      95  
 Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn Tyr Val  
                     100                      105                      110  
 Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val  
 15                      115                      120                      125  
 Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val  
                     130                      135                      140  
 Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys  
 145                      150                      155                      160  
 20 Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu  
                     165                      170                      175  
 Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr Gly Asn  
                     180                      185                      190  
 Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile  
 25                      195                      200                      205  
 Pro Pro Gly Gly Val Glu Glu Lys Ala  
                     210                      215

30                      <210> 894  
                     <211> 156  
                     <212> PRT  
                     <213> Homo sapiens

                    <400> 894  
 35 Leu Gln Gly Gly Asn Gly Pro Ala Val Gly Ile Ser Val Thr Leu Leu  
                     1                      5                      10                      15  
 Gly Leu Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr  
                     20                      25                      30  
 Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr  
 40                      35                      40                      45  
 Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe  
                     50                      55                      60  
 Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr  
 65                      70                      75                      80  
 45 Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu  
                     85                      90                      95  
 Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu  
                     100                      105                      110  
 Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu  
 50                      115                      120                      125  
 Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn  
                     130                      135                      140  
 Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu  
 145                      150                      155

55                      <210> 895  
                     <211> 195  
                     <212> PRT  
                     <213> Homo sapiens

60                      <400> 895  
 Val Leu Gly Leu Glu Thr Gly Ala Ala Phe Val Ser Glu Val Thr Ser  
                     1                      5                      10                      15

Phe Pro Val Val Gln Leu His Met Asn Arg Thr Ala Met Arg Ala Ser  
                   20                  25                  30  
 Gln Lys Asp Phe Glu Asn Ser Met Asn Gln Val Lys Leu Leu Lys Lys  
                   35                  40                  45  
 5 Asp Pro Gly Asn Glu Val Lys Leu Lys Leu Tyr Ala Leu Tyr Lys Gln  
                   50                  55                  60  
 Ala Thr Glu Gly Pro Cys Asn Met Pro Lys Pro Gly Val Phe Asp Leu  
                   65                  70                  75                  80  
 10 Ile Asn Lys Ala Lys Trp Asp Ala Trp Asn Ala Leu Gly Ser Leu Pro  
                   85                  90                  95  
 Lys Glu Ala Ala Arg Gln Asn Tyr Val Asp Leu Val Ser Ser Leu Ser  
                   100                  105                  110  
 Pro Ser Leu Glu Ser Ser Ser Gln Val Glu Pro Gly Thr Asp Arg Lys  
                   115                  120                  125  
 15 Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr  
                   130                  135                  140  
 Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu  
                   145                  150                  155                  160  
 20 Met Tyr His Glu Ile Met Arg Ala Leu Lys Ser Xaa Xaa Gln Xaa Met  
                   165                  170                  175  
 Thr Gln Ser Ser Leu Val Leu Thr Arg Lys Trp Xaa Thr Ile Thr Ser  
                   180                  185                  190  
 Lys Trp Glu  
                   195  
 25  
       <210> 896  
       <211> 176  
       <212> PRT  
       <213> Homo sapiens  
 30  
       <400> 896  
 Asn Asn Xaa Val Leu Leu Arg Xaa Phe Val Xaa Cys Phe Ile Asp Phe  
   1                  5                  10                  15  
 35 Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val Gly Ile Xaa  
                   20                  25                  30  
 Val Thr Leu Leu Gly Leu Phe Asp Xaa Val Tyr Ala Ser Asp Arg Ala  
                   35                  40                  45  
 Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys  
                   50                  55                  60  
 40 Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu  
                   65                  70                  75                  80  
 Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln  
                   85                  90                  95  
 45 Gly Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val  
                   100                  105                  110  
 Trp Thr Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg  
                   115                  120                  125  
 Ile Ser Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala  
                   130                  135                  140  
 50 Val Asn Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp  
                   145                  150                  155                  160  
 Glu Cys Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu  
                   165                  170                  175  
 55  
       <210> 897  
       <211> 217  
       <212> PRT  
       <213> Homo sapiens  
 60  
       <400> 897  
 Met Ala Met Ala Tyr Leu Ala Trp Arg Leu Ala Arg Arg Ser Cys Pro  
   1                  5                  10                  15  
 Ser Ser Leu Gln Val Thr Ser Phe Pro Val Val Gln Leu His Met Asn

20 25 30  
 Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Met Asn  
 35 40 45  
 5 Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys Leu Lys  
 50 55 60  
 Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn Met Pro  
 65 70 75 80  
 Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp Ala Trp  
 85 90 95  
 10 Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn Tyr Val  
 100 105 110  
 Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser Gln Val  
 115 120 125  
 15 Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu Val Val  
 130 135 140  
 Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro Lys Lys  
 145 150 155 160  
 Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg Ala Leu  
 165 170 175  
 20 Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr Gly Asn  
 180 185 190  
 Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr Asp Ile  
 195 200 205  
 Xaa Pro Gly Gly Val Xaa Glu Lys Ala  
 210 215

&lt;210&gt; 898

&lt;211&gt; 158

&lt;212&gt; PRT

30 &lt;213&gt; Homo sapiens

&lt;400&gt; 898

Ala Ser Asp Xaa Ser Gly Asn Gly Pro Ala Val Gly Ile Xaa Val Thr  
 1 5 10 15  
 35 Leu Leu Gly Leu Phe Asp Xaa Val Tyr Ala Ser Asp Arg Ala Thr Phe  
 20 25 30  
 His Thr Pro Phe Ser His Xaa Gly Gln Ser Pro Glu Gly Cys Ser Ser  
 35 40 45  
 Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu  
 50 55 60  
 40 Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu  
 65 70 75 80  
 Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr  
 85 90 95  
 45 Arg Leu Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser  
 100 105 110  
 Lys Glu Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn  
 115 120 125  
 Ala Glu Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys  
 130 135 140  
 50 Thr Asn Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu  
 145 150 155

&lt;210&gt; 899

55 &lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 899

60 Leu Gln Trp Ser Met Val Gln Leu Trp Ala Ser Pro Ser Pro Ser Leu  
 1 5 10 15  
 Gly Leu Phe Asp Ala Val Tyr Ala Ser Asp Arg Ala Thr Phe His Thr  
 20 25 30

Pro Phe Ser His Leu Gly Gln Ser Pro Glu Gly Cys Ser Ser Tyr Thr  
           35                          40                          45  
 Phe Pro Lys Ile Met Ser Pro Ala Lys Ala Thr Glu Met Leu Ile Phe  
       50                          55                          60  
 5 Gly Lys Lys Leu Thr Ala Gly Glu Ala Cys Ala Gln Gly Leu Val Thr  
    65                          70                          75                          80  
 Glu Val Phe Pro Asp Ser Thr Phe Gln Lys Glu Val Trp Thr Arg Leu  
                           85                          90                          95  
 Lys Ala Phe Ala Lys Leu Pro Pro Asn Ala Leu Arg Ile Ser Lys Glu  
 10 Val Ile Arg Lys Arg Glu Arg Glu Lys Leu His Ala Val Asn Ala Glu  
                           100                          105                          110  
                           115                          120                          125  
 Glu Cys Asn Val Leu Gln Gly Arg Trp Leu Ser Asp Glu Cys Thr Asn  
                           130                          135                          140  
 15 Ala Val Val Asn Phe Leu Ser Arg Lys Ser Lys Leu  
    145                          150                          155

<210> 900  
 <211> 108  
 20 <212> PRT  
       <213> Homo sapiens

          <400> 900  
 Leu Leu Lys Asn His Thr Asp Lys Gln Leu Ser Asn Lys Thr Gly Leu  
 25 1                          5                          10                          15  
 Val Gly Phe Leu Ala Cys Leu Thr Asn Met Thr Asp Phe Leu Ser Gln  
                           20                          25                          30  
 Ala Leu Leu Xaa Lys Thr Ser Cys Gly Asn Gln Ala Arg Asp Lys Asn  
                           35                          40                          45  
 30 Ser Ser Leu Met Gln Leu Gly Glu Arg Glu Arg Leu Glu Thr Ser Leu  
    50                          55                          60  
 Ala Ser Asn Ser Thr His Ser His Leu Cys Val Ser Ala Leu Leu Gln  
    65                          70                          75                          80  
 Ala Gln Tyr Ala Xaa Cys Arg Asp Gly Gln Met Phe Arg Val Gly Ser  
 35                          85                          90                          95  
 Gly Thr Phe Gln Pro Ala Lys Ser Ala Glu Val Ile  
                           100                          105

<210> 901  
 40 <211> 77  
       <212> PRT  
       <213> Homo sapiens

          <400> 901  
 Phe Tyr Asn Ala Leu Tyr Leu Ile Lys Glu Phe Ala Phe Phe Val Tyr  
 45 1                          5                          10                          15  
 Thr Gly Met Leu Tyr Ser Leu Cys Ile Leu Gln Gly Tyr Lys Met Ser  
                           20                          25                          30  
 Leu Ile Leu Asn Ile Thr Pro Lys Val Ile Ser Glu Lys Lys Gly Phe  
 50                          35                          40                          45  
 Leu Lys Leu Asn Leu Thr Phe Lys Lys Ser Tyr Gly Gln Thr Thr Phe  
    50                          55                          60  
 Lys Gln Asn Trp Ile Ser Arg Ile Ser Cys Leu Leu Asn  
    65                          70                          75

55 <210> 902  
       <211> 221  
       <212> PRT  
       <213> Homo sapiens

60 <400> 902  
 Gln Asn Asp Asp Ala Glu Val Ser Leu Met Glu Val Arg Phe Tyr Val  
    1                          5                          10                          15

Pro Pro Thr Gln Glu Asp Gly Val Asp Pro Val Glu Ala Phe Ala Gln  
 20 25 30  
 Asn Val Leu Ser Lys Ala Asp Val Ile Gln Ala Thr Gly Asp Ala Ile  
 35 40 45  
 5 Cys Ile Phe Arg Glu Leu Gln Cys Leu Thr Pro Arg Gly Arg Tyr Asp  
 50 55 60  
 Ile Arg Ile Tyr Pro Thr Phe Leu His Leu His Gly Lys Thr Phe Asp  
 65 70 75 80  
 10 Tyr Lys Ile Pro Tyr Thr Thr Val Leu Arg Leu Phe Leu Leu Pro His  
 85 90 95  
 Lys Asp Gln Arg Gln Met Phe Phe Val Ile Ser Leu Asp Pro Pro Ile  
 100 105 110  
 Lys Gln Gly Gln Thr Arg Tyr His Phe Leu Ile Leu Leu Phe Ser Lys  
 115 120 125  
 15 Asp Glu Asp Ile Ser Leu Thr Leu Asn Met Asn Glu Glu Glu Val Glu  
 130 135 140  
 Lys Arg Phe Glu Gly Arg Leu Thr Lys Asn Met Ser Gly Ser Leu Tyr  
 145 150 155 160  
 20 Glu Met Val Ser Arg Val Met Lys Ala Leu Val Asn Arg Lys Ile Thr  
 165 170 175  
 Val Pro Gly Asn Phe Gln Gly His Ser Gly Ala Gln Cys Ile Thr Cys  
 180 185 190  
 Ser Tyr Lys Ala Lys Leu Xaa Thr Ala Leu Pro Ala Gly Ala Gly Leu  
 195 200 205  
 25 His Leu Arg Xaa Gln Ala Thr Cys Ala His Xaa Leu Arg  
 210 215 220

30 <210> 903  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 903  
 Gly Arg Glu Ser Xaa Met Arg Ile Trp Ile Leu His Cys Pro Ala Ser  
 1 5 10 15  
 35 His Pro Xaa Xaa Pro Gln Ile Ile Asn Ser His Pro Trp Glu Ala Ala  
 20 25 30  
 Lys Leu Xaa Arg Leu Pro Thr Ala Leu Gly Thr Tyr Xaa Pro Thr Gly  
 35 40 45  
 40 Xaa His Val Xaa Met Ala Xaa Asn Pro Gly Thr Ala Phe His Glu Xaa  
 50 55 60  
 Lys Leu Val Gln Asn Met Gly Gly Glu Ser Gly Gly Val Lys Arg Gln  
 65 70 75 80  
 45 Ala Gln Xaa Glu Pro Ser Ser Val Ser Thr His Arg Ile Leu Thr Leu  
 85 90 95  
 Lys Pro Xaa Ser Trp Gly Glu Tyr Trp Leu Val Leu Leu Leu Xaa Xaa  
 100 105 110  
 Pro Arg Ser Ser Ser Xaa Xaa Xaa Cys Ser Xaa Ser Leu Pro Glu Lys  
 115 120 125  
 50 Xaa Xaa Ser Leu Xaa Thr Asn Xaa Leu Leu Phe Glu Ala Leu Ala Leu  
 130 135 140  
 Thr Ala Leu Xaa Gly Arg Leu Xaa Ile Xaa Glu Pro Pro Xaa Xaa Gly  
 145 150 155 160  
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60 <210> 904  
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 <212> PRT  
 <213> Homo sapiens

<400> 904  
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				20				25				30	
	Phe	Gln	Glu	Met	Asp	Thr	Val	Met	Lys	Asp	Pro	Tyr	Lys
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	Met	Lys	Gln	Ser	Lys	Leu	Pro	Met	Ser	Leu	Leu	His	Asp
		50				55				60			
	Pro	His	Asn	Leu	Lys	Val	His	Ile	Leu	Asp	Thr	Glu	Ser
	65				70					75			80
10	Thr	Phe	Gly	Pro	Lys	Ser	Gln	Arg	Lys	Arg	Pro	Asn	Leu
				85					90				95
	Asp	Met	Gln	Ser	Leu	Ile	Glu	Asn	Ala	Glu	Met	Ser	Thr
			100					105					110
	Asp	Gln	Gly	Lys	Asp	Arg	Asp	Leu	Val	Thr	Glu	Asp	Thr
15			115				120				125		
	Asn	Glu	Ala	Gln	Glu	Glu	Ile	Tyr	Lys	Lys	Gly	Gln	Ser
	130					135					140		
	Trp	Gly	Glu	Leu	Tyr	Lys	Val	Ile	Asp	Ser	Ser	Asp	Val
	145				150					155			160
20	Val	Leu	Asp	Ala	Arg	Asp	Pro	Met	Gly	Thr	Arg	Ser	Pro
				165						170			175
	Thr	Tyr	Leu	Lys	Lys	Glu	Lys	Pro	Trp	Lys	His	Leu	Ile
			180					185				190	
	Asn	Lys	Cys	Asp	Leu	Val	Pro	Thr	Trp	Ala	Thr	Lys	Arg
25			195				200					205	
	Val	Leu	Phe	Gln	Asp	Tyr	Pro	Thr	Leu	Ala	Xaa	His	Ala
		210				215					220		
	Xaa	Pro	Phe	Gly	Lys	Gly	Ala	Phe	Ile	His	Xaa	Cys	Gly
	225				230					235			240
30	Lys	Leu	Pro	Thr	Xaa	Gln	Glu	Asn	Arg	Ser	Xaa	Val	Gly
				245					250				255
	Phe	Pro	Lys	Val	Gly	Lys	Glu	Xaa	Leu	Gly			
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			<211>	257									
			<212>	PRT									
			<213>	Homo sapiens									
40			<400>	905									
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			20				25				30		
45	Arg	Xaa	Xaa	Lys	Gly	Pro	Val	Pro	Cys	Val	Cys	Leu	Pro
		35				40					45		
	Ser	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Arg	Thr	Leu	Val	Lys	Ser
	50				55					60			
	Xaa	Leu	Ser	Phe	Leu	Gly	Met	Xaa	Trp	Phe	Xaa	Trp	Arg
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	Phe	Glu	Glu	Glu	Leu	Glu	Ser	Phe	Phe	Asp	Glu	Glu	Glu
			85					90				95	
	Glu	Xaa	Gln	Arg	Asp	Xaa	Ala	Glu	Glu	Xaa	Ser	Ser	Glu
			100				105					110	
55	Glu	Asn	Val	Gly	Asn	Asp	Xaa	Lys	Ala	Val	Ile	Lys	Xaa
		115					120				125		
	Lys	Ile	Ala	Lys	Tyr	Gln	Lys	Phe	Leu	Asp	Lys	Ala	Lys
	130				135					140			
	Phe	Ser	Ala	Val	Arg	Ile	Ser	Lys	Gly	Leu	Ser	Glu	Lys
60	145				150					155			160
	Lys	Pro	Glu	Glu	Gln	Xaa	Xaa	Xaa	Leu	Glu	Glu	Asp	Val
				165					170			175	
	Ala	Pro	Ser	Lys	Lys	Gly	Lys	Lys	Arg	Lys	Xaa	Gln	Arg

180 185 190  
 Gln Glu His Ser Asn Lys Ala Pro Arg Xaa Leu Thr Ser Lys Glu Arg  
 195 200 205  
 Arg Arg Ala Val Arg Gln Gln Arg Pro Lys Lys Val Gly Val Arg Xaa  
 210 215 220  
 Tyr Glu Xaa Pro Asn Val Lys Asn Arg Asn Arg Asn Lys Lys Lys Thr  
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 245 250 255  
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 15 <212> PRT  
 <213> Homo sapiens

<400> 906  
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 35 40 45  
 25 Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val Leu Asn Thr Gln  
 50 55 60  
 Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg Lys Glu Leu His  
 65 70 75 80  
 Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln His Asn Gln Leu  
 85 90 95  
 30 Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu Glu Ser Gln Arg  
 100 105 110  
 Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val Leu Thr Ser Glu  
 115 120 125  
 35 Gln Leu Arg Gln Val Glu Glu Leu Lys Lys Lys Asp Gln Glu Asp Asp  
 130 135 140  
 Glu Gln Gln Arg Leu Asn Lys Arg Lys Asp His Lys Lys Ala Asp Val  
 145 150 155 160  
 Glu Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu Thr Gln Glu Glu  
 165 170 175  
 40 Ser Ser Ala Gln Leu Ser Asn Glu Glu Glu His Leu Asp Ser Thr Arg  
 180 185 190  
 Gly Ser Val His Ser Leu Xaa Ala Gly Leu Leu Leu Pro Ser Gly Asp  
 195 200 205  
 45 Pro Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp Gly Leu Arg Arg  
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 Ala Gln Ser Ser Arg Gln Leu Trp Asp Pro Arg Ala His Cys Asn Xaa  
 225 230 235 240  
 Lys Leu

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 <212> PRT  
 55 <213> Homo sapiens

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 20 25 30  
 Pro Xaa Leu Gly Lys Gly Xaa Gly Val Ser Xaa Gly Ala Lys Ser Xaa  
 35 40 45



Pro Xaa Gly Asn Phe Leu Phe Trp Xaa Lys Lys Pro Xaa Xaa Ser Xaa  
 50 55 60  
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 5 Ser Leu Ser Arg  
  
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 Tyr Ile Lys Xaa Pro Phe Met Leu Lys Thr Gln Leu Lys Glu Leu Val  
 20 20 25 30  
 Ser Thr Trp Thr Gly Thr Xaa Xaa Phe Val Tyr Thr Gln Asn Thr Leu  
 35 40 45  
 20 Xaa Xaa Gln Asn Leu Xaa Ser Ser Xaa Xaa Val Phe Xaa Thr Lys Lys  
 50 55 60  
 Gly Asn Ser His Xaa Xaa Gly Ile Leu Pro Gln Xaa Lys Pro Leu Xaa  
 65 70 75 80  
 Leu Ser Leu Asn Xaa Gly Xaa Ile Phe Leu Xaa Xaa Pro Leu Phe Phe  
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 20 25 30  
 Arg Asp Thr Xaa Xaa Cys Leu Tyr Pro Lys His Ile Xaa Xaa Thr Lys  
 40 35 40 45  
 Leu Xaa Lys Leu Xaa Xaa Gly Phe Xaa Tyr Gln Lys Arg Lys Phe Pro  
 50 55 60  
 Xaa Gly Xaa Asp Phe Ala Pro Xaa Glu Thr Pro Xaa Pro Phe Pro Lys  
 65 70 75 80  
 45 Xaa Gly Xaa Asn Phe Phe Xaa Xaa Pro Pro Phe Phe Xaa Xaa Lys Lys  
 85 90 95  
 Asn Phe Leu Glu Gly Gly Pro Xaa Leu Xaa Lys Lys Thr Phe Ile Trp  
 100 105 110  
 Glu Gly  
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 <210> 910  
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 <212> PRT  
 55 <213> Homo sapiens  
  
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 60 Lys Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg  
 20 25 30  
 Gln Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu  
 35 40 45

Glu Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Glu Lys Leu  
 50 55 60  
 Leu Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu  
 65 70 75 80  
 5 Gln Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala  
 85 90 95  
 Ala Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp  
 100 105 110  
 10 Glu Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Glu Gln Lys Arg Gln  
 115 120 125  
 Glu Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala  
 130 135 140  
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 145 150 155 160  
 15 Trp Ile Ser Glu

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 20 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Ser Phe Asn Phe Leu Ser Cys Ser Ser Cys Arg Phe Leu Ala Ala Ser  
 35 40 45  
 30 Ser Phe Ser Phe Phe Ile Leu Asn Ser Ser Cys Ala Phe Cys Ser Leu  
 50 55 60  
 Ser Asn His Ser Ser Cys Asn Leu Cys Leu Ser Leu Ser Asn Ser Phe  
 65 70 75 80  
 Ser Ser Ser Ser Cys Cys Ser Ser Ile Lys Val Ser Ser Ser Ser Ser  
 85 90 95  
 35 Phe Cys Glu Ser Pro Glu Ser Leu Ser Arg Ala Ser Ser Cys Arg Arg  
 100 105 110  
 Phe Phe Arg Phe Ser Phe Phe Arg Ala Ala Leu Tyr Phe Leu Trp Leu  
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 40 Gly Phe Ser Gly Asn Val Ile Phe Ser Gly Ala Ala Ile  
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<210> 912  
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 45 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Ile Ile Phe Gly Xaa Val Ile Xaa Thr Phe Xaa Cys Phe Xaa Ile Gly  
 35 40 45  
 55 Leu Xaa Xaa Pro Leu Gly Xaa Thr Pro Lys Xaa Gly Lys Gly Trp Ala  
 50 55 60  
 Pro Pro Xaa Ile Phe Xaa Xaa Gly Xaa Gly Glu Xaa Lys Xaa Leu Val  
 65 70 75 80  
 Gln Xaa Xaa Pro Xaa Lys Lys Met Gly Asn Pro Lys Gly Lys Xaa Xaa  
 85 90 95  
 60 Val Pro Gly Gly Xaa Xaa Phe Xaa Asn Ala Xaa Gln Lys Xaa Gly Xaa  
 100 105 110  
 Gly Pro Ile Xaa Glu Ala Lys Glu Lys Ile Gly Pro Pro Xaa Gly Pro

115 120 125  
 Pro Pro Gly Ala Gly Ala Pro Gly Xaa Gly Xaa Gly Xaa Gly Xaa Pro  
 130 135 140  
 Gly Xaa Pro Pro Xaa Gly Ala Lys Val Pro Xaa Gly Pro Xaa Xaa Xaa  
 5 145 150 155 160  
 Ala Xaa Gly Gly Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Asn  
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 Pro Xaa Lys Leu Val Xaa Phe Phe  
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 Xaa Pro Cys Xaa Phe Phe His Gly Phe Arg Asn Pro Xaa Asn Tyr Phe  
 20 20 25 30  
 Trp Xaa Gly Asn Xaa Xaa Ile Xaa Leu Phe Pro Xaa Arg Thr Gly Xaa  
 35 40 45  
 Xaa Phe Gly Xaa Asn Ser Gln Xaa Arg Glu Arg Met Gly Pro Pro Xaa  
 50 55 60  
 25 Asp Phe Xaa Xaa Arg Leu Xaa Gly Xaa Lys Xaa Pro Ser Pro Xaa Xaa  
 65 70 75 80  
 Ser Xaa Lys Lys Asn Gly Glu Ser Gln Arg Lys Ser Xaa Xaa Pro Arg  
 85 90 95  
 Gly Xaa Xaa Phe Pro Xaa Arg Xaa Ser Lys Ser Xaa Xaa Xaa Pro Asn  
 100 105 110  
 30 Xaa Arg Ser Lys Gly Lys Asn Arg Ala Pro Xaa Arg Ala Pro Thr Arg  
 115 120 125  
 Gly Arg Gly Thr Arg Xaa Arg Xaa Arg Xaa Arg Xaa Pro Arg Xaa Pro  
 130 135 140  
 35 Pro Xaa Arg Ser Gln Ser Ser Phe Xaa Ser Xaa Xaa Xaa Gly Xaa Arg  
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 Thr Ser Phe Xaa Phe  
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 45 <213> Homo sapiens  
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 20 25 30  
 Trp Leu Arg Xaa Gly Gly Xaa Leu Gly Xaa Arg Xaa Arg Xaa Arg Xaa  
 35 40 45  
 Arg Val Pro Arg Pro Arg Val Gly Ala Leu Xaa Gly Ala Leu Phe Phe  
 50 55 60  
 55 Pro Leu Leu Arg Xaa Leu Gly Xaa Ser Xaa Leu Phe Xaa Gly Arg Xaa  
 65 70 75 80  
 Gly Xaa Xaa Phe Pro Leu Gly Xaa Xaa Leu Phe Leu Trp Asp Ser Pro  
 85 90 95  
 60 Phe Phe Xaa Xaa Xaa Gly Xaa Gly Leu Gly Xaa Xaa Leu Pro Xaa Asn  
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 Leu Xaa

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 10 Glu Lys Glu His Asp Lys Leu His Glu Glu Ile Gln Asn Leu Ile Lys  
 20 25 30  
 Ile Gln Ala Ile Ala Val Cys Met Glu Asn Gly Asn Phe Lys Glu Ala  
 35 40 45  
 15 Glu Glu Val Phe Glu Arg Ile Phe Gly Asp Pro Asn Ser His Met Pro  
 50 55 60  
 Phe Lys Ser Lys Leu Leu Met Ile Ile Ser Gln Lys Asp Thr Phe His  
 65 70 75 80  
 Ser Phe Phe Gln His Phe Ser Tyr Asn His Met Met Glu Lys Ile Lys  
 85 90 95  
 20 Ser Tyr Val Asn Tyr Val Leu Ser Glu Lys Ser Ser Thr Phe Leu Met  
 100 105 110  
 Lys Ala Ala Ala Lys Val Val Glu Ser Lys Arg Thr Arg Thr Ile Thr  
 115 120 125  
 25 Ser Gln Asp Lys Pro Ser Gly Asn Asp Val Glu Met Glu Thr Glu Ala  
 130 135 140  
 Asn Leu Asp Thr Arg Lys Ser Val Ser Asp Lys Gln Ser Ala Val Thr  
 145 150 155 160  
 Glu Ser Ser Glu Gly Thr Val Ser Leu Leu Arg Ser His Lys Asn Leu  
 165 170 175  
 30 Phe Leu Ser Lys Leu Gln His Gly Thr Gln Gln Gln Asp Leu Asn Lys  
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 <213> Homo sapiens

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 45 Glu Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu  
 35 40 45  
 Ser Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys  
 50 55 60  
 Glu Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu  
 65 70 75 80  
 50 Ala Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr  
 85 90 95  
 Gln Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His  
 100 105 110  
 55 Arg Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln  
 115 120 125  
 Glu Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu  
 130 135 140  
 60 Glu Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg  
 145 150 155 160  
 Leu Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg  
 165 170 175  
 Gln Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala

180 185 190  
 Gln Ala Leu Gln Pro Ser Lys Glu Ser Arg Ser Leu Pro Gln Lys Ile  
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 15 Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly Lys Xaa  
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 Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His Gly Arg  
 35 40 45  
 Val His Glu Xaa Met Lys Gln Arg Leu Arg Gln Leu Asp Lys His Ser  
 20 50 55 60  
 Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln Asn Gln  
 65 70 75 80  
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 25 Thr Gln Leu Pro Ser Met Pro Gln Xaa Asp Cys  
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 30 <212> PRT  
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 20 25 30  
 Ile Pro Phe Phe Leu Thr Glu Leu Ser Tyr Phe Arg Ser Gly Phe Leu  
 35 40 45  
 Arg Xaa Leu Val Gln Phe Leu Gly Leu Met Xaa Asn Ile Leu Pro Leu  
 40 50 55 60  
 Thr Phe Val Lys Asn Val Phe Leu Gly Xaa Gln Gln Gln Asn Thr Gly  
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 45 85 90 95  
 Xaa Thr  
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 20 25 30  
 Cys Leu Ser Arg Arg Ser Trp Phe Cys Leu Leu Arg Ser Cys Thr Ser  
 35 40 45  
 Cys Trp Ala Val Ala Trp Leu Cys Leu Ser Ser Cys Leu Ser Leu Cys  
 50 55 60  
 Phe Ile Xaa Ser Cys Thr Leu Pro Cys Trp Thr His Cys Ser Ser Asn  
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5	Phe Ser			
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	20 25 30			
	Ala Asp Thr Gln Gln Arg Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln			
	35 40 45			
20	Val Leu Gln Ile Ser Glu Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu			
	50 55 60			
	Ile Gln Cys Asp Gln Leu Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg			
	65 70 75 80			
	Leu Glu Lys Glu Leu Ala Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys			
	85 90 95			
25	Asp Met Met Lys Lys Glu Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser			
	100 105 110			
	Lys Met Leu Ile Leu Ser Gln Asn Ile Ala Gln Leu Glu Ala Gln Val			
	115 120 125			
30	Glu Lys Val Thr Lys Glu Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu			
	130 135 140			
	Ile Gln Ser Gln Leu Ala Ser Arg Glu Met Asp Val Thr Lys Val Cys			
	145 150 155 160			
	Gly Glu Met Arg Tyr Gln Leu Asn Lys Thr Asn Met Glu Lys Asp Glu			
	165 170 175			
35	Ala Glu Lys Glu His Arg Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu			
	180 185 190			
	Glu Ile Lys Asp Gln Glu Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu			
	195 200 205			
40	Ser Lys His Thr Trp Asn Arg Ser Ser Xaa Arg His Pro Gly Gln Lys			
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	Xaa Val Pro Glu Thr Asn Xaa Thr Ala Gly Arg Ile			
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	20 25 30			
55	Ala Ala Pro Val Pro Ser Val Phe Ala Phe Ile Gln Phe Tyr Ser Gln			
	35 40 45			
	Phe Leu Tyr Phe Leu Ile Phe Asn Phe Lys Ile Pro Val Ser Phe Cys			
	50 55 60			
	Ser Glu Leu Ser Val Leu Leu Phe Cys Leu Ile Leu Leu His Val Gly			
	65 70 75 80			
60	Phe Ile Gln Leu Ile Ala His Phe Ser Thr His Leu Cys Asp Ile His			
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	Phe Pro Arg Ser Gln Leu Ala Leu Asn Phe Leu Gln Leu Ile Asn Ser			
	100 105 110			

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 20 25 30  
 Arg Pro Arg Lys Xaa Ser Arg Ser Cys Xaa Arg Asn Xaa Ala Asn Gly  
 35 40 45  
 Ser Pro Ala Cys Gln Asn Xaa Lys Met Thr Ser Phe Xaa Cys Cys Xaa  
 50 55 60  
 15 Pro Arg Ile His Phe Cys Lys Val Lys Glu Arg Met Leu Tyr Ile Ser  
 65 70 75 80  
 Gln Glu Thr Gly Pro Xaa Ser Gln Lys Thr Arg Phe Glu Ile Ala Gln  
 85 90 95  
 20 Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly Lys Xaa Gln  
 100 105 110  
 Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His Gly Arg Val  
 115 120 125  
 His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys His Ser Gln  
 130 135 140  
 25 Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln Asn Gln Leu  
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 20 25 30  
 Ile Pro Phe Phe Leu Thr Glu Leu Ser Tyr Phe Lys Ser Gly Phe Leu  
 35 40 45  
 45 Arg Xaa Trp Ser Ser Phe Leu Ala Asn Val Gln His Ser Phe Phe Asn  
 50 55 60  
 Phe Ala Lys Met Tyr Ser Gly Xaa Ala Thr Xaa Lys Thr Gly His Phe  
 65 70 75 80  
 Xaa Val Leu Ala Cys Trp Ala Ser Ile Cys Xaa Ile Ser Xaa Ala Thr  
 85 90 95  
 50 Pro Ala Xaa Phe Ser Trp Pro Xaa Arg Leu Gly Pro Phe Phe Leu Xaa  
 100 105 110  
 Lys Xaa Leu Xaa Lys Ala Asn Phe Phe Leu Leu Gly Xaa Xaa Xaa Leu  
 115 120 125  
 55 Xaa Leu Lys Ile Pro Xaa Gln  
 130 135

<210> 924  
 <211> 159  
 60 <212> PRT  
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 Pro Glu Leu Glu Pro Gly Pro Gly Pro Gly Ser Ala Leu Glu Xaa Gly  
 20 25 30  
 5 Glu Glu Phe Glu Ile Val Asp Arg Ser Gln Leu Pro Gly Pro Gly Asp  
 35 40 45  
 Leu Arg Ser Ala Thr Arg Pro Arg Ala Ala Glu Gly Trp Ser Ala Pro  
 50 55 60  
 10 Ile Leu Thr Leu Ala Arg Arg Ala Thr Gly Asn Leu Ser Ala Ser Cys  
 65 70 75 80  
 Gly Ser Ala Leu Arg Ala Ala Ala Gly Leu Gly Gly Gly Asp Ser Gly  
 85 90 95  
 Asp Gly Thr Ala Arg Ala Ala Ser Lys Cys Gln Met Met Glu Glu Arg  
 100 105 110  
 15 Ala Asn Leu Met His Met Met Lys Leu Ser Ile Lys Val Leu Leu Gln  
 115 120 125  
 Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala Asp His Ala Pro Leu  
 130 135 140  
 Gln Gln Phe Phe Cys Ser Asp Gly Ala Leu Pro Gln Thr Trp Ala  
 145 150 155

&lt;210&gt; 925

&lt;211&gt; 154

&lt;212&gt; PRT

25 &lt;213&gt; Homo sapiens

&lt;400&gt; 925

Gly Ser Ala Pro Ser Leu Gln Lys Asn Cys Cys Lys Gly Ala Trp Ser  
 1 5 10 15  
 30 Ala Ser Arg Leu Arg Pro Arg Leu Arg Ala Asp Trp Ser Asn Thr Leu  
 20 25 30  
 Met Leu Ser Phe Ile Met Cys Ile Arg Leu Ala Arg Ser Ser Ile Ile  
 35 40 45  
 Trp His Leu Glu Ala Ala Arg Ala Val Pro Ser Pro Leu Ser Pro Pro  
 50 55 60  
 35 Pro Ser Pro Ala Ala Ala Arg Ser Ala Leu Pro Gln Leu Ala Asp Arg  
 65 70 75 80  
 Phe Pro Val Ala Leu Arg Ala Arg Val Arg Met Gly Ala Asp Gln Pro  
 85 90 95  
 40 Ser Ala Ala Arg Gly Leu Val Ala Leu Arg Arg Ser Pro Gly Pro Gly  
 100 105 110  
 Ser Trp Leu Arg Ser Thr Ile Ser Asn Ser Ser Xaa Gly Ser Ser Ala  
 115 120 125  
 Asp Pro Gly Pro Gly Pro Gly Ser Ser Ser Gly Ser Ser Ser Arg Pro  
 130 135 140  
 45 Arg Pro Ala Ala Gln Pro Pro Ser Arg Ser  
 145 150

&lt;210&gt; 926

50 &lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 926

Leu Ser Ser Pro Cys Leu Arg Gln Cys Ser Ile Thr Thr Lys Glu Leu  
 1 5 10 15  
 Leu Gln Gly Gly Met Val Arg Ile Gln Ala Ala Ala Gln Ala Gln Ser  
 20 25 30  
 Arg Leu Glu Gln His Leu Asp Ala Glu Phe His His Val His Gln Val  
 35 40 45  
 60 Gly Thr Leu Leu His His Leu Ala Leu Arg Ser Cys Ala Arg Arg Ala  
 50 55 60  
 Val Pro Ala Val Pro Ala Ala Gln Pro Arg Gly Arg Ala Gln Arg Ala



	65	70	75	80
	Pro Ala Ala Arg Arg Gln Val Pro Gly Gly Pro Ala Cys Gln Gly Gln			
		85	90	95
5	Asp Gly Arg Arg Pro Ala Leu Gly Arg Pro Arg Pro Arg Cys Ala Pro			
		100	105	110
	Gln Val Ala Trp Ala Gly Gln Leu Ala Ser Val His Asp Leu Lys Leu			
		115	120	125
	Phe Ser Xaa Leu Lys Arg			
	130			
10	<210> 927			
	<211> 424			
	<212> PRT			
	<213> Homo sapiens			
15	<400> 927			
	Ile Arg Tyr Leu Glu Val Leu Cys Thr Lys Lys Val Ser Glu Lys Met			
	1 5 10 15			
20	Glu Phe Phe Asn Ile Ser Val Asp Asn Thr Cys Ser Leu Phe Arg Gly			
		20 25 30		
	Leu Gln Lys Glu Glu Val Val Leu Thr His Gly Asp Ser Val Asp			
		35 40 45		
	Lys Val Ala Asp Gly Phe Lys Val Val Ala Arg Ser Gly Asn Ile Val			
		50 55 60		
25	Ala Gly Ile Ala Asn Glu Ser Lys Lys Leu Tyr Gly Ala Gln Phe His			
		65 70 75 80		
	Pro Glu Val Gly Leu Thr Glu Asn Gly Lys Val Ile Leu Lys Asn Phe			
		85 90 95		
30	Leu Tyr Asp Ile Thr Gly Cys Ser Gly Thr Phe Thr Val Gln Asn Arg			
		100 105 110		
	Glu Leu Glu Cys Ile Arg Glu Ile Lys Glu Arg Val Gly Thr Ser Lys			
		115 120 125		
	Val Leu Val Leu Leu Ser Gly Gly Val Asp Ser Thr Val Cys Thr Ala			
		130 135 140		
35	Leu Leu Asn Arg Ala Leu Asn Gln Glu Gln Val Ile Ala Val His Ile			
		145 150 155 160		
	Asp Asn Gly Phe Met Arg Lys Arg Glu Ser Gln Ser Val Glu Glu Ala			
		165 170 175		
40	Leu Lys Lys Leu Gly Ile Gln Val Lys Val Ile Asn Ala Ala His Ser			
		180 185 190		
	Phe Tyr Asn Gly Thr Thr Thr Leu Pro Ile Ser Asp Glu Asp Arg Thr			
		195 200 205		
	Pro Arg Lys Arg Ile Ser Lys Thr Leu Asn Met Thr Thr Ser Pro Glu			
		210 215 220		
45	Glu Lys Arg Lys Ile Ile Gly Asp Thr Phe Val Lys Ile Ala Asn Glu			
		225 230 235 240		
	Val Ile Gly Glu Met Asn Leu Lys Pro Glu Glu Val Phe Leu Ala Gln			
		245 250 255		
50	Gly Thr Leu Arg Pro Asp Leu Ile Glu Ser Ala Ser Leu Val Ala Ser			
		260 265 270		
	Gly Lys Ala Glu Leu Ile Lys Thr His His Asn Asp Thr Glu Leu Ile			
		275 280 285		
	Lys Lys Leu Arg Glu Glu Gly Lys Val Ile Glu Pro Leu Lys Asp Phe			
		290 295 300		
55	His Lys Asp Glu Val Arg Ile Leu Gly Arg Glu Leu Gly Leu Pro Glu			
		305 310 315 320		
	Glu Leu Val Ser Arg His Pro Phe Pro Gly Pro Gly Leu Ala Ile Arg			
		325 330 335		
60	Val Ile Cys Ala Glu Glu Pro Tyr Ile Cys Lys Asp Phe Pro Glu Thr			
		340 345 350		
	Asn Asn Ile Leu Lys Ile Val Ala Asp Phe Ser Ala Ser Val Lys Lys			
		355 360 365		
	Pro His Thr Leu Leu Gln Arg Val Lys Ala Cys Thr Thr Glu Glu Asp			

370 375 380  
 Gln Glu Lys Leu Met Gln Ile Thr Ser Leu His Ser Leu Asn Ala Phe  
 385 390 395 400  
 Leu Leu Pro Ile Lys Thr Val Xaa Val Gln Gly Asp Cys Arg Ser Tyr  
 405 410 415  
 5 Ser Tyr Arg Val Trp Asn Xaa Gln  
 420  
 <210> 928  
 10 <211> 191  
 <212> PRT  
 <213> Homo sapiens  
 <400> 928  
 15 Pro Arg Ser Ala Ala Val Ala Pro Phe Gly Ala Phe Leu Ala Ala Gly  
 1 5 10 15  
 Ser Ser Pro Leu Pro Ala Ala Pro Arg Pro Gly Leu Leu Leu Asn Leu  
 20 20 25 30  
 Ser Pro Arg Arg Arg Pro Phe Arg His Pro Pro Ala Pro Ser Arg Thr  
 35 40 45  
 20 Val Ala Val Thr Ala Ala Ala Pro Ala Leu Ala Pro Met Ala Leu Cys  
 50 55 60  
 Asn Gly Asp Ser Lys Leu Glu Asn Ala Gly Gly Asp Leu Lys Asp Gly  
 65 70 75 80  
 25 His His His Tyr Glu Gly Ala Val Val Ile Leu Asp Ala Gly Ala Gln  
 85 90 95  
 Tyr Gly Lys Val Ile Asp Arg Arg Val Arg Glu Leu Phe Val Gln Ser  
 100 105 110  
 Glu Ile Phe Pro Leu Glu Thr Pro Ala Phe Ala Ile Lys Glu Gln Gly  
 115 120 125  
 30 Phe Arg Ala Ile Ile Ile Ser Gly Gly Pro Asn Ser Val Tyr Ala Glu  
 130 135 140  
 Asp Ala Pro Trp Phe Asp Pro Thr Ile Phe Thr Ile Gly Lys Pro Val  
 145 150 155 160  
 35 Leu Gly Ile Cys Tyr Gly Met Gln Met Met Asn Lys Val Phe Gly Gly  
 165 170 175  
 Thr Val His Lys Lys Ser Val Arg Lys Asp Gly Val Phe Gln His  
 180 185 190  
 <210> 929  
 40 <211> 203  
 <212> PRT  
 <213> Homo sapiens  
 <400> 929  
 45 Arg Pro Leu Asn Asn Glu His Val Leu Ser Thr Leu Met Leu Lys Asn  
 1 5 10 15  
 Ser Ile Phe Ser Asp Thr Phe Phe Val His Ser Thr Ser Lys Tyr Leu  
 20 25 30  
 50 Ile His His Leu His Thr Ile Ala Asn Ser Lys Asn Arg Leu Ala Asn  
 35 40 45  
 Ser Glu Tyr Cys Trp Ile Lys Pro Gly Ser Ile Phe Ser Ile His Arg  
 50 55 60  
 Ile Arg Ser Ser Arg Asp Asp Asn Ser Thr Glu Ser Leu Phe Leu Tyr  
 65 70 75 80  
 55 Ser Lys Cys Trp Cys Phe Gln Gly Glu Asn Phe Arg Leu His Glu Gln  
 85 90 95  
 Phe Pro His Ser Ser Val Tyr Asp Phe Pro Val Leu Ser Thr Ser Ile  
 100 105 110  
 60 Gln Asn Asp Asn Ser Ser Phe Ile Val Val Val Ala Ile Leu Lys Val  
 115 120 125  
 Ser Ser Ser Ile Leu Gln Leu Gly Val Ser Val Ala Gln Ser His Arg  
 130 135 140

Gly Gln Gly Arg Ser Arg Gly Gly Asp Gly Asp Ser Thr Arg Arg Gly  
 145 150 155 160  
 Gly Arg Val Pro Glu Gly Ser Ala Pro Arg Ala Glu Val Glu Lys Glu  
 165 170 175  
 5 Ala Trp Ser Arg Ser Ser Arg Gln Arg Arg Gly Ala Ser Arg Gln Lys  
 180 185 190  
 Ser Ala Glu Trp Ser Asn Ser Ser Gly Ala Arg  
 195 200

10 <210> 930  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens

15 <400> 930  
 Pro Arg Ser Ala Ala Val Ala Pro Phe Gly Ala Phe Leu Ala Ala Gly  
 1 5 10 15  
 Ser Ser Pro Leu Pro Ala Ala Pro Arg Pro Gly Leu Leu Leu Asn Leu  
 20 25 30  
 Ser Pro Arg Arg Arg Pro Phe Arg His Pro Pro Ala Pro Ser Arg Thr  
 35 40 45  
 Val Ala Val Thr Ala Ala Ala Pro Ala Leu Ala Pro Met Ala Leu Cys  
 50 55 60  
 Asn Gly Asp Ser Lys Leu Glu Asn Ala Gly Gly Asp Leu Lys Asp Gly  
 65 70 75 80  
 25 His His His Tyr Glu Gly Ala Val Val Ile Leu Asp Ala Gly Ala Gln  
 85 90 95  
 Tyr Gly Lys Val Ile Asp Arg Arg Val Arg Glu Leu Phe Val Gln Ser  
 100 105 110  
 30 Glu Ile Phe Pro Leu Glu Thr Pro Ala Phe Ala Ile Lys Glu Gln Gly  
 115 120 125  
 Phe Arg Ala Ile Ile Ile Ser Gly Gly Pro Asn Ser Val Tyr Ala Glu  
 130 135 140  
 Asp Ala Pro Trp Phe Asp Pro Thr Ile Phe Thr Ile Gly Lys Pro Val  
 145 150 155 160  
 35 Leu Gly Ile Cys Tyr Gly Met Xaa Met Met Asn Xaa Val Phe Gly Gly  
 165 170 175  
 Thr Val His Lys Lys Lys Cys Gln Lys Arg Trp Ser Phe Ser Thr Leu  
 180 185 190  
 40 Val Xaa Ile Ile His Val His Tyr Ser Xaa Ala Phe Xaa Lys Glu Lys  
 195 200 205  
 Leu Val Leu Ala Tyr Thr Trp Glu Asn Ser Val Lys Gln Ser Asn Leu  
 210 215 220  
 Met Glu Xaa Lys Val Gly Ala Pro Phe Trp Xaa Lys  
 225 230 235

45 <210> 931  
 <211> 189  
 <212> PRT  
 50 <213> Homo sapiens

<400> 931  
 Lys Thr Pro Ser Phe Leu Thr Leu Phe Phe Val His Ser Thr Ser Lys  
 1 5 10 15  
 55 Tyr Xaa Ile His His Xaa His Thr Ile Ala Asn Ser Lys Asn Arg Leu  
 20 25 30  
 Ala Asn Ser Glu Tyr Cys Trp Ile Lys Pro Gly Ser Ile Phe Ser Ile  
 35 40 45  
 His Arg Ile Arg Ser Ser Arg Asp Asp Asn Ser Thr Glu Ser Leu Phe  
 50 55 60  
 60 Leu Tyr Ser Lys Cys Trp Cys Phe Gln Gly Glu Asn Phe Arg Leu His  
 65 70 75 80  
 Glu Gln Phe Pro His Ser Ser Val Tyr Asp Phe Pro Val Leu Ser Thr

85 90 95  
 Ser Ile Gln Asn Asp Asn Ser Ser Phe Ile Val Val Val Ala Ile Leu  
 100 105 110  
 5 Lys Val Ser Ser Ile Leu Gln Leu Gly Val Ser Val Ala Gln Ser  
 115 120 125  
 His Arg Gly Gln Gly Arg Ser Arg Gly Gly Asp Gly Asp Ser Thr Arg  
 130 135 140  
 Arg Gly Gly Arg Val Pro Glu Gly Ser Ala Pro Arg Ala Glu Val Glu  
 145 150 155 160  
 10 Lys Glu Ala Trp Ser Arg Ser Ser Arg Gln Arg Arg Gly Ala Ser Arg  
 165 170 175  
 Gln Lys Ser Ala Glu Trp Ser Asn Ser Ser Gly Ala Arg  
 180 185  
 15 <210> 932  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens  
 20 <400> 932  
 Val Cys Arg Gly Leu Trp Phe Pro Gln Leu Gly Gly Xaa Xaa Ser Ser  
 1 5 10 15  
 Lys Asn Asp Pro Xaa Trp Glu Xaa Leu Xaa Phe Xaa Xaa Arg Leu Xaa  
 20 25 30  
 25 Pro Gly Met Cys His Asn Val Asn Xaa Val Val Tyr Ile Phe Gly Xaa  
 35 40 45  
 Pro Val Lys Xaa Pro Xaa Thr Xaa Val Thr Pro Pro Phe Leu Thr Thr  
 50 55 60  
 Gly Xaa Val Ser Thr Leu Arg Gln Xaa Asp Phe Xaa Ala His Asn Ile  
 65 70 75 80  
 30 Phe Arg Glu Phe Gly Tyr Xaa Gly Lys Ile Xaa Gln Xaa Pro Xaa Ile  
 85 90 95  
 Leu Xaa Pro Leu His Phe Asp Xaa Xaa Leu Gln Xaa Gln Pro Xaa  
 100 105 110  
 35 Cys Xaa Arg Phe Xaa Val Ile Arg Xaa Phe Ile Xaa Xaa Asp Phe Met  
 115 120 125  
 Thr Xaa Xaa Pro Ala Xaa Pro Gly Asn Glu Ile Pro Val Lys Xaa Val  
 130 135 140  
 Leu Xaa Met Val Xaa Xaa Ile Xaa Xaa Ile Pro Xaa Ile Xaa Arg Ile  
 145 150 155 160  
 40 Met Tyr Asp Leu Thr Ser Lys Pro Pro Gly Thr Xaa Glu Xaa Xaa  
 165 170 175  
 45 <210> 933  
 <211> 202  
 <212> PRT  
 <213> Homo sapiens  
 50 <400> 933  
 Gly Asn Ile Val Ala Gly Ile Ala Asn Glu Ser Lys Lys Leu Tyr Gly  
 1 5 10 15  
 Ala Gln Phe His Pro Glu Val Gly Leu Thr Glu Asn Gly Lys Val Ile  
 20 25 30  
 Leu Lys Asn Phe Leu Tyr Asp Ile Ala Gly Cys Ser Gly Thr Phe Thr  
 35 40 45  
 55 Val Gln Asn Arg Glu Leu Glu Cys Ile Arg Glu Ile Lys Glu Arg Val  
 50 55 60  
 Gly Thr Ser Lys Val Leu Val Leu Leu Ser Gly Gly Val Asp Ser Thr  
 65 70 75 80  
 60 Val Cys Thr Ala Leu Leu Asn Arg Ala Leu Asn Gln Glu Gln Val Ile  
 85 90 95  
 Ala Val His Ile Asp Asn Gly Phe Met Arg Lys Arg Glu Ser Gln Ser  
 100 105 110

Val Glu Glu Ala Leu Lys Lys Leu Gly Ile Gln Val Lys Val Ile Asn  
           115                          120                          125  
 Ala Ala His Ser Phe Tyr Asn Gly Thr Thr Thr Leu Pro Ile Ser Asp  
           130                          135                          140  
 5 Glu Asp Arg Thr Pro Arg Lys Arg Ile Ser Lys Thr Leu Asn Met Thr  
    145                          150                          155                          160  
 Thr Ser Pro Glu Glu Lys Arg Lys Ile Ile Gly Asp Thr Phe Val Lys  
                           165                          170                          175  
 10 Ile Ala Asn Glu Val Ile Gly Glu Met Asn Leu Lys Pro Xaa Glu Val  
                           180                          185                          190  
 Phe Leu Ala Gln Gly Leu Tyr Xaa Leu Ile  
           195                          200  
  
       <210> 934  
 15       <211> 152  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 934  
 20 Pro Ala Xaa Tyr Phe Xaa Lys Lys Met Val Gly Phe Lys Lys Xaa Pro  
    1                          5                          10                          15  
 Xaa Pro Lys Lys Lys Val Phe Ser Ser Thr Tyr Tyr Phe Xaa Ile Ala  
           20                          25                          30  
 25 Gln Ala Gln Xaa Pro Gly Lys Trp Lys Ala Trp Lys Thr Asn Xaa Xaa  
    35                          40                          45  
 Trp Lys Val Gln Val Xaa Trp Pro Lys Asn Ser His Phe Ile Phe Asn  
    50                          55                          60  
 Glu Ile Phe Pro Xaa Val Leu Ile Thr Phe Pro Xaa Xaa Ser Gln Leu  
    65                          70                          75                          80  
 30 Phe Asp Glu Leu Xaa Val Ile Val Met Gly Phe Asp Glu Ser Ser Phe  
           85                          90                          95  
 Ala Thr Cys Asn Lys Xaa Trp His Phe Gln Leu Asp Gln Xaa Val Lys  
           100                          105                          110  
 35 Thr Leu Gly Lys Glu Asn Leu Xaa Trp Phe Gln Val His Phe Ser Asn  
    115                          120                          125  
 Tyr Phe Ile Gly Asn Leu Asn Lys Ser Ile Pro Asn Asp Phe Ser Phe  
    130                          135                          140  
 Leu Phe Arg Thr Cys Gly His Ile  
    145                          150  
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       <210> 935  
       <211> 176  
       <212> PRT  
       <213> Homo sapiens  
 45  
       <400> 935  
 Val Cys Arg Val Thr Val Val Pro Thr Val Thr Cys Val Glu Ser Pro  
    1                          5                          10                          15  
 Val Lys Met Asn Leu Thr Gly Asn His Phe Ile Phe Leu Ala Arg Leu  
           20                          25                          30  
 50 Ile Pro Arg Met Cys His Asn Val Asn Arg Val Val Tyr Ile Phe Gly  
    35                          40                          45  
 Pro Pro Val Lys Glu Pro Pro Thr Asp Val Thr Pro Thr Phe Leu Thr  
    50                          55                          60  
 55 Thr Gly Val Leu Ser Thr Leu Arg Gln Ala Asp Phe Glu Ala His Asn  
    65                          70                          75                          80  
 Ile Leu Arg Glu Ser Gly Tyr Ala Gly Lys Ile Ser Gln Met Pro Val  
           85                          90                          95  
 60 Ile Leu Thr Pro Leu His Phe Asp Arg Asp Pro Leu Gln Lys Gln Pro  
           100                          105                          110  
 Ser Cys Gln Arg Ser Val Val Ile Arg Thr Phe Ile Thr Ser Asp Phe  
           115                          120                          125  
 Met Thr Gly Ile Pro Ala Thr Pro Gly Asn Glu Ile Pro Val Glu Val

130 135 140  
 Val Leu Lys Met Val Thr Glu Ile Lys Lys Ile Pro Gly Ile Ser Arg  
 145 150 155 160  
 Ile Met Tyr Asp Leu Thr Ser Lys Pro Pro Gly Thr Thr Glu Trp Glu  
 165 170 175  
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 <210> 936  
 <211> 218  
 <212> PRT  
 10 <213> Homo sapiens  
 <400> 936  
 Arg Thr Pro Arg Lys Arg Ile Ser Lys Thr Leu Asn Met Thr Thr Ser  
 1 5 10 15  
 15 Pro Glu Glu Lys Arg Lys Ile Ile Gly Asp Thr Phe Val Lys Ile Ala  
 20 25 30  
 Asn Glu Val Ile Gly Glu Met Asn Leu Lys Pro Glu Glu Val Phe Leu  
 35 40 45  
 Ala Gln Gly Thr Leu Arg Pro Asp Leu Ile Glu Ser Ala Ser Leu Val  
 50 55 60  
 20 Ala Ser Gly Lys Ala Glu Leu Ile Lys Thr His His Asn Asp Thr Glu  
 65 70 75 80  
 Leu Ile Arg Lys Leu Arg Glu Glu Gly Lys Val Ile Glu Pro Leu Lys  
 85 90 95  
 25 Asp Phe His Lys Asp Glu Val Arg Ile Leu Gly Arg Glu Leu Gly Leu  
 100 105 110  
 Pro Glu Glu Leu Val Ser Arg His Pro Phe Pro Gly Pro Gly Leu Ala  
 115 120 125  
 Ile Arg Val Ile Cys Ala Glu Glu Pro Tyr Ile Cys Lys Asp Phe Pro  
 130 135 140  
 30 Glu Thr Asn Asn Ile Leu Lys Ile Val Ala Asp Phe Ser Ala Ser Val  
 145 150 155 160  
 Lys Lys Pro His Thr Leu Leu Gln Arg Val Lys Ala Cys Thr Thr Glu  
 165 170 175  
 35 Glu Asp Gln Glu Lys Leu Met Gln Ile Thr Ser Leu His Ser Leu Asn  
 180 185 190  
 Ala Phe Leu Leu Pro Ile Lys Thr Val Xaa Val Gln Gly Asp Cys Arg  
 195 200 205  
 Ser Tyr Ser Tyr Arg Val Trp Asn Xaa Gln  
 210 215  
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 <210> 937  
 <211> 246  
 <212> PRT  
 45 <213> Homo sapiens  
 <400> 937  
 Ala Ala Ala Pro Ala Leu Ala Pro Met Ala Leu Cys Asn Gly Asp Ser  
 1 5 10 15  
 50 Lys Leu Glu Asn Ala Gly Gly Asp Leu Lys Asp Gly His His His Tyr  
 20 25 30  
 Glu Gly Ala Val Val Ile Leu Asp Ala Gly Ala Gln Tyr Gly Lys Val  
 35 40 45  
 Ile Asp Arg Arg Val Arg Glu Leu Phe Val Gln Ser Glu Ile Phe Pro  
 50 55 60  
 55 Leu Glu Thr Pro Ala Phe Ala Ile Lys Glu Gln Gly Phe Arg Ala Ile  
 65 70 75 80  
 Ile Ile Ser Gly Gly Pro Asn Ser Val Tyr Ala Glu Asp Ala Pro Trp  
 85 90 95  
 60 Phe Asp Pro Ala Ile Phe Thr Ile Gly Lys Pro Val Leu Gly Ile Cys  
 100 105 110  
 Tyr Gly Met Gln Met Met Asn Lys Val Phe Gly Gly Thr Val His Lys  
 115 120 125

Lys Ser Val Arg Glu Asp Gly Val Phe Asn Ile Ser Val Asp Asn Thr  
 130 135 140  
 Cys Ser Leu Phe Arg Gly Leu Gln Lys Glu Val Val Leu Leu Thr  
 145 150 155 160  
 5 His Gly Asp Ser Val Asp Lys Val Ala Asp Gly Phe Lys Val Val Ala  
 165 170 175  
 Arg Ser Gly Asn Ile Val Ala Gly Ile Ala Asn Glu Ser Lys Lys Leu  
 180 185 190  
 Tyr Gly Ala Gln Phe His Pro Glu Val Gly Leu Thr Glu Asn Gly Lys  
 195 200 205  
 10 Val Ile Leu Lys Asn Phe Leu Tyr Asp Ile Thr Trp Met Gln Trp Asn  
 210 215 220  
 Leu His Arg Ala Xaa Thr Glu Lys Leu Glu Cys Xaa Xaa Glu Ile Lys  
 225 230 235 240  
 15 Arg Glu Ser Xaa Ala Arg  
 245

<210> 938  
 <211> 145  
 20 <212> PRT  
 <213> Homo sapiens

<400> 938  
 Thr Cys Ile Ile His Thr Asn Val Glu Asn Ser Ile Phe Ser Asp Thr  
 1 5 10 15  
 Phe Phe Val His Ser Thr Ser Lys Tyr Leu Ile His His Leu His Thr  
 20 25 30  
 Ile Ala Asn Ser Lys Asn Arg Leu Ala Asn Ser Glu Tyr Cys Trp Ile  
 35 40 45  
 30 Lys Pro Gly Ser Ile Phe Ser Ile His Arg Ile Arg Ser Ser Arg Asp  
 50 55 60  
 Asp Asn Ser Thr Glu Ser Leu Phe Leu Tyr Ser Lys Cys Trp Cys Phe  
 65 70 75 80  
 Gln Gly Glu Asn Phe Arg Leu His Glu Gln Phe Pro His Ser Ser Val  
 85 90 95  
 35 Tyr Asp Phe Pro Val Leu Ser Thr Ser Ile Gln Asn Asp Asn Ser Ser  
 100 105 110  
 Phe Ile Val Val Val Ala Ile Leu Lys Val Ser Ser Ser Ile Leu Gln  
 115 120 125  
 40 Leu Gly Val Ser Val Ala Gln Ser His Arg Gly Gln Gly Arg Ser Arg  
 130 135 140  
 Gly  
 145

45 <210> 939  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens

<400> 939  
 Thr Met Glu Ala Lys Asp Gln Lys Lys His Arg Lys Lys Asn Ser Gly  
 1 5 10 15  
 Pro Lys Ala Ala Lys Lys Lys Lys Arg Leu Leu Gln Asp Leu Gln Leu  
 20 25 30  
 55 Gly Asp Glu Glu Asp Ala Arg Lys Arg Asn Pro Lys Ala Phe Ala Val  
 35 40 45  
 Gln Ser Ala Val Arg Met Ala Arg Ser Phe His Arg Thr Gln Asp Leu  
 50 55 60  
 Lys Thr Lys Lys His His Ile Pro Val Val Asp Arg Thr Pro Leu Glu  
 65 70 75 80  
 60 Pro Pro Pro Ile Val Val Val Met Gly Pro Pro Lys Val Gly Lys  
 85 90 95  
 Ser Thr Leu Ile Gln Cys Leu Ile Arg Asn Phe Thr Arg Gln Lys Leu

100 105 110  
 Thr Glu Ile Arg Gly Pro Val Thr Ile Val Ser Gly Lys Lys Arg Arg  
 115 120 125  
 Leu Thr Ile Ile Glu Cys Gly Cys Asp Ile Asn Met Met Ile Asp Leu  
 130 135 140  
 Ala Lys Val Ala Asp Leu Val Leu Met Leu Ile Asp Ala Ser Phe Gly  
 145 150 155 160  
 Phe Glu Met Glu Thr Phe Glu Phe Leu Asn Ile Cys Gln Val His Gly  
 165 170 175  
 10 Phe Pro Lys Ile Met Gly Val Leu Thr His Leu Asp Phe Phe Lys His  
 180 185 190  
 Asn Lys Pro Thr Gly Gly Arg Gln Arg Ser Arg Leu Lys His Arg Phe  
 195 200 205  
 Trp Thr Xaa Lys Phe Thr Pro Gly Ala Gln Ala Val  
 15 210 215 220  
  
 <210> 940  
 <211> 156  
 <212> PRT  
 20 <213> Homo sapiens  
  
 <400> 940  
 Asn Cys Leu Pro Pro Gln Ile Gln Gly Gln Ser Leu Gln Ser Lys Gly  
 1 5 10 15  
 25 Ser Leu Gln Leu Ala Leu Ser Pro Leu Gln Thr Gly Leu Leu Val Ser  
 20 25 30  
 Ser Phe Leu Leu Pro Leu Asn Ser Glu Glu Leu Leu Pro Glu Val Leu  
 35 40 45  
 Leu Pro Leu Gln Leu Leu Leu Leu Leu Leu Leu Gly Ser Glu Val  
 50 55 60  
 30 Leu Phe Ile Val Gln Val Pro Leu Leu Leu Gly Leu Leu His Leu Leu  
 65 70 75 80  
 Thr Met His Arg Thr Gln Ser Ile Gln Gln Cys Lys Asp Leu Ser Phe  
 85 90 95  
 35 Met Arg Leu Ala Tyr Asp Gly Arg Ser Pro Pro Val Leu Trp His Leu  
 100 105 110  
 Ala Cys Leu Cys Leu Gly Leu Gly Leu Val Leu Lys Trp Gln Gly Leu  
 115 120 125  
 Leu Gln Xaa Phe Trp Asn Val Gln Xaa Ile Lys Met Phe Leu Leu Pro  
 130 135 140  
 40 Gln Asp Gly Leu Tyr Xaa Lys Val Leu Gly Xaa Leu  
 145 150 155  
  
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 45 <211> 132  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 941  
 50 Gly Gln Lys Glu Xaa Phe Leu Ile Ser Xaa Ala Xaa Ser Gln Asn Xaa  
 1 5 10 15  
 Leu Pro Xaa Gly Xaa Ser Xaa Phe Lys Xaa Gln Ala Gln Ala Pro Asn  
 20 25 30  
 Gln Lys Ala Gly Lys Val Pro Lys Gly Gln Ala Glu Pro Gly Xaa His  
 35 40 45  
 55 Thr Arg Ala Phe Met Lys Xaa Arg Ser Leu Ala Leu Leu Asp Ala Leu  
 50 55 60  
 Ser Thr Val His Ser Gln Lys Met Lys Lys Ala Lys Glu Gln Arg Xaa  
 65 70 75 80  
 60 Leu Xaa Asn Lys Glu Pro Phe Arg Ala Lys Gln Lys Glu Glu Glu Glu  
 85 90 95  
 Lys Leu Lys Arg Gln Lys Asp Leu Arg Lys Lys Leu Phe Arg Ile Gln  
 100 105 110



Gly Gln Lys Glu Arg Arg Asn Gln Lys Ser Ser Leu Lys Gly Ala Glu  
           115                          120                          125  
 Gly Gln Xaa Gln  
           130

5

<210> 942  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

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<400> 942  
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 Ser Leu Xaa Leu Ala Leu Ser Pro Leu Gln Thr Gly Leu Leu Val Ser  
 15                  20                          25                          30  
 Ser Phe Leu Leu Pro Leu Asn Ser Glu Glu Leu Leu Pro Glu Val Leu  
           35                          40                          45  
 Leu Pro Leu Gln Leu Leu Leu Leu Leu Leu Leu Gly Ser Glu Gly  
           50                          55                          60  
 20 Leu Phe Ile Xaa Gln Xaa Pro Leu Leu Leu Gly Leu Leu His Leu Leu  
   65                          70                          75                          80  
 Thr Met His Arg Thr Gln Ser Ile Gln Gln Cys Lys Gly Ser Xaa Phe  
                           85                          90                          95  
 His Glu Gly Ser Arg Met Xaa Ala Gly Leu Arg Leu Ser Phe Trp His  
 25                          100                          105                          110  
 Leu Ala Cys Leu Leu Val Trp Gly Leu Gly Leu Xaa Leu Lys Xaa Gly  
                           115                          120                          125  
 Xaa Ala Xaa Trp Gln Xaa Val Leu Gly Xaa Gly Xaa Gly Asn  
           130                          135                          140

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<210> 943  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

35

<400> 943  
 Ala Lys Arg Asn Leu Phe Asn Ser Leu Xaa His Ser Gln Xaa Xaa Cys  
   1                  5                          10                          15  
 Xaa Arg Xaa Xaa His Xaa Arg Pro Ser Pro Ser Pro Ser Lys Gly Arg  
 40                  20                          25                          30  
 Gln Gly Ala Lys Asp Arg Arg Arg Pro Ala Val Ile Arg Glu Pro His  
           35                          40                          45  
 Glu Arg Lys Ile Leu Ala Leu Leu Asp Ala Leu Ser Thr Val His Ser  
           50                          55                          60  
 45 Gln Lys Met Lys Lys Ala Lys Glu Gln Arg His Leu His Asn Lys Glu  
   65                          70                          75                          80  
 His Phe Arg Ala Lys Gln Lys Glu Glu Glu Lys Leu Lys Arg Gln  
                           85                          90                          95  
 Lys Asp Leu Arg Lys Lys Leu Phe Arg Ile Gln Gly Gln Lys Glu Arg  
 50                          100                          105                          110  
 Arg Asn Gln Lys Ser Ser Leu Lys Gly Ala Glu Gly Gln Leu Gln  
           115                          120                          125

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<210> 944  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

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<400> 944  
 Asn Cys Leu Pro Pro Gln Ile Gln Gly Gln Ser Leu Gln Ser Lys Gly  
   1                  5                          10                          15  
 Ser Leu Gln Leu Ala Leu Ser Pro Leu Gln Thr Gly Leu Leu Val Ser  
           20                          25                          30

	Ser	Phe	Leu	Leu	Pro	Leu	Asn	Ser	Glu	Glu	Leu	Leu	Pro	Glu	Val	Leu
			35					40					45			
	Leu	Pro	Leu	Gln	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Glu	Val
		50					55					60				
5	Leu	Phe	Ile	Val	Gln	Val	Pro	Leu	Leu	Leu	Gly	Leu	Leu	His	Leu	Leu
	65					70					75				80	
	Thr	Met	His	Arg	Thr	Gln	Ser	Ile	Gln	Gln	Cys	Lys	Asp	Leu	Ser	Phe
					85					90					95	
	Met	Arg	Leu	Ala	Tyr	Asp	Gly	Arg	Ser	Pro	Pro	Val	Phe	Gly	Thr	Leu
10				100					105					110		
	Pro	Ala	Phe	Ala	Trp	Ala	Trp	Ala	Trp	Ser	Xaa	Met	Xaa	Xaa	Pro	Xaa
		115					120						125			
	Ala	Xaa	Xaa	Leu	Gly	Met	Xaa	Lys	Gly	Ile	Lys	Lys	Val	Ser	Phe	Gly
		130					135					140				
15	Leu	Arg	Ile	Gly	Leu	Phe	Lys	Xaa	Val	Leu	Gly	Arg	Leu	Leu	Xaa	
	145					150					155					

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20      <210> 945
        <211> 250
        <212> PRT
        <213> Homo sapiens

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	<400> 945															
25	Ile	Asn	Tyr	Val	Leu	Val	Val	Tyr	Gly	Leu	Ala	Ile	Ser	Leu	Leu	Gly
	1				5					10					15	
	Ile	Gly	Gln	Pro	Glu	Glu	Leu	Ser	Glu	Ala	Glu	Asn	Gln	Phe	Lys	Arg
				20					25					30		
	Ile	Ile	Glu	His	Tyr	Pro	Ser	Glu	Gly	Leu	Asp	Cys	Leu	Ala	Tyr	Cys
			35					40					45			
30	Gly	Ile	Gly	Lys	Val	Tyr	Leu	Lys	Lys	Asn	Arg	Phe	Leu	Glu	Ala	Leu
		50					55					60				
	Asn	His	Phe	Glu	Lys	Ala	Arg	Thr	Leu	Ile	Tyr	Arg	Leu	Pro	Gly	Val
	65					70					75				80	
	Leu	Thr	Trp	Pro	Thr	Ser	Asn	Val	Ile	Ile	Glu	Glu	Ser	Gln	Pro	Gln
35					85					90					95	
	Lys	Ile	Lys	Met	Leu	Leu	Glu	Lys	Phe	Val	Glu	Glu	Cys	Lys	Phe	Pro
				100					105					110		
	Pro	Val	Pro	Asp	Ala	Ile	Cys	Cys	Tyr	Gln	Lys	Cys	His	Gly	Tyr	Ser
			115					120					125			
40	Lys	Ile	Gln	Ile	Tyr	Ile	Thr	Asp	Pro	Asp	Phe	Lys	Gly	Phe	Ile	Arg
		130					135					140				
	Ile	Ser	Cys	Cys	Gln	Tyr	Cys	Lys	Ile	Glu	Phe	His	Met	Asn	Cys	Trp
	145					150					155				160	
45	Lys	Lys	Leu	Lys	Thr	Thr	Thr	Phe	Asn	Asp	Lys	Ile	Asp	Lys	Asp	Phe
					165					170					175	
	Leu	Gln	Gly	Ile	Cys	Leu	Thr	Pro	Asp	Cys	Glu	Xaa	Val	Ile	Ser	Lys
				180					185					190		
	Ile	Ile	Ile	Phe	Ser	Ser	Gly	Gly	Glu	Val	Lys	Cys	Glu	Phe	Glu	His
			195					200					205			
50	Lys	Val	Ile	Lys	Glu	Lys	Val	Xaa	Ser	Arg	Pro	Ile	Leu	Lys	Gln	Lys
		210					215					220				
	Cys	Ser	Ser	Leu	Xaa	Lys	Leu	Arg	Leu	Glu	Glu	Asp	Lys	Lys	Leu	Glu
	225					230					235					240
	Glu	Lys	Gly	Xaa	Gln	Lys	Lys	Glu	Pro	Lys						
55					245					250						

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        <210> 946
        <211> 128
        <212> PRT
60      <213> Homo sapiens

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<400> 946  
Arg Ala Ser Asn Ser Ser Thr Ser Cys Arg Arg Trp Ser Gly Thr Ala  
356

1                      5                      10                      15  
 Asn Gly Pro Ala Xaa Ser Glu Phe Arg Leu Leu Trp Ser Ser Leu Glu  
                          20                      25                      30  
 Val Met Ile Ser Leu Phe Glu Val Thr Glu Val Val Pro Asp Pro Thr  
 5                      35                      40                      45  
 Asn Ile Gly Phe Glu Ser Phe Gly Phe Phe Phe Leu Leu Leu Xaa Phe  
                          50                      55                      60  
 Thr Leu Val Glu Leu Asn Gly Ala Ser Pro Leu Ser Cys Phe Leu Asn  
 65                      70                      75                      80  
 10 Thr Val Gln Ala Gly Val His Tyr Ile Lys Arg Ile His Leu Lys His  
                          85                      90                      95  
 Tyr Ala Met Leu Gly Asn Leu Gly Phe Trp Gly Leu Leu Xaa Xaa Xaa  
                          100                      105                      110  
 15 Ile Leu Asn Lys Pro Gly Leu Ser Phe Lys Xaa Lys Pro Gly Leu Pro  
                          115                      120                      125

&lt;210&gt; 947

&lt;211&gt; 127

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 947

Ala Val Met Gln Pro Ser Ser Val Gln Tyr Ser Cys Gln Ser Gln Gln  
 1                      5                      10                      15  
 25 Asn Glu Gly Ile Pro Arg Glu Lys Val Leu Asn Leu Leu Leu Phe Leu  
                          20                      25                      30  
 Val Ser Val Glu Phe Leu Leu Gly Lys Thr His Ile Leu Gln Arg Thr  
                          35                      40                      45  
 Ser Cys Tyr Ser Cys Pro Arg Asp His Val Pro Pro Lys Thr Glu Arg  
 30                      50                      55                      60  
 Ser Asn His Ile Glu Leu Asn Ile Phe Val Leu Gly Ser Cys Pro Ile  
 65                      70                      75                      80  
 Ala Ser Tyr Cys Gly Gln His Ile Arg Tyr Cys Val Gly His Arg Glu  
                          85                      90                      95  
 35 Leu Arg Ile Leu Leu His Leu Ala Glu Asp Gly Gln Ala Leu Gln Met  
                          100                      105                      110  
 Gly Leu Xaa Asn Leu Asn Phe Asp Cys Tyr Gly Leu His Leu Lys  
                          115                      120                      125

40 &lt;210&gt; 948

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

45 &lt;400&gt; 948

Trp Thr Pro Ala Cys Thr Val Leu Arg Lys Gln Asp Ser Gly Glu Ala  
 1                      5                      10                      15  
 Pro Phe Ser Ser Thr Lys Val Lys Xaa Lys Ser Lys Lys Lys Lys Pro  
                          20                      25                      30  
 50 Lys Asp Ser Lys Pro Met Leu Val Gly Ser Gly Thr Thr Ser Val Thr  
                          35                      40                      45  
 Ser Asn Asn Glu Ile Ile Thr Ser Ser Glu Asp His Ser Asn Arg Asn  
                          50                      55                      60  
 Ser Asp Xaa Ala Gly Pro Phe Ala Val Pro Asp His Leu Arg Gln Asp  
 55                      65                      70                      75                      80  
 Val Glu Glu Phe Glu Ala Leu Tyr Asp Gln His Ser Asn Glu Tyr Val  
                          85                      90                      95  
 Val Arg Asn Lys Lys Leu Trp Asp Met Asn Pro Lys Gln Lys Cys Ser  
                          100                      105                      110  
 60 Thr Leu Tyr Asp Tyr Phe Ser Gln Phe Leu Glu Glu His Gly Pro Leu  
                          115                      120                      125  
 Asp Met Ser Asn Lys Met Phe Ser Ala Glu Tyr Glu Phe Phe Pro Glu  
                          130                      135                      140

Glu Thr Arg Gln Ile Leu Glu Lys Ala Gly Gly Leu Lys Pro Phe Leu  
 145 150 155 160  
 Leu Gly Cys Pro Arg Phe Val Val Ile Asp Asn Cys Ile Ala Leu Lys  
 165 170 175  
 5 Lys Val Ala Ser Arg Leu Lys  
 180  
 <210> 949  
 <211> 219  
 10 <212> PRT  
 <213> Homo sapiens  
 <400> 949  
 15 Leu Leu Asn Gly Leu Asp Pro Gln Lys Ile Lys Gln Leu Asn Leu Ala  
 1 5 10 15  
 Met Ile Asn Tyr Val Leu Val Val Tyr Gly Leu Ala Ile Ser Leu Leu  
 20 20 25 30  
 Gly Ile Gly Gln Pro Glu Glu Leu Ser Glu Ala Glu Asn Gln Phe Lys  
 35 40 45  
 20 Arg Ile Ile Glu His Tyr Pro Ser Glu Gly Leu Asp Cys Leu Ala Tyr  
 50 55 60  
 Cys Gly Ile Gly Lys Val Tyr Leu Lys Lys Asn Arg Phe Leu Glu Ala  
 65 70 75 80  
 Leu Asn His Phe Glu Lys Ala Arg Thr Leu Ile Tyr Arg Leu Pro Gly  
 85 90 95  
 25 Val Leu Thr Trp Pro Thr Ser Asn Val Ile Ile Glu Glu Ser Gln Pro  
 100 105 110  
 Gln Lys Ile Lys Met Leu Leu Glu Lys Phe Val Glu Glu Cys Lys Phe  
 115 120 125  
 30 Pro Pro Val Pro Asp Ala Ile Cys Cys Tyr Gln Lys Cys His Gly Tyr  
 130 135 140  
 Ser Lys Ile Gln Ile Tyr Ile Thr Asp Pro Asp Phe Lys Gly Phe Ile  
 145 150 155 160  
 Arg Ile Ser Cys Cys Gln Tyr Cys Lys Ile Glu Phe His Met Asn Cys  
 165 170 175  
 35 Trp Lys Lys Leu Lys Thr Thr Thr Phe Asn Asp Lys Ile Asp Lys Gly  
 180 185 190  
 Phe Ser Thr Arg Glu Tyr Val Leu Pro Leu Thr Val Xaa Gly Ser Phe  
 195 200 205  
 40 Leu Xaa Ile Ile Ile Phe Ser Ser Gly Trp Val  
 210 215  
 <210> 950  
 <211> 116  
 45 <212> PRT  
 <213> Homo sapiens  
 <400> 950  
 50 Arg Ala Ser Asn Ser Ser Thr Ser Cys Arg Arg Trp Ser Gly Thr Ala  
 1 5 10 15  
 Asn Gly Pro Ala Glu Ser Glu Phe Arg Leu Leu Trp Ser Ser Leu Glu  
 20 25 30  
 Val Met Ile Ser Leu Phe Glu Val Thr Glu Val Val Pro Asp Pro Thr  
 35 40 45  
 55 Asn Ile Gly Phe Glu Ser Phe Gly Phe Phe Phe Leu Leu Phe Phe  
 50 55 60  
 Thr Leu Val Glu Leu Asn Xaa Ala Ser Pro Leu Ser Cys Phe Leu Asn  
 65 70 75 80  
 Thr Val Gln Arg Val Pro Leu Tyr Gln Arg Ile His Leu Lys His Tyr  
 85 90 95  
 60 Ala Met Leu Gly Asn Leu Ala Leu Gly Ser Ser Ser Thr Ile Leu Asn  
 100 105 110  
 Asn Gly Phe Leu

115

&lt;210&gt; 951

&lt;211&gt; 127

5 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 951

Ala Val Met Gln Pro Ser Ser Val Gln Tyr Ser Cys Gln Ser Gln Gln  
 1 5 10 15  
 Asn Glu Gly Ile Pro Arg Glu Lys Val Leu Asn Leu Leu Leu Phe Leu  
 20 25 30  
 Val Ser Val Glu Phe Leu Leu Gly Lys Thr His Ile Leu Gln Arg Thr  
 35 40 45  
 15 Ser Cys Tyr Ser Cys Pro Arg Asp His Val Pro Pro Lys Thr Glu Arg  
 50 55 60  
 Ser Asn His Ile Glu Leu Asn Ile Phe Val Leu Gly Ser Cys Pro Ile  
 65 70 75 80  
 Ala Ser Tyr Cys Gly Gln His Ile Arg Tyr Cys Val Gly His Arg Glu  
 85 90 95  
 20 Leu Arg Ile Leu Leu His Leu Ala Glu Asp Gly Gln Ala Leu Gln Met  
 100 105 110  
 Gly Leu Gln Asn Leu Asn Phe Asp Cys Tyr Gly Leu His Leu Lys  
 115 120 125

25

&lt;210&gt; 952

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

30

&lt;400&gt; 952

Tyr Asn Gly Thr Arg Cys Thr Val Leu Arg Lys Gln Asp Ser Gly Glu  
 1 5 10 15  
 Xaa Pro Phe Ser Ser Thr Lys Val Lys Asn Lys Ser Lys Lys Lys  
 20 25 30  
 35 Pro Lys Asp Ser Lys Pro Met Leu Val Gly Ser Gly Thr Thr Ser Val  
 35 40 45  
 Thr Ser Asn Asn Glu Ile Ile Thr Ser Ser Glu Asp His Ser Asn Arg  
 50 55 60  
 40 Asn Ser Asp Ser Ala Gly Pro Phe Ala Val Pro Asp His Leu Arg Gln  
 65 70 75 80  
 Asp Val Glu Glu Phe Glu Ala Leu Tyr Asp Gln His Ser Asn Glu Tyr  
 85 90 95  
 Val Val Arg Asn Lys Lys Leu Trp Asp Met Asn Pro Lys Gln Lys Cys  
 100 105 110  
 45 Ser Thr Leu Tyr Asp Tyr Phe Ser Gln Phe Leu Glu Glu His Gly Pro  
 115 120 125  
 Leu Asp Met Ser Asn Lys Met Phe Ser Ala Glu Tyr Glu Phe Phe Pro  
 130 135 140  
 50 Glu Glu Thr Arg Gln Ile Leu Glu Lys Ala Gly Gly Leu Lys Pro Phe  
 145 150 155 160  
 Leu Leu Gly Cys Pro Arg Phe Val Val Ile Asp Asn Cys Ile Ala Leu  
 165 170 175  
 Lys Lys Val Ala Ser Arg Leu Lys  
 180

55

&lt;210&gt; 953

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

60

&lt;400&gt; 953

Tyr Asn Xaa Xaa Pro Leu Val Leu Val Leu Arg Lys Gln Asp Ser Gly

	1		5		10		15									
	Glu	Xaa	Pro	Phe	Ser	Ser	Thr	Lys	Val	Lys	Asn	Lys	Ser	Lys	Lys	
				20					25					30		
5	Lys	Pro	Lys	Asp	Ser	Lys	Pro	Met	Leu	Val	Gly	Ser	Gly	Thr	Thr	Ser
			35					40					45			
	Val	Thr	Ser	Asn	Asn	Glu	Ile	Ile	Thr	Ser	Ser	Glu	Asp	His	Ser	Asn
			50				55					60				
	Arg	Asn	Ser	Asp	Ser	Ala	Gly	Pro	Phe	Ala	Val	Pro	Asp	His	Leu	Arg
	65					70					75				80	
10	Gln	Asp	Val	Glu	Glu	Phe	Glu	Ala	Leu	Tyr	Asp	Gln	His	Ser	Asn	Glu
					85					90					95	
	Tyr	Val	Val	Arg	Asn	Lys	Lys	Leu	Trp	Asp	Met	Asn	Pro	Lys	Gln	Lys
				100					105					110		
	Cys	Ser	Thr	Leu	Tyr	Asp	Tyr	Phe	Ser	Gln	Phe	Leu	Glu	Glu	His	Gly
15			115					120					125			
	Pro	Leu	Asp	Met	Ser	Asn	Lys	Met	Phe	Ser	Ala	Glu	Tyr	Glu	Phe	Phe
		130					135						140			
	Pro	Glu	Glu	Thr	Arg	Gln	Ile	Leu	Glu	Lys	Ala	Gly	Gly	Leu	Lys	Pro
	145					150					155				160	
20	Phe	Leu	Leu	Gly	Cys	Pro	Arg	Phe	Val	Val	Ile	Asp	Asn	Cys	Ile	Ala
					165					170					175	
	Leu	Lys	Lys	Val	Ala	Ser	Arg	Leu	Lys							
				180					185							
25				<210>	954											
				<211>	125											
				<212>	PRT											
				<213>	Homo sapiens											
30				<400>	954											
	Met	Gln	Pro	Ser	Ser	Val	Gln	Tyr	Ser	Cys	Gln	Ser	Gln	Gln	Asn	Glu
	1				5					10					15	
	Gly	Ile	Pro	Arg	Glu	Lys	Val	Leu	Asn	Leu	Leu	Leu	Phe	Leu	Val	Ser
				20					25					30		
35	Val	Glu	Phe	Leu	Leu	Gly	Lys	Thr	His	Ile	Leu	Gln	Arg	Thr	Ser	Cys
			35					40					45			
	Tyr	Ser	Cys	Pro	Arg	Asp	His	Val	Pro	Pro	Lys	Thr	Glu	Arg	Ser	Asn
			50				55					60				
	His	Ile	Glu	Leu	Asn	Ile	Phe	Val	Leu	Gly	Ser	Cys	Pro	Ile	Ala	Ser
40	65					70					75				80	
	Tyr	Cys	Gly	Gln	His	Ile	Arg	Tyr	Cys	Val	Gly	His	Arg	Glu	Leu	Arg
					85					90					95	
	Ile	Leu	Leu	His	Leu	Ala	Glu	Asp	Gly	Gln	Ala	Leu	Gln	Met	Gly	Leu
				100					105					110		
45	Gln	Asn	Leu	Asn	Phe	Asp	Cys	Tyr	Gly	Leu	His	Leu	Lys			
			115					120					125			
				<210>	955											
				<211>	212											
50				<212>	PRT											
				<213>	Homo sapiens											
				<400>	955											
	Glu	Asp	Glu	Lys	Arg	Arg	Arg	Lys	Glu	Glu	Glu	Glu	Arg	Arg	Met	Lys
55	1				5					10					15	
	Leu	Glu	Met	Glu	Ala	Lys	Arg	Lys	Gln	Glu	Glu	Glu	Glu	Arg	Lys	Lys
				20					25					30		
	Arg	Glu	Asp	Asp	Glu	Lys	Arg	Ile	Gln	Ala	Glu	Val	Glu	Ala	Gln	Leu
			35					40					45			
60	Ala	Arg	Gln	Lys	Glu	Glu	Glu	Ser	Gln	Gln	Gln	Ala	Val	Leu	Glu	Gln
			50				55					60				
	Glu	Arg	Arg	Asp	Arg	Glu	Leu	Ala	Leu	Arg	Ile	Ala	Gln	Ser	Glu	Ala
	65					70					75				80	

Glu Leu Ile Ser Asp Glu Ala Gln Ala Asp Leu Ala Leu Arg Ser Leu  
                     85                    90                    95  
 Asp Ser Tyr Pro Val Thr Ser Lys Asn Asp Gly Thr Arg Pro Lys Met  
                     100                    105                    110  
 5 Thr Pro Glu Gln Met Ala Lys Glu Met Ser Glu Phe Leu Ser Arg Gly  
                     115                    120                    125  
 Pro Ala Val Leu Ala Thr Lys Ala Ala Ala Gly Thr Lys Lys Tyr Asp  
                     130                    135                    140  
 10 Leu Ser Lys Trp Lys Tyr Ala Glu Leu Arg Asp Thr Ile Asn Thr Ser  
                     145                    150                    155                    160  
 Cys Asp Ile Glu Leu Leu Ala Ala Cys Arg Glu Glu Phe His Arg Arg  
                     165                    170                    175  
 Leu Lys Val Tyr His Ala Trp Lys Ser Lys Asn Lys Lys Arg Asn Leu  
                     180                    185                    190  
 15 Glu Gln Ser Asn Val Leu Gln Ser Leu Leu Leu Ile Met Leu Ser Lys  
                     195                    200                    205  
 Thr Gln Gln Leu  
                     210  
  
 20 <210> 956  
       <211> 121  
       <212> PRT  
       <213> Homo sapiens  
  
 25 <400> 956  
 His Phe Phe Gly His Leu Phe Arg Cys His Phe Gly Ser Cys Ser Ile  
   1                    5                    10                    15  
 Ile Phe Arg Ser Tyr Arg Ile Gly Ile Gln Ala Pro Gln Arg Gln Val  
                     20                    25                    30  
 30 Gly Leu Gly Leu Ile Thr Asp Glu Leu Gly Phe Thr Leu Gly Asn Pro  
                     35                    40                    45  
 Gln Gly Gln Leu Pro Val Pro Ala Leu Leu Leu Gln Asn Cys Leu Leu  
                     50                    55                    60  
 35 Leu Gly Phe Leu Leu Leu Leu Ser Gly Gln Leu Cys Leu His Phe Ser  
                     65                    70                    75                    80  
 Leu Asn Ala Phe Phe Ile Ile Phe Pro Phe Leu Ser Leu Phe Phe Phe  
                     85                    90                    95  
 Leu Phe Ser Leu Cys Phe His Leu Lys Phe His Pro Pro Phe Leu Leu  
                     100                    105                    110  
 40 Phe Leu Ser Ser Thr Phe Phe Val Phe  
                     115                    120  
  
       <210> 957  
       <211> 221  
       <212> PRT  
       <213> Homo sapiens  
  
 45 <400> 957  
 Glu Arg Lys Arg Arg Glu Glu Asp Glu Lys Arg Arg Arg Lys Glu Glu  
   1                    5                    10                    15  
 Glu Glu Arg Arg Met Lys Leu Glu Met Glu Ala Lys Arg Lys Gln Glu  
                     20                    25                    30  
 Glu Glu Glu Arg Lys Lys Arg Glu Asp Asp Glu Lys Arg Ile Gln Ala  
                     35                    40                    45  
 55 Glu Val Glu Ala Gln Leu Ala Arg Gln Lys Glu Glu Glu Ser Gln Gln  
                     50                    55                    60  
 Gln Ala Val Leu Glu Gln Glu Arg Arg Asp Arg Glu Leu Ala Leu Arg  
                     65                    70                    75                    80  
 Ile Ala Gln Ser Glu Ala Glu Leu Ile Ser Asp Glu Ala Gln Ala Asp  
                     85                    90                    95  
 60 Leu Ala Leu Arg Arg Gly Pro Ala Val Leu Ala Thr Lys Ala Ala Ala  
                     100                    105                    110  
 Gly Thr Lys Lys Tyr Asp Leu Ser Lys Trp Lys Tyr Ala Glu Leu Arg

115 120 125  
 Asp Thr Ile Asn Thr Ser Cys Asp Ile Glu Leu Leu Ala Ala Cys Arg  
 130 135 140  
 Glu Glu Phe His Arg Arg Leu Lys Val Tyr His Ala Trp Lys Ser Lys  
 145 150 155 160  
 5 Asn Lys Lys Arg Asn Thr Glu Thr Glu Gln Arg Ala Pro Lys Ser Val  
 165 170 175  
 Thr Asp Tyr Ala Gln Gln Asn Pro Ala Ala Gln Ile Pro Ala Arg Gln  
 180 185 190  
 10 Arg Glu Ile Glu Met Asn Pro Thr Ala Thr Leu Leu Ser His Xaa Ile  
 195 200 205  
 His Ser Ala Leu Pro Asp Gln Tyr Lys Arg Pro Ser Glu  
 210 215 220  
  
 15 <210> 958  
 <211> 93  
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 <213> Homo sapiens  
  
 20 <400> 958  
 Phe Ser Lys Cys Ser Ala Ser Asn Ile Phe Leu Phe Lys Lys Phe Leu  
 1 5 10 15  
 Val Ser Phe Leu Ala Phe Glu Val Leu Val Ile Val Asp Leu Phe His  
 20 25 30  
 25 Lys Leu Cys Asn Ser Glu Ile Leu Val Phe Ser Lys Cys Leu Phe Tyr  
 35 40 45  
 Ile Thr Asp Asn Phe Lys Met Phe Ser Leu Cys Ala Val Ser Ile Asp  
 50 55 60  
 Ser Asn Val Ser Ser Phe Lys Pro Asn Ile Tyr Asp Phe His Ile Trp  
 65 70 75 80  
 30 Asn Leu Lys Thr Lys Ile His Gln Gly Val Met Leu Thr  
 85 90  
  
 <210> 959  
 35 <211> 93  
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 40 Phe Ser Lys Cys Ser Ala Ser Asn Ile Phe Leu Phe Lys Lys Phe Leu  
 1 5 10 15  
 Val Ser Phe Leu Ala Phe Glu Val Leu Val Ile Val Asp Leu Phe His  
 20 25 30  
 Lys Leu Cys Asn Ser Glu Ile Leu Val Phe Ser Lys Cys Leu Phe Tyr  
 35 40 45  
 45 Ile Thr Asp Asn Phe Lys Met Phe Ser Leu Cys Ala Val Ser Ile Asp  
 50 55 60  
 Ser Asn Val Ser Ser Phe Lys Pro Asn Ile Tyr Asp Phe His Ile Trp  
 65 70 75 80  
 50 Asn Leu Lys Thr Lys Ile His Gln Gly Val Met Leu Thr  
 85 90  
  
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 <213> Homo sapiens  
  
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 60 Trp Trp Asn His Phe Arg Ser Lys Asn Val Arg Arg Ile Asn Leu Gln  
 1 5 10 15  
 Lys Asn Ile Ile Gly Ser Ser Pro Val Ala Asp Phe Ser Ala Ile Lys  
 20 25 30  
 Glu Leu Asp Thr Leu Asn Asn Glu Ile Val Asp Leu Gln Arg Glu Lys  
 362



35 40 45  
 Asn Asn Val Glu Gln Asp Leu Lys Glu Lys Glu Asp Thr Ile Lys Gln  
 50 55 60  
 Arg Thr Ser Glu Val Gln Asp Leu Gln Asp Glu Val Gln Arg Glu Asn  
 5 65 70 75 80  
 Thr Asn Leu Gln Lys Leu Gln Ala Gln Lys Gln Gln Val Gln Glu Leu  
 85 90 95  
 Leu Asp Glu Leu Asp Glu Gln Lys Ala Gln Leu Glu Glu Gln Leu Lys  
 100 105 110  
 10 Glu Val Arg Lys Lys Cys Ala Glu Glu Ala Gln Leu Ile Ser Ser Leu  
 115 120 125  
 Lys Ala Glu Leu Thr Ser Gln Glu Ser Gln Ile Ser Thr Tyr Glu Glu  
 130 135 140  
 Glu Leu Ala Lys Ala Arg Glu Glu Leu Ser Arg Leu Gln Gln Glu Thr  
 15 145 150 155 160  
 Gln Asn Trp Arg Xaa Ser Val Lys Ser Gly Lys Ala Gln Phe Xaa Thr  
 165 170 175  
 Xaa Leu Ala Ala Pro Thr Arg Phe Thr Xaa Lys Leu Val Gln Cys  
 180 185 190  
 20 Gln

<210> 961  
 <211> 82  
 25 <212> PRT  
 <213> Homo sapiens

<400> 961  
 Leu Thr Tyr Arg Gly Lys Arg Ile Met Trp Asn Arg Thr Leu Arg Arg  
 30 1 5 10 15  
 Arg Lys Ile Leu Leu Asn Arg Gly Gln Val Arg Phe Arg Ile Phe Lys  
 20 25 30  
 Met Lys Phe Lys Gly Arg Ile Leu Ile Cys Lys Asn Tyr Arg Pro Arg  
 35 35 40 45  
 Asn Ser Arg Tyr Arg Asn Ser Leu Met Asn Trp Met Ser Arg Lys Pro  
 50 55 60  
 Ser Trp Arg Ser Asn Ser Arg Lys Ser Glu Arg Asn Val Leu Arg Arg  
 65 70 75 80  
 Pro Asn

<210> 962  
 <211> 219  
 <212> PRT  
 45 <213> Homo sapiens

<400> 962  
 Ala Ala Gln Leu Ser Leu Thr Gln Leu Ser Ser Gly Asn Pro Val Tyr  
 1 5 10 15  
 50 Glu Lys Tyr Tyr Arg Gln Val Asp Thr Gly Asn Thr Gly Arg Val Leu  
 20 25 30  
 Ala Ser Asp Ala Ala Ala Phe Leu Lys Lys Ser Gly Leu Pro Asp Leu  
 35 40 45  
 Ile Leu Gly Lys Ile Trp Asp Leu Ala Asp Thr Asp Gly Lys Gly Ile  
 55 50 55 60  
 Leu Asn Lys Gln Glu Phe Phe Val Ala Leu Arg Leu Val Ala Cys Ala  
 65 70 75 80  
 Gln Asn Gly Leu Glu Val Ser Leu Ser Ser Leu Asn Leu Ala Val Pro  
 85 90 95  
 60 Pro Pro Arg Phe His Asp Thr Ser Ser Pro Leu Leu Ile Ser Gly Thr  
 100 105 110  
 Ser Ala Ala Glu Leu Pro Trp Ala Val Lys Pro Glu Asp Lys Ala Lys  
 115 120 125

Tyr Asp Ala Ile Phe Asp Ser Leu Ser Pro Val Asn Gly Phe Leu Ser  
 130 135 140  
 Gly Asp Lys Val Lys Pro Val Leu Leu Asn Ser Lys Leu Pro Val Asp  
 145 150 155 160  
 5 Ile Leu Gly Arg Val Trp Glu Leu Ser Asp Ile Asp His Asp Gly Met  
 165 170 175  
 Leu Asp Arg Xaa Xaa Phe Ala Val Ala Met Phe Leu Val Tyr Xaa Ala  
 180 185 190  
 Thr Gly Lys Lys Asn Leu Cys Gln Cys Pro Cys Xaa Gln Pro Trp Val  
 195 200 205  
 10 Pro Pro Ile Leu Arg Lys Lys Thr Xaa Val Gly  
 210 215  
 <210> 963  
 15 <211> 109  
 <212> PRT  
 <213> Homo sapiens  
 <400> 963  
 20 Leu Ala Lys Asp Tyr Trp Tyr His Glu Ile Leu Val Glu Glu Gln Pro  
 1 5 10 15  
 Gly Ser Asn Tyr Leu Val Lys Leu Pro Ile His Ser Gly His Met Pro  
 20 25 30  
 Gln Asp Ala Lys Gln Gln Arg Ile Leu Val Cys Ser Gly Tyr Leu Cys  
 35 40 45  
 25 His Leu Cys Arg Leu Asn Pro Lys Ser Phe Gln Val Ser Ser Leu Glu  
 50 55 60  
 Ala Leu Ile Phe Ser Gly Lys Gln Gln His Gln Lys Pro Thr Pro Phe  
 65 70 75 80  
 30 Gln Tyr Cys Leu Tyr Gln Pro Val Tyr Ser Ile Phe His Ile Gln Asp  
 85 90 95  
 Ser His Leu Ile Thr Val Ser Glu Arg Ala Gly Pro Pro  
 100 105  
 35 <210> 964  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens  
 <400> 964  
 40 Pro Thr Xaa Val Phe Phe Leu Lys Met Gly Gly Thr Gln Gly Xaa Arg  
 1 5 10 15  
 Gln Gly His Trp His Arg Phe Phe Phe Pro Val Xaa Gln Tyr Thr Lys  
 20 25 30  
 45 Asn Met Ala Thr Ala Xaa Ser Xaa Leu Ser Ser Ile Pro Ser Trp Ser  
 35 40 45  
 Ile Ser Leu Asn Ser Gln Thr Leu Pro Arg Ile Ser Thr Gly Asn Leu  
 50 55 60  
 Glu Leu Ser Asn Thr Gly Phe Thr Leu Ser Pro Asp Arg Asn Pro Phe  
 65 70 75 80  
 50 Thr Gly Leu Lys Leu Ser Asn Ile Ala Ser Tyr Leu Ala Leu Ser Ser  
 85 90 95  
 Gly Phe Thr Ala His Gly Ser Ser Ala Ala Glu Val Pro Leu Ile Ser  
 100 105 110  
 55 Lys Gly Leu Leu Val Ser  
 115  
 <210> 965  
 <211> 78  
 60 <212> PRT  
 <213> Homo sapiens  
 <400> 965

Thr Gly Gln Gly Pro Xaa Lys Xaa Arg Met Ala Ala Met Leu Xaa Leu  
 1 5 10 15  
 Leu Leu Ala Leu Tyr Leu Met Xaa Ile Phe Xaa Gly Xaa Lys Phe Xaa  
 20 25 30  
 5 Pro Xaa Leu Ser Leu Lys Arg Asn Ile Xaa Phe Xaa Thr Xaa Phe Val  
 35 40 45  
 Arg Asn Arg Xaa Xaa Phe Ile Ser Gln Pro Pro Trp Xaa Gly Phe Gly  
 50 55 60  
 Gly Pro Lys Asn Xaa Xaa Lys Xaa Xaa Phe Phe Lys  
 10 65 70 75

&lt;210&gt; 966

&lt;211&gt; 181

&lt;212&gt; PRT

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 966

Glu Leu Thr Val Phe Gln Ser Lys Asp Val Pro Glu Lys Thr Ser Ser  
 1 5 10 15  
 20 Pro Glu Glu Ser Ile Arg Met Thr Lys Gly Ile Thr Met Ala Thr Ala  
 20 25 30  
 Lys Ala Val Ala Ala Gly Asn Ser Cys Arg Gln Glu Asp Val Ile Ala  
 35 40 45  
 Thr Ala Asn Leu Ser Arg Lys Ala Val Ser Asp Met Leu Thr Ala Cys  
 50 55 60  
 25 Lys Gln Ala Ser Phe His Pro Asp Val Ser Asp Glu Val Arg Thr Arg  
 65 70 75 80  
 Ala Leu Arg Phe Gly Thr Glu Cys Thr Leu Gly Tyr Leu Asp Leu Leu  
 85 90 95  
 30 Glu His Val Leu Val Ile Leu Gln Lys Pro Thr Pro Glu Phe Lys Gln  
 100 105 110  
 Gln Leu Ala Ala Phe Ser Lys Arg Val Ala Gly Ala Val Thr Glu Leu  
 115 120 125  
 Ile Gln Ala Ala Glu Ala Met Lys Gly Thr Glu Trp Val Asp Pro Glu  
 130 135 140  
 35 Asp Pro Thr Val Ile Ala Glu Thr Glu Leu Leu Gly Ala Ala Ala Ser  
 145 150 155 160  
 Ile Glu Ala Ala Ala Lys Lys Leu Glu Gln Leu Lys Pro Arg Ala Lys  
 165 170 175  
 40 Pro Lys Gln Ala Gly  
 180

&lt;210&gt; 967

&lt;211&gt; 90

&lt;212&gt; PRT

45 &lt;213&gt; Homo sapiens

&lt;400&gt; 967

Leu Ser Thr Gly Ser Arg Gly Phe Val Trp Met Thr Leu Cys Glu Leu  
 1 5 10 15  
 Lys Gln Pro Leu Gln Gly Lys Glu Pro Thr Asp Cys Ile Thr Ala Pro  
 20 25 30  
 Ala His Gln Ala Pro Thr Ala Phe Arg Asn Xaa Ala Leu Trp Thr Thr  
 35 40 45  
 55 Glu Glu Gln Asn Asn Arg Ser Val Phe Trp Ala Thr Lys Tyr Xaa Met  
 50 55 60  
 Gly Leu Gly Cys Thr Arg Ser Leu His Thr Glu Ala Xaa Lys Arg Ala  
 65 70 75 80  
 Asn Arg Gly Gly Asn Phe Ser Pro Pro Gly  
 85 90

&lt;210&gt; 968

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 968

5 Asn Ser Leu Cys Arg Val Arg Ser Pro Gln Thr Val Leu Gln Pro Leu  
 1 5 10 15  
 Leu Thr Lys Pro Arg Arg Pro Ser Ala Thr Xaa Pro Phe Gly Leu Arg  
 20 25 30  
 Arg Asn Lys Ile Ile Val Gln Phe Ser Gly Pro Gln Asn Thr Xaa Trp  
 35 40 45  
 10 Val Trp Val Val Gln Gly Ala Tyr Thr Arg Arg Gln Xaa Ser Val Gln  
 50 55 60  
 Thr Gly Ala Gly Ile Phe His Pro Leu Gly Glu Pro Val Leu Lys Thr  
 65 70 75 80  
 15 Trp Lys Glu Asp Leu Ser His Pro Pro Gly Val His Thr Gly Leu Cys  
 85 90 95  
 Phe Trp Leu Leu  
 100

&lt;210&gt; 969

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 969

25 Gly Leu Lys Xaa Xaa Ala Lys Met Arg Pro Xaa Gly Asn Ala Xaa Gly  
 1 5 10 15  
 Xaa Ile Gly Gln Thr Val Phe Xaa Lys Xaa Trp Ala Xaa Ser Glu Thr  
 20 25 30  
 30 Xaa Pro Xaa Xaa Pro Gly Xaa Ser Xaa Lys Xaa Xaa Gly Val Val Phe  
 35 40 45  
 Thr Phe Leu Ser Arg Gly His Xaa Trp Asn Val Arg Met Ser Xaa Val  
 50 55 60  
 Lys Cys Xaa Thr Gln Asn Ser Phe Ala Xaa Ser Xaa His Ala Ser Xaa  
 65 70 75 80  
 35 Cys Xaa Arg Lys Xaa Gly Cys Thr Phe His Gly Leu Val Thr Asn Lys  
 85 90 95  
 Glu Lys Ser Val Leu Cys Cys Xaa Gln Thr Leu Trp Leu Leu Val  
 100 105 110  
 40 Leu Leu Leu Gly Leu Leu Leu Asp Leu Phe Met Ile Leu  
 115 120 125

&lt;210&gt; 970

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 970

50 Asn Xaa Pro Xaa Xaa Ser Arg Xaa Lys Xaa Glu Xaa Xaa Gly Gly Cys  
 1 5 10 15  
 Phe His Ile Phe Val Pro Trp Ala Xaa Val Glu Cys Ser Tyr Val Xaa  
 20 25 30  
 Gly Lys Met Xaa Tyr Pro Lys Phe Phe Cys Arg Xaa Xaa Ser Cys Leu  
 35 40 45  
 55 Xaa Val Xaa Gln Lys Xaa Gly Val His Val Ser Trp Thr Cys Tyr Gln  
 50 55 60  
 Gln Arg Lys Val Ser Ile Met Leu Xaa Ser Asp Thr Leu Ala Phe Val  
 65 70 75 80  
 Gly Pro Ser Leu Arg Pro Ala Pro Gly Pro Leu Tyr Asp Ile Val Ile  
 85 90 95  
 60 Gly Lys Lys Ile Ile Asp Val Ile Glu Tyr Ser Ser Ser Ser Gln Glu  
 100 105 110  
 Lys Thr Glu Ala Gly Val Gly His Gly Ser

115 120

5 <210> 971  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens

<400> 971

10 Cys Ile Lys Gln Glu Leu Thr Val Phe Gln Ser Lys Asp Val Pro Glu  
 1 5 10 15  
 Lys Thr Ser Ser Pro Glu Glu Ser Ile Xaa Met Thr Lys Gly Ile Thr  
 20 25 30  
 Met Ala Thr Ala Lys Ala Val Ala Ala Gly Asn Ser Cys Xaa Gln Glu  
 35 40 45  
 15 Asp Val Ile Ala Thr Ala Asn Leu Ser Arg Lys Ala Val Ser Asp Met  
 50 55 60  
 Leu Thr Ala Cys Lys Gln Ala Ser Phe His Pro Asp Val Ser Asp Glu  
 65 70 75 80  
 Val Arg Thr Xaa Ala Leu Arg Phe Gly Thr Glu Cys Thr Leu Gly Tyr  
 85 90 95  
 20 Leu Asp Leu Leu Glu His Val Leu Val Ile Leu Gln Lys Pro Thr Pro  
 100 105 110  
 Glu Phe Lys Gln Gln Leu Ala Ala Phe Ser Lys Arg Val Ala Gly Ala  
 115 120 125  
 25 Val Thr Glu Leu Ile Gln Ala Ala Glu Ala Met Lys Gly Thr Glu Trp  
 130 135 140  
 Val Asp Pro Glu Asp Pro Thr Val Ile Ala Glu Thr Glu Leu Leu Gly  
 145 150 155 160  
 Ala Ala Ala Ser Ile Glu Ala Ala Cys  
 165

30 <210> 972  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 972

40 Arg Gly Glu Asn Xaa Ser Leu Ala Phe Arg Asp Gly Val His Pro Trp  
 1 5 10 15  
 Leu Leu Gly Pro Pro Gly Ala Arg Leu Gly Asp Ser Ser Glu Thr Asn  
 20 25 30  
 Pro Arg Ile Gln Ala Ala Ala Gly Arg Phe Leu Gln Ala Ser Arg Arg  
 35 40 45  
 Arg Cys Asp Arg Ala His Pro Gly Gly Gly Ser His Glu Arg Asn Arg  
 50 55 60  
 Val Gly Gly Ser Arg Arg Pro Asn Cys His Cys Arg Asn Arg Val Thr  
 65 70 75 80  
 Gly Gly Cys Ser Ile His Arg Ser Cys Leu Leu Lys Lys Leu Glu Gln  
 85 90 95  
 50 Leu Lys Pro Arg Ala Lys Pro Lys Gln Ala Asp Glu Thr Leu Gly Leu  
 100 105 110

55 <210> 973  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 973

60 Leu Cys Phe Cys Asn Asp Ser Trp Val Phe Trp Ile His Pro Leu Cys  
 1 5 10 15  
 Ser Phe His Gly Phe Arg Arg Leu Asp Glu Leu Cys His Ser Ala Gly  
 20 25 30  
 Asp Ser Leu Gly Glu Ser Gly Gln Leu Leu Glu Phe Trp Gly Trp

35 40 45  
 Phe Leu Lys Asn His Gln Asp Val Leu Gln Glu Val Gln Val Ala Lys  
 50 55 60  
 Gly Ala Leu Arg Pro Glu Thr Gln Gly Xaa Gly Ser His Leu Val Thr  
 5 65 70 75 80  
 Asp Ile Gly Val Glu Gly Cys Leu Leu Ala Ser Arg Gln His Ile  
 85 90 95  
  
 <210> 974  
 10 <211> 95  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 974  
 15 Pro Arg Val His Ser Val Pro Lys Arg Lys Ala Xaa Val Leu Thr Ser  
 1 5 10 15  
 Ser Leu Thr Ser Gly Trp Lys Asp Ala Cys Leu Gln Ala Val Asn Ile  
 20 20 25 30  
 Ser Asp Thr Ala Phe Arg Leu Arg Leu Ala Val Ala Ile Thr Ser Ser  
 35 40 45  
 Cys Xaa His Glu Phe Pro Ala Ala Thr Ala Leu Ala Val Ala Met Val  
 50 55 60  
 Met Pro Phe Val Ile Xaa Met Asp Ser Ser Gly Asp Asp Val Phe Ser  
 65 70 75 80  
 25 Gly Thr Ser Phe Asp Trp Asn Thr Val Ser Ser Cys Phe Met His  
 85 90 95  
  
 <210> 975  
 <211> 159  
 30 <212> PRT  
 <213> Homo sapiens  
  
 <400> 975  
 35 Arg Xaa Xaa Gly Gly Thr Gln Lys Gly Xaa Pro Gln Xaa Met Ala Pro  
 1 5 10 15  
 Xaa Xaa Asn Trp Thr Asn Lys Phe Ser Xaa Lys Val Gly Pro Leu Ser  
 20 25 30  
 Trp Lys Xaa Ala Pro Xaa Xaa Pro Gly Xaa Ser Leu Glu Xaa Leu Xaa  
 35 40 45  
 40 Xaa Leu Phe Ser His Phe Leu Ser Pro Trp Ala Xaa Gly Gly Met Phe  
 50 55 60  
 Xaa Met Ser His Gly Tyr Asn Cys Leu Thr His Lys Phe Phe Cys Arg  
 65 70 75 80  
 Xaa Pro Ser Cys Xaa Xaa Val Xaa Gln Xaa Xaa Gly Val His Val Ser  
 85 90 95  
 45 Trp Thr Cys Tyr Gln Gln Arg Lys Val Ser Ile Met Leu Phe Ser Asp  
 100 105 110  
 Thr Leu Ala Phe Val Gly Pro Ser Leu Arg Pro Ala Pro Gly Pro Leu  
 115 120 125  
 50 Tyr Asp Ile Val Ile Gly Lys Lys Ile Ile Asp Val Ile Glu Tyr Ser  
 130 135 140  
 Ser Ser Ser Gln Glu Lys Thr Glu Ala Gly Val Gly His Gly Ser  
 145 150 155  
  
 55 <210> 976  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens  
  
 60 <400> 976  
 Xaa Trp Asn Pro Lys Gly Glu Xaa Pro Gly Xaa Gly Pro Trp Xaa Xaa  
 1 5 10 15  
 Leu Asp Lys Gln Val Phe Xaa Lys Gly Trp Ala Ile Lys Leu Glu Thr

20 25 30  
 Xaa Pro Xaa Xaa Ser Arg Val Xaa Pro Gly Xaa Pro Xaa Xaa Phe Val  
 35 40 45  
 Phe Thr Phe Phe Val Pro Val Gly His Xaa Trp Asn Val Arg Xaa Val  
 5 50 55 60  
 Thr Arg Val Gln Leu Ser Tyr Pro Gln Ile Leu Leu Pro Xaa Pro Phe  
 65 70 75 80  
 Met Xaa His Xaa Xaa Ser Glu Xaa Arg Gly Ala Arg Phe Met Asp Leu  
 85 90 95  
 10 Leu Pro Thr Lys Lys Ser Gln Tyr Tyr Val Val Leu Arg His Phe Gly  
 100 105 110  
 Phe Cys Trp Ser Phe Ser  
 115  
 15 <210> 977  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens  
 20 <400> 977  
 Trp Leu Xaa Ala Ser Xaa Cys Ser Val Leu Met Cys Val Ser Trp Lys  
 1 5 10 15  
 Xaa Ala Arg Leu Ala Ala Gln Arg Gly Gln Ser Val Arg Leu Trp Leu  
 20 25 30  
 25 Xaa Arg Gly Cys Arg Arg Xaa Leu Trp Gly Xaa Arg Leu Xaa Leu Arg  
 35 40 45  
 Gly Arg Leu Arg Gly Arg Arg Gly Leu Trp Gly Leu Leu Arg Gly Trp  
 50 55 60  
 Arg Arg Arg Leu Leu Leu Gly His Pro His Val Ala Arg Ala Arg Arg  
 65 70 75 80  
 30 Gly Gly Arg Gly Ala Ala Asp Ala Val Ala Ala Arg Val Gly Asp Leu  
 85 90 95  
 Ala Val Arg Gly Arg His Pro Arg Val Ala Val Gly Arg Gln Val Leu  
 100 105 110  
 35 Val Lys Leu Val Asp Ile Glu Gly Leu Asp Val Gly Asp Asp Val Ala  
 115 120 125  
 Ala Gln Leu Ala Asp Val His Val Ala Glu Val Asp Arg  
 130 135 140  
 40 <210> 978  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens  
 45 <400> 978  
 Leu Glu Xaa Gly Pro Ala Ser Cys Ser Ala Trp Ser Glu Cys Ala Pro  
 1 5 10 15  
 Val Ala Ala Xaa Gly Val Pro Pro Xaa Ala Val Gly Xaa Pro Pro Thr  
 20 25 30  
 50 Xaa Ala Gly Ala Pro Ala Gly Pro Ala Gly Pro Val Gly Ala Ala Ala  
 35 40 45  
 Gly Val Ala Ala Ala Pro Ala Ala Trp Thr Ser Thr Arg Gly Pro Arg  
 50 55 60  
 Ser Pro Gly Trp Pro Arg Cys Cys  
 55 65 70  
 <210> 979  
 <211> 96  
 <212> PRT  
 60 <213> Homo sapiens  
 <400> 979  
 Pro Ile Asp Phe Arg Asp Val Asp Ile Gly Glu Leu Ser Ser Asp Val

1 5 10 15  
 Ile Ser Asn Ile Glu Thr Phe Asp Val Asn Glu Phe Asp Gln Tyr Leu  
 20 30  
 Pro Pro Asn Gly His Pro Gly Val Pro Ala Thr His Gly Gln Val Thr  
 35 40 45  
 Tyr Thr Gly Ser Tyr Gly Ile Ser Ser Thr Ala Ala Thr Pro Ala Ser  
 50 55 60  
 Ala Gly His Val Trp Met Ser Lys Gln Gln Ala Pro Pro Pro Pro Pro  
 65 70 75 80  
 10 Gln Gln Pro Pro Gln Ala Pro Pro Ala Pro Gln Ala Pro Pro Gln Xaa  
 85 90 95

15 <210> 980  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 980  
 20 Ala Ala Thr Ser Ser Pro Thr Ser Arg Pro Ser Met Ser Thr Ser Leu  
 1 5 10 15  
 Thr Ser Thr Cys Arg Pro Thr Ala Thr Arg Gly Cys Arg Pro Arg Thr  
 20 25 30  
 Ala Arg Ser Pro Thr Arg Ala Ala Thr Ala Ser Ala Ala Pro Arg Pro  
 35 40 45  
 25 Pro Arg Arg Ala Arg Ala Thr Cys Gly Cys Pro Ser Arg Arg Arg  
 50 55 60  
 Arg His Pro Arg Ser Ser Pro His Arg Pro Arg Arg Pro Arg Arg Arg  
 65 70 75 80  
 Pro Arg Xaa Arg Arg Arg Xaa Pro His Ser Xaa Arg Arg His Pro Xaa  
 30 85 90 95  
 Ser Ser His Arg Arg Thr Leu  
 100

35 <210> 981  
 <211> 164  
 <212> PRT  
 <213> Homo sapiens

<400> 981  
 40 Asp Ala Gly Ala His Ala Gly Ala Arg Gln Arg Leu Gln Gln Glu Gln  
 1 5 10 15  
 Ala Ala Arg Gln Ala Ala His Glu Arg Leu His Gly Val Gly Ala Gly  
 20 25 30  
 Gly Ala Gln Glu Ala Arg Gly Pro Val Pro Ala Leu Ala Gln Arg Arg  
 35 40 45  
 45 Ala Gln Gln Asp Ala Gly Gln Ala Leu Glu Thr Ser Glu Arg Glu Arg  
 50 55 60  
 Glu Ala Ala Leu Arg Gly Gly Gly Ala Ala Arg Ala Ala Gln  
 65 70 75 80  
 50 Glu Gly Pro Pro Gly Leu Gln Val Pro Ala Ala Ala Glu Glu Val Gly  
 85 90 95  
 Glu Glu Arg Ala Gly Gly Gly Arg Gly Gly His Gly Ala Asp Ala His  
 100 105 110  
 Leu Pro Gln Arg His Leu Gln Gly Ala Ala Gly Arg Leu Ala Thr Leu  
 115 120 125  
 55 Leu Xaa Arg His Glu Arg Gly Ala Leu Pro Arg Arg Ala Leu Gly Ala  
 130 135 140  
 Ile Pro Gly Pro Thr Asp Pro Thr His His Pro Gln Asn Arg Arg Ala  
 145 150 155 160  
 60 Ala Gly Gln Gly

<210> 982



<211> 192  
 <212> PRT  
 <213> Homo sapiens

5           <400> 982  
 Thr Leu Val Pro Met Pro Val Arg Val Asn Gly Ser Ser Lys Asn Lys  
   1                   5                   10                   15  
 Pro His Val Lys Arg Pro Met Asn Ala Phe Met Val Trp Ala Gln Ala  
               20                   25                   30  
 10 Ala Arg Arg Lys Leu Ala Asp Gln Tyr Pro His Leu His Asn Ala Glu  
               35                   40                   45  
 Leu Ser Lys Thr Leu Gly Lys Leu Trp Arg Leu Leu Asn Glu Ser Glu  
               50                   55                   60  
 Lys Arg Pro Phe Val Glu Glu Ala Glu Arg Leu Arg Val Gln His Lys  
 15 65                   70                   75                   80  
 Lys Asp His Pro Asp Tyr Lys Tyr Gln Pro Arg Arg Arg Lys Ser Val  
                   85                   90                   95  
 Lys Asn Gly Gln Ala Glu Ala Glu Glu Ala Thr Glu Gln Thr His Ile  
               100                   105                   110  
 20 Ser Pro Asn Ala Ile Phe Lys Ala Leu Gln Ala Asp Ser Pro His Ser  
               115                   120                   125  
 Ser Xaa Gly Met Ser Glu Val His Ser Pro Gly Glu His Ser Gly Gln  
               130                   135                   140  
 Ser Gln Gly Pro Pro Thr Pro Pro Thr Thr Pro Lys Thr Asp Val Gln  
 25 145                   150                   155                   160  
 Pro Gly Lys Ala Asp Leu Lys Arg Glu Gly Arg Pro Leu Pro Glu Gly  
                   165                   170                   175  
 Gly Arg Gln Ala Pro Tyr Arg Leu Ser Arg Arg Gly His Xaa Ala Ser  
                   180                   185                   190

30           <210> 983  
             <211> 196  
             <212> PRT  
             <213> Homo sapiens

35           <400> 983  
 Arg Arg Cys Ser Ala Arg Xaa Met Ser Thr Ser Arg Lys Ser Ile Gly  
   1                   5                   10                   15  
 Gly Leu Ser Ala Pro Leu Trp Gln Gly Ala Pro Leu Ser Leu Gln Val  
 40                20                   25                   30  
 Ser Leu Ala Arg Leu His Val Gly Phe Gly Gly Gly Gly Trp Gly Arg  
               35                   40                   45  
 Trp Ala Leu Gly Leu Pro Arg Val Leu Ala Gly Gly Val His Leu Ala  
               50                   55                   60  
 45 His Ala Xaa Gly Gly Val Trp Arg Val Gly Leu Gln Arg Leu Glu Asp  
               65                   70                   75                   80  
 Gly Val Gly Gly Asp Val Arg Leu Leu Arg Gly Leu Leu Cys Leu Arg  
                   85                   90                   95  
 Leu Pro Val Leu His Arg Leu Pro Pro Pro Arg Leu Val Leu Val Ile  
 50                100                   105                   110  
 Arg Val Val Leu Leu Val Leu His Ala Gln Pro Leu Arg Leu Leu His  
               115                   120                   125  
 Glu Gly Pro Leu Leu Ala Leu Val Gln Lys Ser Pro Glu Leu Ala Gln  
               130                   135                   140  
 55 Arg Leu Ala Glu Leu Gly Val Val Gln Val Arg Val Leu Val Arg Glu  
               145                   150                   155                   160  
 Leu Pro Ala Arg Arg Leu Arg Pro His His Glu Gly Val His Gly Pro  
                   165                   170                   175  
 Leu Asp Val Arg Leu Val Leu Ala Gly Ala Val Asp Ala His Arg His  
 60                180                   185                   190  
 Gly His Gln Arg  
               195

<210> 984  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens

5

<400> 984  
 Met Ser Leu Arg Lys Lys Lys Lys Lys Lys Lys Gln Xaa Gln Asn Lys  
 1 5 10 15  
 Lys Xaa Lys Lys Thr Pro Met Ser Lys Gly Glu Phe Trp Val Xaa Ser  
 10 20 25 30  
 Phe Ser Phe Phe Gly Leu Phe Phe Arg Asp His Leu Xaa His Xaa Arg  
 35 40 45  
 Pro Leu Trp Gly Gly Pro Pro Gln Xaa Ser Xaa Trp Lys Leu Gly Xaa  
 50 55 60  
 Xaa Thr Gly Phe Val Xaa Lys Xaa Leu Gly Gly Leu Gly Gly Xaa Xaa  
 15 65 70 75 80  
 Pro Gly Met Xaa Lys Gly Asp Pro His Xaa Gly Val Arg Ala Xaa Xaa  
 85 90 95  
 Gly Gly Trp

20

<210> 985  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

25

<400> 985  
 Gly Arg Arg Arg Arg Arg Lys Asn Lys Xaa Lys Ile Lys Lys Xaa Lys  
 1 5 10 15  
 Lys His Gln Cys Pro Lys Gly Asn Ser Gly Xaa Gly Pro Ser Leu Ser  
 30 20 25 30  
 Ser Gly Tyr Phe Leu Gly Ile Ile Xaa Ala Xaa Xaa Ala Leu Cys Gly  
 35 40 45  
 Glu Ala Leu Leu Xaa Gly Pro Xaa Gly Asn Leu Gly Xaa Xaa Pro Gly  
 50 55 60  
 Leu Xaa Pro Asn Xaa Trp Gly Gly Leu Val Gly Xaa Xaa Arg Gly Xaa  
 65 70 75 80  
 Gly Lys Gly Thr Pro Ile Xaa Val Phe Gly Pro Xaa Xaa Gly Gly Gly  
 85 90 95

40

<210> 986  
 <211> 133  
 <212> PRT  
 <213> Homo sapiens

45

<400> 986  
 Gly His Pro Glu Gly Pro Gly Ala His Leu Asp Met Asn Ser Leu Asp  
 1 5 10 15  
 Arg Ala Gln Ala Ala Lys Asn Lys Gly Asn Lys Tyr Phe Lys Ala Gly  
 50 20 25 30  
 Lys Tyr Glu Gln Ala Ile Gln Cys Tyr Thr Glu Ala Ile Ser Leu Cys  
 35 40 45  
 Pro Thr Glu Lys Asn Val Asp Leu Ser Thr Phe Tyr Gln Asn Arg Ala  
 50 55 60  
 Ala Ala Phe Glu Gln Leu Gln Lys Trp Lys Glu Val Ala Gln Asp Cys  
 55 65 70 75 80  
 Thr Lys Ala Val Glu Leu Asn Pro Lys Tyr Val Lys Ala Leu Phe Arg  
 85 90 95  
 Arg Ala Lys Ala His Glu Lys Leu Asp Asn Lys Lys Glu Cys Leu Glu  
 100 105 110  
 Asp Val Thr Ala Val Cys Ile Leu Glu Gly Phe Gln Asn Gln Gln Ser  
 115 120 125  
 Met Leu Leu Ala Arg

130

5 <210> 987  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 987  
 10 Leu Leu Met Gly Phe Cys Thr Ser Lys Glu Ser Phe His Ile Phe Gly  
 1 5 10 15  
 Ile Lys Phe Asn Ser Phe Cys Thr Val Leu Cys His Phe Phe Pro Phe  
 20 25 30  
 Leu Gln Leu Phe Lys Gly Ser Ser Ser Val Leu Ile Lys Cys Arg Lys  
 35 40 45  
 15 Val Asn Ile Leu Leu Cys Arg Ala Gln Ala Asn Ser Leu Ser Ile Ala  
 50 55 60  
 Leu Asn Ser Leu Phe Ile Phe Ser Cys Phe Lys Ile Phe Ile Ala Phe  
 65 70 75 80  
 20 Ile Leu Gly Cys Leu Gly Ser Ile Lys Arg Val His Val Gln Val Ser  
 85 90 95  
 Thr Gly Thr Phe Arg Val Ser  
 100

25 <210> 988  
 <211> 64  
 <212> PRT  
 <213> Homo sapiens

<400> 988  
 30 Asn Gly Thr Cys Phe Ser Phe Leu Cys Val Ser Leu Pro Asn Pro Lys  
 1 5 10 15  
 Met Lys Glu Gly Arg Arg Val Glu Glu Asn Val Ser Val Asn Val Asn  
 20 25 30  
 Thr Ala Met Gln Ile Lys Thr Phe Leu Lys Ser Glu Val Ile Gln Arg  
 35 35 40 45  
 Cys Arg Thr Phe Leu Tyr Leu Gly Val Ile Arg Arg Cys Ile Ile Ser  
 50 55 60

40 <210> 989  
 <211> 77  
 <212> PRT  
 <213> Homo sapiens

<400> 989  
 45 Met Thr Ser Asp Phe Lys Lys Val Phe Ile Cys Met Ala Val Phe Thr  
 1 5 10 15  
 Leu Thr Leu Thr Phe Ser Ser Thr Leu Leu Pro Ser Phe Ile Leu Gly  
 20 25 30  
 Leu Gly Arg Glu Thr Gln Arg Lys Leu Lys His Val Pro Phe Tyr Thr  
 35 40 45  
 50 Val Ile Pro Asn Ser His Gly Leu Leu Pro Val Val Lys Met Phe Glu  
 50 55 60  
 Thr Ala Leu Lys Ala Ala Ser Val Cys Ile Phe Leu Leu  
 65 70 75

55 <210> 990  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

60 <400> 990  
 Pro Gly Ser Gly His Pro Glu Gly Pro Gly Ala His Leu Asp Met Asn  
 1 5 10 15

Ser Leu Asp Arg Ala Gln Ala Ala Lys Asn Lys Gly Asn Lys Tyr Phe  
                             20                            25                            30  
 Lys Ala Gly Lys Tyr Glu Gln Ala Ile Gln Cys Tyr Thr Glu Ala Ile  
                             35                            40                            45  
 5 Ser Leu Cys Pro Thr Glu Lys Asn Val Asp Leu Ser Thr Phe Tyr Gln  
                             50                            55                            60  
 Asn Arg Ala Ala Ala Phe Glu Gln Leu Gln Lys Trp Lys Glu Val Ala  
                             65                            70                            75                            80  
 10 Gln Asp Cys Thr Lys Ala Val Glu Leu Asn Pro Lys Tyr Val Lys Ala  
                             85                            90                            95  
 Leu Phe Arg Arg Ala Lys Ala His Glu Lys Leu Asp Asn Lys Lys Glu  
                             100                            105                            110  
 Cys Leu Glu Asp Val Thr Ala Val Cys Ile Leu Glu Gly Phe Gln Asn  
                             115                            120                            125  
 15 Gln Gln Ser Met Leu Leu Ala Asp Lys Val Leu Lys Leu Leu Gly Lys  
                             130                            135                            140  
 Glu Lys Ala Lys Glu Lys Tyr Lys Asn Arg Glu Pro Leu Met Pro Ser  
                             145                            150                            155                            160  
 20 Pro Gln Phe Ile Lys Ser Tyr Phe Ser Ser Phe Thr Asp Asp Ile Ile  
                             165                            170                            175  
 Ser Gln Pro Met Leu Lys Gly Glu Lys Ser Asp Glu Asp Lys Asp Lys  
                             180                            185                            190  
 Glu Gly Xaa Ala Leu Glu Val Lys Arg Lys Phe Trp Ile Leu Lys Xaa  
                             195                            200                            205  
 25 Pro Thr Val Tyr Xaa Arg Arg Lys Leu Arg  
                             210                            215  
  
                             <210> 991  
                             <211> 268  
 30                              <212> PRT  
                             <213> Homo sapiens  
  
                             <400> 991  
 35 Glu Asn Ile Met Val Phe Asn Trp Trp Ala Leu Phe Ser Glu Lys Ala  
                             1                            5                            10                            15  
 Val His Leu Gln Glu Glu Leu Ile Ala Ile Asn Ser Lys Lys Glu Glu  
                             20                            25                            30  
 Leu Asn Gln Ser Val Asn Arg Val Lys Glu Leu Glu Leu Glu Leu Glu  
                             35                            40                            45  
 40 Ser Val Lys Ala Gln Ser Leu Ala Ile Thr Lys Gln Asn His Met Leu  
                             50                            55                            60  
 Asn Glu Lys Val Lys Glu Met Ser Asp Tyr Ser Leu Leu Lys Glu Glu  
                             65                            70                            75                            80  
 45 Lys Leu Glu Leu Leu Ala Gln Asn Lys Leu Leu Lys Gln Gln Leu Glu  
                             85                            90                            95  
 Glu Ser Arg Asn Glu Asn Leu Arg Leu Leu Asn Arg Leu Ala Gln Pro  
                             100                            105                            110  
 Ala Pro Glu Leu Ala Val Phe Gln Lys Glu Leu Arg Lys Ala Glu Lys  
                             115                            120                            125  
 50 Ala Ile Val Val Glu His Glu Glu Phe Glu Ser Cys Arg Gln Ala Leu  
                             130                            135                            140  
 His Lys Gln Leu Gln Asp Glu Ile Glu His Ser Ala Gln Leu Lys Ala  
                             145                            150                            155                            160  
 Gln Ile Leu Gly Tyr Lys Ala Ser Val Lys Ser Leu Thr Thr Gln Val  
                             165                            170                            175  
 55 Ala Asp Leu Lys Leu Gln Leu Lys Gln Thr Gln Thr Ala Leu Glu Asn  
                             180                            185                            190  
 Glu Val Tyr Cys Asn Pro Lys Gln Ser Val Ile Asp Arg Ser Val Asn  
                             195                            200                            205  
 60 Gly Leu Ile Asn Gly Asn Val Val Pro Cys Asn Gly Glu Ile Ser Gly  
                             210                            215                            220  
 Asp Phe Leu Asn Asn Pro Phe Lys Gln Glu Asn Val Leu Ala Arg Met  
                             225                            230                            235                            240

Gly Ala Ser Arg Ile Thr Asn Tyr Pro Thr Ala Trp Val Glu Gly Ser  
 245 250 255  
 Ser Pro Asp Ser Asp Leu Glu Phe Val Ala Gln Tyr  
 260 265

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<210> 992  
 <211> 219  
 <212> PRT  
 <213> Homo sapiens

10

<400> 992  
 Val Lys Ala Gln Ser Leu Ala Ile Thr Lys Gln Asn His Met Leu Asn  
 1 5 10 15  
 Glu Lys Val Lys Glu Met Ser Asp Tyr Ser Leu Leu Lys Glu Glu Lys  
 20 25 30  
 Leu Glu Leu Leu Ala Gln Asn Lys Leu Leu Lys Gln Gln Leu Glu Glu  
 35 40 45  
 Ser Arg Asn Glu Asn Leu Arg Leu Leu Asn Arg Leu Ala Gln Pro Ala  
 50 55 60  
 Pro Glu Leu Ala Val Phe Gln Lys Glu Leu Arg Lys Ala Glu Lys Ala  
 65 70 75 80  
 Ile Val Val Glu His Glu Glu Phe Glu Ser Cys Arg Gln Ala Leu His  
 85 90 95  
 Lys Gln Leu Gln Asp Glu Ile Glu His Ser Ala Gln Leu Lys Ala Gln  
 100 105 110  
 Ile Leu Gly Tyr Lys Ala Ser Val Lys Ser Leu Thr Thr Gln Val Ala  
 115 120 125  
 Asp Leu Lys Leu Gln Leu Lys Gln Thr Gln Thr Ala Leu Glu Asn Glu  
 130 135 140  
 Val Tyr Cys Asn Pro Lys Gln Ser Val Ile Asp Arg Ser Val Asn Gly  
 145 150 155 160  
 Leu Ile Asn Gly Asn Val Val Pro Cys Asn Gly Glu Ile Ser Gly Asp  
 165 170 175  
 Phe Leu Asn Asn Pro Phe Lys Gln Glu Asn Val Leu Ala Arg Met Gly  
 180 185 190  
 Ala Ser Arg Ile Thr Asn Tyr Xaa Thr Ala Trp Val Xaa Gly Ser Ser  
 195 200 205  
 Pro Asp Ser Asp Leu Glu Phe Val Ala Gln Tyr  
 210 215

20

25

30

35

40

<210> 993  
 <211> 194  
 <212> PRT  
 <213> Homo sapiens

45

<400> 993  
 Met Arg Ser Leu Asn His Leu Phe Gly Phe Cys Arg Glu His Ala Lys  
 1 5 10 15  
 Ala Ser Trp Xaa Met Gly Gly Leu Ser Pro Ala Gly Xaa Tyr Val Ser  
 20 25 30  
 Cys Gly Arg Cys Cys Ser Cys Leu Cys Pro Ser His Ile Ser Thr Gln  
 35 40 45  
 Gly Val Asp Gln Lys Gln Ile Glu Xaa Gln Lys Glu Glu Glu Lys Ile  
 50 55 60  
 Arg Glu Gln Gln Val Lys Glu Arg Arg Gln Arg Glu Glu Arg Arg Gln  
 65 70 75 80  
 Ser Asn Leu Gln Glu Val Leu Glu Arg Glu Arg Arg Glu Leu Glu Lys  
 85 90 95  
 Leu Tyr Gln Glu Arg Lys Met Ile Glu Glu Ser Leu Lys Ile Lys Ile  
 100 105 110  
 Lys Lys Glu Leu Glu Met Glu Asn Glu Leu Glu Met Ser Asn Gln Glu  
 115 120 125  
 Ile Lys Asp Lys Ser Ala His Ser Glu Asn Pro Leu Glu Lys Tyr Met

50

55

60

130 135 140  
 Lys Ile Ile Gln Gln Glu Gln Asp Gln Glu Ser Ala Asp Lys Ser Ser  
 145 150 155 160  
 Lys Lys Met Val Gln Glu Gly Ser Leu Val Asp Thr Leu Gln Ser Ser  
 165 170 175  
 5 Asp Lys Val Glu Ser Leu Thr Gly Phe Ser His Glu Glu Leu Asp Asp  
 180 185 190  
 Ser Trp  
 10  
 <210> 994  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 994  
 Glu Asn Ile Met Val Phe Asn Trp Trp Ala Leu Phe Ser Glu Lys Ala  
 1 5 10 15  
 Val His Leu Gln Glu Leu Ile Ala Ile Asn Ser Lys Lys Glu Glu  
 20 20 25 30  
 Leu Asn Gln Ser Val Asn Arg Val Lys Glu Leu Glu Leu Glu Leu Glu  
 35 40 45  
 Ser Val Lys Ala Gln Ser Leu Ala Ile Thr Lys Gln Asn His Met Leu  
 50 55 60  
 25 Asn Glu Lys Val Lys Glu Met Ser Asp Tyr Ser Leu Leu Lys Glu Glu  
 65 70 75 80  
 Lys Leu Glu Leu Leu Ala Gln Asn Lys Leu Leu Lys Gln Gln Leu Glu  
 85 90 95  
 Glu Ser Arg Asn Glu Asn Leu Arg Leu Leu Asn Arg Leu Ala Gln Pro  
 100 105 110  
 30 Ala Pro Glu Leu Ala Val Phe Gln Lys Glu Leu Arg Lys Ala Glu Lys  
 115 120 125  
 Ala Ile Val Val Glu His Glu Glu Phe Glu Ser Cys Arg Gln Ala Leu  
 130 135 140  
 35 His Lys Gln Leu Gln Asp Glu Ile Glu His Ser Ala Gln Leu Lys Ala  
 145 150 155 160  
 Gln Ile Leu Gly Tyr Lys Ala Ser Val Lys Ser Leu Thr Thr Xaa Val  
 165 170 175  
 Ala Asp Leu Lys Leu Gln Leu Lys Gln Thr Gln Thr Pro  
 180 185  
 40  
 <210> 995  
 <211> 125  
 <212> PRT  
 45 <213> Homo sapiens  
 <400> 995  
 Lys Thr Glu Gly Arg Glu Lys Glu Arg Arg Gln Ser Asn Xaa Gln Glu  
 1 5 10 15  
 50 Val Leu Glu Arg Glu Arg Arg Glu Leu Glu Lys Leu Tyr Gln Glu Arg  
 20 25 30  
 Lys Met Ile Glu Glu Ser Leu Lys Ile Lys Ile Lys Lys Glu Leu Glu  
 35 40 45  
 Met Glu Asn Glu Leu Glu Met Ser Asn Gln Glu Ile Lys Asp Lys Ser  
 50 55 60  
 55 Ala His Ser Glu Asn Pro Leu Glu Lys Tyr Met Lys Ile Ile Gln Gln  
 65 70 75 80  
 Glu Gln Asp Gln Glu Ser Ala Asp Lys Ser Ser Lys Lys Met Val Gln  
 85 90 95  
 60 Glu Gly Ser Leu Val Asp Thr Leu Gln Ser Ser Asp Lys Val Glu Ser  
 100 105 110  
 Leu Thr Gly Phe Xaa His Glu Glu Leu Asp Asp Ser Trp  
 115 120 125

<210> 996  
 <211> 466  
 <212> PRT  
 5 <213> Homo sapiens  
  
 <400> 996  
 Thr Ile His Gln Val Ser Leu Asp Leu Asp Ser Leu Ala Glu Ser Pro  
 1 5 10 15  
 10 Glu Ser Asp Phe Met Ser Ala Val Asn Glu Phe Val Ile Glu Glu Asn  
 20 25 30  
 Leu Ser Ser Pro Asn Pro Ile Ser Asp Pro Gln Ser Pro Glu Met Met  
 35 40 45  
 15 Val Glu Ser Leu Tyr Ser Ser Val Ile Asn Ala Ile Asp Ser Arg Arg  
 50 55 60  
 Met Gln Asp Thr Asn Val Cys Gly Lys Glu Asp Phe Gly Asp His Thr  
 65 70 75 80  
 Ser Leu Asn Val Gln Leu Glu Arg Cys Arg Val Val Ala Gln Asp Ser  
 85 90 95  
 20 His Phe Ser Ile Gln Thr Ile Lys Glu Asp Leu Cys His Phe Arg Thr  
 100 105 110  
 Phe Val Gln Lys Glu Gln Cys Asp Phe Ser Asn Ser Leu Lys Cys Thr  
 115 120 125  
 25 Ala Val Glu Ile Arg Asn Ile Ile Glu Lys Val Lys Cys Ser Leu Glu  
 130 135 140  
 Ile Thr Leu Lys Glu Lys His Gln Lys Glu Leu Ser Leu Lys Asn  
 145 150 155 160  
 Glu Tyr Glu Gly Lys Leu Asp Gly Leu Ile Lys Glu Thr Glu Glu Asn  
 165 170 175  
 30 Glu Asn Lys Ile Lys Lys Leu Lys Gly Glu Leu Val Cys Leu Glu Glu  
 180 185 190  
 Val Leu Gln Asn Lys Asp Asn Glu Phe Ala Leu Val Lys His Glu Lys  
 195 200 205  
 35 Glu Ala Val Ile Cys Leu Gln Asn Glu Lys Asp Gln Lys Leu Xaa Glu  
 210 215 220  
 Met Glu Asn Ile Met His Ser Gln Asn Cys Glu Ile Lys Glu Leu Lys  
 225 230 235 240  
 Gln Ser Arg Glu Ile Val Leu Glu Asp Leu Lys Lys Leu His Val Glu  
 245 250 255  
 40 Asn Asp Glu Lys Leu Gln Leu Leu Arg Ala Glu Leu Gln Ser Leu Glu  
 260 265 270  
 Gln Ser His Leu Lys Glu Leu Glu Asp Thr Leu Gln Val Arg His Ile  
 275 280 285  
 45 Gln Glu Phe Glu Lys Val Met Thr Asp His Arg Val Ser Leu Glu Glu  
 290 295 300  
 Leu Lys Lys Glu Asn Gln Gln Ile Ile Asn Gln Ile Gln Glu Ser His  
 305 310 315 320  
 Ala Glu Ile Ile Gln Glu Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu  
 325 330 335  
 50 Lys Val Ser Asp Leu Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu  
 340 345 350  
 Ala Leu Lys Glu Ala Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu  
 355 360 365  
 55 Ser Arg Ala Gln Gln Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu  
 370 375 380  
 Thr Glu Asn Leu Arg Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln  
 385 390 395 400  
 Asp Asn Asn Glu Asn Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu  
 405 410 415  
 60 Met Thr Ile Glu Lys Asp Gln Cys Ile Ser Glu Leu Ile Ser Arg His  
 420 425 430  
 Glu Glu Glu Ser Asn Ile Leu Lys Ala Glu Leu Asn Lys Ser Tyr Ile  
 435 440 445

Phe Cys Ile Thr Gln Pro Phe Xaa Ile Glu Lys Asn Leu Lys Glu Pro  
 450 455 460  
 Ile Xaa  
 465

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 <210> 997  
 <211> 237  
 <212> PRT  
 <213> Homo sapiens

10  
 <400> 997  
 His Ser Gln Asn Cys Glu Ile Lys Glu Leu Lys Gln Ser Arg Glu Ile  
 1 5 10 15  
 Val Leu Glu Asp Leu Lys Lys Leu His Val Glu Asn Asp Glu Lys Leu  
 15 20 25 30  
 Gln Leu Leu Arg Ala Glu Leu Gln Ser Leu Glu Gln Ser His Leu Lys  
 35 40 45  
 Glu Leu Glu Asp Thr Leu Gln Val Arg His Ile Gln Glu Phe Glu Lys  
 50 55 60  
 20 Val Met Thr Asp His Arg Val Ser Leu Glu Glu Leu Lys Lys Glu Asn  
 65 70 75 80  
 Gln Gln Ile Ile Asn Gln Ile Gln Glu Ser His Ala Glu Ile Ile Gln  
 85 90 95  
 Glu Lys Glu Lys Gln Leu Gln Glu Leu Lys Leu Lys Val Ser Asp Leu  
 100 105 110  
 25 Ser Asp Thr Arg Cys Lys Leu Glu Val Glu Leu Ala Leu Lys Glu Ala  
 115 120 125  
 Glu Thr Asp Glu Ile Lys Ile Leu Leu Glu Glu Ser Arg Ala Gln Gln  
 130 135 140  
 30 Lys Glu Thr Leu Lys Ser Leu Leu Glu Gln Glu Thr Glu Asn Leu Arg  
 145 150 155 160  
 Thr Glu Ile Ser Lys Leu Asn Gln Lys Ile Gln Asp Asn Asn Glu Asn  
 165 170 175  
 Tyr Gln Val Gly Leu Ala Glu Leu Arg Thr Leu Met Thr Ile Glu Lys  
 180 185 190  
 35 Asp Gln Cys Ile Ser Glu Leu Ile Ser Xaa His Glu Glu Glu Ser Asn  
 195 200 205  
 Ile Leu Lys Ala Glu Xaa Asn Lys Ser Tyr Ile Phe Cys Ile Thr Gln  
 210 215 220  
 40 Pro Phe Xaa Ile Glu Lys Asn Leu Lys Glu Pro Ile Xaa  
 225 230 235

<210> 998  
 <211> 278  
 <212> PRT  
 <213> Homo sapiens

45  
 <400> 998  
 Thr Ile His Gln Val Ser Leu Asp Leu Asp Ser Leu Ala Glu Ser Pro  
 1 5 10 15  
 Glu Ser Asp Phe Met Ser Ala Val Asn Glu Phe Val Ile Glu Glu Asn  
 20 25 30  
 Leu Ser Ser Pro Asn Pro Ile Ser Asp Pro Gln Ser Pro Glu Met Met  
 35 40 45  
 55 Val Glu Ser Leu Tyr Ser Ser Val Ile Asn Ala Ile Asp Ser Arg Arg  
 50 55 60  
 Met Gln Asp Thr Asn Val Cys Gly Lys Glu Asp Phe Gly Asp His Thr  
 65 70 75 80  
 Ser Leu Asn Val Gln Leu Glu Arg Cys Arg Val Val Ala Gln Asp Ser  
 85 90 95  
 60 His Phe Ser Ile Gln Thr Ile Lys Glu Asp Leu Cys His Phe Arg Thr  
 100 105 110  
 Phe Val Gln Lys Glu Gln Cys Asp Ser Asn Ser Leu Lys Cys Thr



115 120 125  
 Ala Val Glu Ile Arg Asn Ile Ile Glu Lys Val Lys Cys Ser Leu Glu  
 130 135 140  
 Ile Thr Leu Lys Glu Lys His Gln Lys Glu Leu Leu Ser Leu Lys Asn  
 5 145 150 155 160  
 Glu Tyr Glu Gly Lys Leu Asp Gly Leu Ile Lys Glu Thr Glu Glu Asn  
 165 170 175  
 Glu Asn Lys Ile Lys Lys Leu Lys Gly Glu Leu Val Cys Leu Glu Glu  
 180 185 190  
 10 Val Leu Gln Asn Lys Asp Asn Glu Phe Ala Leu Val Lys His Glu Lys  
 195 200 205  
 Glu Ala Val Ile Cys Leu Gln Asn Glu Lys Asp Gln Lys Leu Xaa Glu  
 210 215 220  
 Met Glu Asn Ile Met Pro Ser Gln Asn Trp Glu Ile Xaa Glu Leu Lys  
 15 225 230 235 240  
 Gln Ser Arg Glu Ile Gly Leu Glu Asp Leu Lys Lys Leu Met Trp Lys  
 245 250 255  
 Met Met Arg Ser Xaa Gly Phe Gly Gly Xaa Thr Xaa Val Leu Gly Pro  
 260 265 270  
 20 Lys Ser Xaa Xaa Gly Ile  
 275  
 <210> 999  
 <211> 168  
 25 <212> PRT  
 <213> Homo sapiens  
 <400> 999  
 Xaa Xaa Xaa His Glu Glu Glu Xaa Asn Xaa Leu Lys Gly Glu Leu Asn  
 30 1 5 10 15  
 Lys Xaa Thr Ser Leu His Asn Gln Ala Phe Glu Ile Glu Lys Xaa Leu  
 20 25 30  
 Lys Xaa Gln Ile Ile Xaa Leu Xaa Ser Lys Xaa Asp Ser Xaa Leu Xaa  
 35 35 40 45  
 Ala Xaa Glu Ser Gln Lys Asp Glu Lys Ile Xaa Pro Gln Glu Glu Lys  
 50 55 60  
 Xaa Glu Xaa Xaa Xaa Gln Thr Leu Glu Lys Xaa Ser Gln Lys Leu Val  
 65 70 75 80  
 Xaa Ser Gln Glu Gln Xaa Xaa Xaa Gln Leu Ile Gln Lys Xaa Asn Cys  
 40 85 90 95  
 Glu Lys Xaa Glu Ala Ile Gln Xaa Ala Leu Lys Xaa Phe Lys Leu Xaa  
 100 105 110  
 Xaa Xaa Val Val Xaa Lys Xaa Xaa Leu Glu Lys Val Xaa Xaa Xaa Glu  
 115 120 125  
 45 Asn Gln Xaa Ala Lys Ser Pro Ala Xaa Asp Xaa Xaa Xaa Gly Asp Phe  
 130 135 140  
 Ser Ser Leu Xaa Xaa Glu Leu Gln Xaa Lys Leu Gln Glu Xaa Lys Xaa  
 145 150 155 160  
 Lys Phe Leu Xaa Xaa Leu Glu Glu  
 50 165  
 <210> 1000  
 <211> 194  
 <212> PRT  
 55 <213> Homo sapiens  
 <400> 1000  
 Glu Gly Lys Leu Gln Lys Ala Leu Glu Asp Ala Phe Leu Ala Ile Asp  
 1 5 10 15  
 60 Ala Lys Leu Thr Thr Glu Glu Val Ile Lys Glu Leu Ala Gln Ile Ala  
 20 25 30  
 Gly Arg Pro Thr Glu Asp Glu Asp Glu Lys Glu Lys Val Ala Asp Glu  
 35 40 45

Asp Asp Val Asp Asn Glu Glu Ala Ala Leu Leu His Glu Glu Ala Thr  
 50 55 60  
 Met Thr Ile Glu Glu Leu Leu Thr Arg Tyr Gly Gln Asn Cys His Lys  
 65 70 75 80  
 5 Gly Pro Pro His Ser Lys Ser Gly Gly Gly Thr Gly Glu Glu Pro Gly  
 85 90 95  
 Ser Gln Gly Leu Asn Gly Glu Ala Gly Pro Glu Asp Ser Thr Arg Glu  
 100 105 110  
 Thr Pro Ser Gln Glu Asn Gly Pro Thr Ala Lys Ala Tyr Thr Gly Phe  
 115 120 125  
 10 Ser Ser Asn Ser Glu Arg Gly Thr Glu Ala Gly Gln Val Gly Glu Pro  
 130 135 140  
 Gly Ile Pro Thr Gly Glu Ala Gly Pro Ser Cys Ser Ser Ala Ser Asp  
 145 150 155 160  
 15 Lys Leu Leu Glu Leu Leu Ser Pro Ser Ser Leu Arg Thr Val Arg Met  
 165 170 175  
 Ser Gln Met Lys Arg Arg Lys Lys Lys Lys Thr Val Arg Asn Ala Ala  
 180 185 190  
 Arg Lys

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<210> 1001  
 <211> 73  
 <212> PRT  
 <213> Homo sapiens

25

<400> 1001  
 Arg Val Ser Ser Ser Ser Ile Val Met Val Ala Ser Ser Cys Ser Ser  
 1 5 10 15  
 30 Ala Ala Ser Ser Leu Ser Thr Ser Ser Ser Ser Ala Thr Phe Ser Phe  
 20 25 30  
 Ser Ser Ser Ser Ser Val Gly Arg Pro Ala Ile Cys Ala Ser Ser Leu  
 35 35 40 45  
 Met Thr Ser Ser Val Val Asn Leu Ala Ser Ile Ala Lys Lys Ala Ser  
 50 55 60  
 Ser Lys Ala Phe Cys Ser Leu Pro Ser  
 65 70

40

<210> 1002  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 1002  
 His Lys Xaa Val Xaa Phe Thr Glu Ala Xaa Asn Ser Trp Ser Leu Pro  
 1 5 10 15  
 Gly Gly Xaa Trp Asn Val Met Thr Thr Gln Lys Val Val Asp Phe Ile  
 20 25 30  
 Gln Ser Lys Ile Ser Gln Ala Xaa Glu Asn Gly Lys Phe Gly Ile Val  
 35 40 45  
 50 Ile His Cys Glu Xaa Leu Leu Asp Gln Cys Xaa Ala Pro Asp Thr Phe  
 50 55 60  
 Gly Asp Gly Thr Gly Cys Asp Asn Met Thr Cys Ile Ile Ile Xaa Phe  
 65 70 75 80  
 55 Lys Pro Arg Asn Thr Ala Glu Leu Gln Pro Glu Ser Gly Lys Arg Lys  
 85 90 95  
 Leu Glu Glu Val Leu Ser Thr Glu Gly Ala Glu Glu Asn Gly Asn Ser  
 100 105 110  
 Asp Lys Lys Lys Lys Ala Lys Arg Asp  
 115 120

60

<210> 1003  
 <211> 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1003

5 Arg Arg Cys Ser Leu Leu Arg Gly Leu Lys Lys Met Ala Thr Ala Thr  
 1 5 10 15  
 Arg Arg Arg Arg Pro Ser Glu Thr Ser Ser His Pro Asp Pro Cys Pro  
 20 25 30  
 Pro Arg Leu Phe Xaa Glu Pro Ser Gly Pro Glu Thr Glu Phe Cys Leu  
 10 35 40 45  
 Phe Pro Leu Ala Leu Ala Val Gly Xaa Arg Cys Ala Gly Gly Ala Gly  
 50 55 60  
 Trp Leu His Ser Ala His Ser Lys Glu Gly Ser Pro Ser Thr Leu Gln  
 65 70 75 80  
 15 Pro Gly Ala Xaa Ala Val Leu Pro Ser Arg Xaa Cys Ser Ser Gly Ser  
 85 90 95  
 Ser Pro Val Leu Cys Leu Cys Ser Val Val Leu Glu Gly Arg Thr Gly  
 100 105 110  
 Gly Ser Gly Phe Tyr Ser Val Asn Phe Ile  
 115 120  
 20

&lt;210&gt; 1004

&lt;211&gt; 176

&lt;212&gt; PRT

25 &lt;213&gt; Homo sapiens

&lt;400&gt; 1004

Ala Ala Gln Leu Arg Met Val Asp Asp Gly Ser Gly Lys Val Glu Val  
 1 5 10 15  
 30 Trp Cys Ile Gln Asp Leu His Arg Gln Pro Val Asp Pro Lys Arg His  
 20 25 30  
 Gly Gln Leu Cys Ala Gly Asn Cys Tyr Leu Val Leu Tyr Thr Tyr Gln  
 35 35 40 45  
 Arg Leu Gly Arg Val Gln Tyr Ile Leu Tyr Leu Trp Gln Gly His Gln  
 50 55 60  
 Ala Thr Ala Asp Xaa Ile Glu Ala Leu Asn Ser Asn Ala Glu Glu Leu  
 65 70 75 80  
 Asp Val Met Tyr Gly Gly Val Leu Val Gln Glu His Val Thr Met Gly  
 85 90 95  
 40 Ser Glu Pro Pro His Phe Leu Ala Ile Phe Gln Gly Gln Leu Val Ile  
 100 105 110  
 Phe Gln Glu Arg Ala Gly His His Gly Lys Gly Gln Ser Ala Ser Thr  
 115 120 125  
 Thr Arg Leu Phe Gln Val Gln Gly Thr Asp Ser His Asn Thr Arg Thr  
 130 135 140  
 45 Met Glu Val Pro Ala Arg Ala Ser Ser Leu Asn Ser Ser Asp Ile Phe  
 145 150 155 160  
 Leu Leu Val Thr Ser Gln Arg Leu Leu Pro Leu Val Trp Glu Gly Leu  
 165 170 175  
 50

&lt;210&gt; 1005

&lt;211&gt; 143

&lt;212&gt; PRT

55 &lt;213&gt; Homo sapiens

&lt;400&gt; 1005

Pro Pro Pro Val Pro Ser His Val Asp His His Tyr Ser Pro Ser Gln  
 1 5 10 15  
 Thr Arg Gly Ser Arg Arg Trp Leu Val Thr Ser Lys Lys Met Ser Leu  
 20 25 30  
 Glu Leu Arg Asp Glu Ala Arg Ala Gly Thr Ser Met Val Leu Val Leu  
 35 40 45  
 Trp Leu Ser Val Pro Cys Thr Trp Lys Ser Leu Val Val Asp Ala Asp  
 50

50                      55                      60  
 Cys Pro Phe Pro Trp Cys Pro Ala Leu Ser Trp Lys Ile Thr Ser Trp  
 65                      70                      75                      80  
 Pro Trp Lys Met Ala Arg Lys Trp Gly Gly Ser Leu Pro Met Val Thr  
 85                      90                      95  
 Cys Ser Cys Thr Arg Thr Pro Pro Tyr Met Thr Ser Ser Ser Ser Ala  
 100                      105                      110  
 Leu Leu Phe Arg Ala Ser Xaa Ser Ser Ala Val Ala Trp Trp Pro Cys  
 115                      120                      125  
 10 His Arg Tyr Arg Met Tyr Trp Thr Arg Pro Ser Leu Trp Tyr Val  
 130                      135                      140

15                      <210> 1006  
                      <211> 145  
                      <212> PRT  
                      <213> Homo sapiens

20                      <400> 1006  
 Pro Xaa Val Pro Gln Glu Ser Gly Glu Trp Gln Pro Gly Lys Gln His  
 1                      5                      10                      15  
 Gln Pro Xaa Phe Glu Ile Thr Ala Glu Val Asn Asn Leu Gly Leu Ser  
 20                      25                      30  
 Xaa Trp Pro Gly Asn Gly Arg Ala Gly Ala Val Ala Leu Gln Ala Leu  
 35                      40                      45  
 25 Lys Gly Ser Gln Asp Ser Ser Xaa Asn Asp Leu Val Arg Ser Pro Lys  
 50                      55                      60  
 Ser Ala Gly Ser Arg Thr Ser Xaa Ser Val Ser Ser Thr Xaa Ala Thr  
 65                      70                      75                      80  
 Ile Asn Gly Gly Leu Arg Arg Glu Gln Xaa Met His Gln Ala Val Glu  
 85                      90                      95  
 30 Asp Leu Pro Xaa Xaa Val Asp Pro Ala Arg Arg Glu Phe Tyr Xaa Ser  
 100                      105                      110  
 Asp Xaa Asp Phe Gln Asp Xaa Phe Gly Lys Ser Lys Glu Glu Phe Tyr  
 115                      120                      125  
 35 Ser Met Ala Thr Trp Arg Gln Arg Gln Glu Lys Lys Gln Leu Gly Phe  
 130                      135                      140  
 Phe  
 145

40                      <210> 1007  
                      <211> 98  
                      <212> PRT  
                      <213> Homo sapiens

45                      <400> 1007  
 Cys Thr Arg Leu Leu Arg Thr Cys Xaa Arg Xaa Trp Thr Leu Pro Ala  
 1                      5                      10                      15  
 Gly Ser Ser Xaa Xaa Gln Thr Xaa Thr Ser Lys Ile Xaa Leu Gly Asn  
 20                      25                      30  
 50 Pro Arg Arg Asn Phe Thr Ala Trp Pro Arg Gly Gly Ser Gly Arg Arg  
 35                      40                      45  
 Lys Ser Ser Trp Ala Phe Phe Glu Pro Lys Pro Xaa Arg Leu Pro Leu  
 50                      55                      60  
 Ser Pro Gly Pro Gln His Thr Tyr Asn Ala Gly Glu Ala Leu Leu Pro  
 55 65                      70                      75                      80  
 Leu Pro Ser Xaa Ala Phe Gly His Pro Leu Xaa Val Ser Lys Ser Arg  
 85                      90                      95  
 Gln Pro

60                      <210> 1008  
                      <211> 65  
                      <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1008

5 Ser Thr Cys Arg Gly Pro Lys Val Xaa Asn His Pro Met Lys Gly Gly  
 1 5 10 15  
 Glu Ala Leu Trp Pro Cys Leu Xaa Xaa Thr Asn Xaa Cys Xaa Pro Gly  
 20 25 30  
 Phe Leu Pro Leu Xaa Gly Xaa Lys Ser Phe Lys Xaa Thr Ser Leu Xaa  
 35 40 45  
 10 Pro Lys Ala Asn Pro Pro Xaa Phe Pro Xaa Xaa Phe Cys Xaa Phe Ser  
 50 55 60  
 Pro  
 65

15 &lt;210&gt; 1009

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

20 &lt;400&gt; 1009

Tyr Leu Val Ala Leu Asp Lys Leu Asn Pro Tyr Thr Leu Tyr Thr Phe  
 1 5 10 15  
 Arg Ile Arg Cys Ser Thr Glu Thr Phe Trp Lys Trp Ser Lys Trp Ser  
 20 25 30  
 25 Asn Lys Lys Gln His Leu Thr Thr Glu Ala Ser Pro Ser Lys Gly Pro  
 35 40 45  
 Asp Thr Trp Arg Glu Trp Ser Ser Asp Gly Lys Asn Leu Ile Ile Tyr  
 50 55 60  
 Trp Lys Pro Leu Pro Ile Asn Glu Ala Asn Gly Lys Ile Leu Ser Tyr  
 30 65 70 75 80  
 Asn Val Ser Cys Ser Ser Asp Glu Glu Thr Gln Ser Leu Ser Glu Ile  
 85 90 95  
 Pro Asp Pro Gln His Lys Ala Glu Ile Arg Leu Asp Lys Asn Asp Tyr  
 100 105 110  
 35 Ile Ile Ser Val Val Ala Lys Asn Ser Val Gly Ser Ser Pro Pro Ser  
 115 120 125  
 Lys Ile Ala Ser Met Glu Ile Pro Asn Asp Asp Leu Lys Ile Glu Gln  
 130 135 140  
 Val Val Gly Met Gly Lys Gly Ile Leu Leu Thr Trp His Tyr Asp Pro  
 40 145 150 155 160  
 Asn Met Thr Cys Asp Tyr Val Ile Lys Trp Cys Asn Ser Ser Arg Ser  
 165 170 175  
 Glu Pro Cys Leu Met Asp Trp Arg Lys Val Pro Gln Thr Ala Leu Lys  
 180 185 190  
 45 Leu

50 &lt;210&gt; 1010

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1010

55 Xaa Phe Pro Arg Asn Val Phe Pro Phe Xaa Leu Xaa Ile Glu Ser Ala  
 1 5 10 15  
 Xaa Val Ser Phe Thr Ser Lys Phe Gly His Gln Trp Glu Pro Ile Xaa  
 20 25 30  
 Leu Tyr Ile Gln Ser Trp Ser Val Ile Ile Asp Ile Leu Asp Phe Cys  
 35 40 45  
 60 Ile His Thr Gly Lys Asn Tyr Ile Leu Tyr Leu Val Glu Thr His Gln  
 50 55 60  
 Ile Leu Leu Gln Phe Gln Cys Cys Leu Arg Asn Phe Ser Pro Val His  
 65 70 75 80

Lys Ala Trp Phe Arg Pro Arg Arg Val Thr Pro Leu Asn Asp Val Val  
                     85                    90                    95  
 Ala Ser His Val Gly Val Val Met Pro Gly Glu Glu Asn Pro Leu Ser  
                     100                    105                    110  
 5 His Pro Asn Asn Leu Phe Tyr Phe Glu Ile Ile Ile Trp Asn Phe His  
                     115                    120                    125  
 Thr Arg Tyr Phe Gly Arg Trp  
                     130                    135  
  
 10 <210> 1011  
       <211> 80  
       <212> PRT  
       <213> Homo sapiens  
  
 15 <400> 1011  
 Xaa Asn His Xaa Thr Arg Gly Lys Arg Pro Lys Val Xaa Trp Ile Trp  
   1                    5                    10                    15  
 Ser Pro Arg Gly Xaa Xaa Xaa Val Gly Cys Xaa Pro Ser Gln Gly Ile  
                     20                    25                    30  
 20 Leu Pro Leu Trp Xaa Met Ser Xaa His Ser Glu Ser Phe Pro Gln Pro  
                     35                    40                    45  
 Pro Xaa Leu Val Pro Ser Ser His Phe Lys Tyr Lys Thr Lys Xaa Arg  
                     50                    55                    60  
 Met Leu Leu Thr Gly Pro Val Pro Lys Gly Cys Phe Leu Glu Leu Ser  
 25 65                    70                    75                    80  
  
       <210> 1012  
       <211> 77  
       <212> PRT  
 30 <213> Homo sapiens  
  
       <400> 1012  
 Xaa Leu Thr Ile Xaa Pro Gly Val Ser Gly Gln Lys Xaa Asp Gly Phe  
   1                    5                    10                    15  
 35 Gly Pro Pro Glu Glu Xaa Xaa Pro Trp Val Xaa Pro Gln Ala Arg Val  
                     20                    25                    30  
 Phe Cys Pro Phe Xaa Xaa Cys Xaa Pro Thr Gln Ser Leu Phe Leu Ser  
                     35                    40                    45  
 Pro His Xaa Leu Ser Arg Pro His Ile Leu Asn Ile Lys Leu Xaa Arg  
                     50                    55                    60  
 40 Glu Cys Phe Leu Gln Asp Gln Tyr Pro Arg Ala Val Ser  
   65                    70                    75  
  
       <210> 1013  
 45 <211> 117  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 1013  
 50 Leu Ile His Tyr Leu Gln Ile His Tyr Arg Ile Ser Asp Asp Lys Lys  
   1                    5                    10                    15  
 Gln Thr Thr Asn Gln Lys Lys Gln Thr Lys Lys Thr Tyr Leu Ile Arg  
                     20                    25                    30  
 Thr Leu Lys Ile Phe Lys Tyr Phe Cys Leu Lys Tyr Glu Lys Val Lys  
                     35                    40                    45  
 55 Tyr Ile Gly Asn Leu Arg Ala Gly Lys Ile Gln Asp His Phe Leu Val  
                     50                    55                    60  
 Phe Pro Ser Ala Phe Pro Arg Thr Thr Ile Thr Pro Asp Ile Ala Tyr  
   65                    70                    75                    80  
 60 Glu Lys Gln Gly Trp Ala Glu Asp Ala Val Leu Lys Ala Ile Asn Ser  
                     85                    90                    95  
 Ala Gln Leu Thr Lys Gln Leu Leu Pro Cys Asn Thr Gly Cys Pro Trp  
                     100                    105                    110

Ile Gln Ile Ser Leu  
115

5 <210> 1014  
<211> 212  
<212> PRT  
<213> Homo sapiens

<400> 1014

10 Ile Ser Asp Asn Ser Lys Ile Asn Phe Arg Leu Lys Pro Leu Asp Val  
1 5 10 15  
Ala Phe Met Lys Ala Ile His Asn Lys Val Asn Ile Val Pro Val Ile  
20 25 30  
Ala Lys Ala Asp Thr Leu Thr Leu Lys Glu Arg Glu Arg Leu Lys Lys  
15 35 40 45  
Arg Ile Leu Asp Glu Ile Glu Glu His Asn Ile Lys Ile Tyr His Leu  
50 55 60  
Pro Asp Ala Glu Ser Asp Glu Asp Glu Asp Phe Lys Glu Gln Thr Arg  
65 70 75 80  
20 Leu Leu Lys Ala Ser Ile Pro Phe Ser Val Val Gly Ser Asn Gln Leu  
85 90 95  
Ile Glu Ala Lys Gly Lys Lys Val Arg Gly Arg Leu Tyr Pro Trp Gly  
100 105 110  
Val Val Glu Val Glu Asn Pro Glu His Asn Asp Phe Leu Lys Leu Arg  
115 120 125  
25 Thr Met Leu Ile Thr His Met Gln Asp Leu Gln Glu Val Thr Gln Asp  
130 135 140  
Leu His Tyr Glu Asn Phe Arg Ser Glu Arg Leu Lys Arg Gly Gly Arg  
145 150 155 160  
30 Lys Val Glu Asn Glu Asp Met Asn Lys Asp Gln Ile Leu Leu Glu Lys  
165 170 175  
Glu Ala Glu Leu Arg Arg Met Gln Xaa Met Ile Ala Arg Met Gln Ala  
180 185 190  
Pro Asn Ala Asp Ala Xaa Cys Xaa Ala Gly Asp Gly Xaa Gly Gly Ala  
195 200 205  
35 Phe Arg Ala Thr  
210

<210> 1015  
40 <211> 143  
<212> PRT  
<213> Homo sapiens

<400> 1015

45 Gly Gly Pro Lys Ser Pro Ala Xaa Ala Ile Pro Gly Xaa Ala Xaa Gly  
1 5 10 15  
Ile Cys Ile Trp Gly Leu His Pro Cys Asn His Xaa Leu His Ala Ala  
20 25 30  
Glu Leu Ser Phe Phe Phe Gln Gln Asp Leu Val Phe Ile His Val Leu  
35 40 45  
50 Ile Leu His Phe Pro Ala Ala Ser Leu Glu Ser Leu Arg Thr Glu Val  
50 55 60  
Phe Ile Met Lys Val Leu Gly His Leu Leu Glu Ile Leu His Val Gly  
65 70 75 80  
55 Asp Glu His Gly Ser Gln Leu Gln Lys Val Ile Val Leu Trp Val Leu  
85 90 95  
His Phe His Asn Thr Pro Gly Val Glu Ala Ala Ser Asp Leu Leu Ser  
100 105 110  
Phe Gly Phe Asn Gln Leu Ile Gly Ser Asn His Arg Glu Trp Asp Ala  
115 120 125  
60 Ser Leu Glu Lys Ser Ser Leu Leu Phe Lys Ile Phe Ile Phe Ile  
130 135 140

<210> 1016  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1016  
 His Thr Phe Ile Asn Tyr Tyr Tyr Leu Thr Ala Ser Phe Tyr Gly Phe  
 1 5 10 15  
 Ser Ser Pro His Lys Asn Glu Lys Thr Leu Ser His Pro Gln Ile Lys  
 10 20 25 30  
 His Phe Leu His Leu Pro Thr Gln Pro Leu Ala Pro Phe Ile Trp Gln  
 35 40 45  
 Phe Leu Gly Gly Glu Phe Pro Thr Ser Val Xaa Met Asp Xaa Lys Arg  
 50 55 60  
 15 His Pro Leu Glu Xaa Ser Leu Arg Gly Pro Gln Xaa Lys Xaa Gly Thr  
 65 70 75 80  
 Leu Arg Xaa Pro Gly Xaa Xaa Lys Thr Lys Pro Gly Xaa Gly Xaa Asn  
 85 90 95  
 Gly Ala Asp Leu Ala Pro Tyr Pro Leu Leu Gln Asn Leu Lys Xaa Val  
 100 105 110  
 20 Phe Pro Phe Asp Leu Ala Xaa Arg  
 115 120

<210> 1017  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

25

<400> 1017  
 Val Phe Ser Lys Tyr Ile Ser Ile Gly Arg Asp Tyr Val Leu Val Lys  
 1 5 10 15  
 Glu Gln Leu Ser Ile Ile Lys Ser Ile Tyr Leu Asp Leu Gly Ser Lys  
 20 25 30  
 Thr Lys Gly Asp Gln Lys Cys Ser Val Gly Pro Pro Ser Leu His  
 35 35 40 45  
 Ser Cys Tyr Gln Glu Ala Ala Cys Leu Lys Tyr Phe His Ser His Met  
 50 55 60  
 Arg Gly Leu Val Thr Ser Lys Leu Val Phe Leu Phe Tyr Arg Phe Ser  
 65 70 75 80  
 40 Ser Lys Val Ile Lys Cys Gln Thr Gln Ile Met Asp Ser Ala Trp Met  
 85 90 95  
 Tyr Ser Glu Val Met Glu His His Phe Leu Val Thr Phe Thr Gln  
 100 105 110

<210> 1018  
 <211> 219  
 <212> PRT  
 <213> Homo sapiens

45

<400> 1018  
 Arg Glu Arg Val Thr Gln Ser Ala Leu Val Pro Val Leu Ala Met Ala  
 1 5 10 15  
 Ser Phe Val Thr Glu Val Leu Ala His Ser Gly Arg Leu Glu Lys Glu  
 20 25 30  
 55 Asp Leu Gly Thr Arg Ile Ser Arg Leu Thr Arg Arg Val Glu Glu Ile  
 35 40 45  
 Lys Gly Glu Val Cys Asn Met Ile Ser Lys Lys Tyr Ser Glu Phe Leu  
 50 55 60  
 Pro Ser Met Gln Ser Ala Gln Gly Leu Ile Thr Gln Val Asp Lys Leu  
 65 70 75 80  
 60 Ser Glu Asp Ile Asp Leu Leu Lys Ser Arg Ile Glu Ser Glu Val Arg  
 85 90 95  
 Arg Asp Leu His Val Ser Thr Gly Glu Phe Thr Asp Leu Lys Gln Gln



100 105 110  
 Leu Glu Arg Asp Ser Val Val Leu Ser Leu Leu Lys Gln Leu Gln Glu  
 115 120 125  
 Phe Ser Thr Ala Ile Glu Glu Tyr Asn Cys Ala Leu Thr Glu Lys Lys  
 130 135 140  
 5 Tyr Val Thr Gly Ala Gln Arg Leu Glu Glu Ala Gln Lys Cys Leu Lys  
 145 150 155 160  
 Leu Leu Lys Ser Arg Lys Cys Phe Asp Leu Lys Ile Leu Lys Ser Leu  
 165 170 175  
 10 Ser Met Glu Leu Thr Ile Gln Glu Thr Glu His Thr Leu Ser Pro Trp  
 180 185 190  
 Arg Arg Val Ala Glu Ala Asp Cys Met Glu Val Pro Thr Ile Lys Arg  
 195 200 205  
 Tyr Gln Pro Val Trp Glu Ser Leu Pro Tyr Lys  
 15 210 215

&lt;210&gt; 1019

&lt;211&gt; 99

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 1019

Arg Ser Arg Arg Thr Ser Leu Ser Ile Leu Asp Phe Ser Arg Ser Met  
 1 5 10 15  
 25 Ser Ser Asp Ser Leu Ser Thr Trp Val Ile Arg Pro Cys Ala Leu Cys  
 20 25 30  
 Met Leu Gly Arg Asn Ser Leu Tyr Phe Leu Leu Ile Ile Leu His Thr  
 35 40 45  
 30 Ser Pro Leu Ile Ser Ser Thr Arg Arg Val Arg Arg Leu Ile Arg Val  
 50 55 60  
 Pro Arg Ser Ser Phe Ser Ser Leu Pro Glu Cys Ala Lys Thr Ser Val  
 65 70 75 80  
 Thr Asn Glu Ala Met Ala Lys Thr Gly Thr Asn Ala Asp Trp Val Thr  
 85 90 95  
 35 Leu Ser Leu

&lt;210&gt; 1020

&lt;211&gt; 131

&lt;212&gt; PRT

40 &lt;213&gt; Homo sapiens

&lt;400&gt; 1020

Ser Gln Thr Ser Lys Met Tyr Trp Phe Thr Lys Thr Asn Gly Arg Phe  
 1 5 10 15  
 Lys Glu Val Phe Lys Gly Xaa Ile Met Pro Arg Glu Glu Ser Thr Tyr  
 20 25 30  
 Ser Arg His Ser Phe Leu Lys Lys Met Glu Leu Phe Asn Phe Ser Lys  
 35 40 45  
 50 Gly Ser Cys Ser Ser Phe Leu Cys Leu Lys Gln Gly Arg Ile Lys Ala  
 50 55 60  
 Leu Leu His Trp Lys Xaa Thr His Cys Gln Gly Xaa Phe Xaa Ile Trp  
 65 70 75 80  
 Pro Thr Asp Pro Asn Xaa Leu Pro Ser Trp Leu Trp Glu Pro Ser Ser  
 85 90 95  
 55 Ser Asn Ser Leu Glu Trp Leu Pro Phe Leu Ala His Xaa Thr Gly Asn  
 100 105 110  
 Leu Phe Leu Lys Phe Xaa Gly Ala Trp Leu Ser Ser Lys Xaa Lys Gly  
 115 120 125  
 60 Gln Xaa Pro  
 130

&lt;210&gt; 1021

<211> 222  
 <212> PRT  
 <213> Homo sapiens

5           <400> 1021  
 Pro Leu Glu Pro Ala Val Gly Pro Lys Ala Ala Cys Pro Leu Asp Ser  
   1                  5                  10                  15  
 Glu Ser Ala Glu Gly Val Val Pro Pro Ala Ser Gly Gly Gly Arg Val  
           20                  25                  30  
 10 Gln Asn Ser Pro Pro Val Gly Arg Lys Thr Leu Pro Leu Thr Thr Ala  
       35                  40                  45  
 Pro Glu Ala Gly Glu Val Thr Pro Ser Asp Ser Gly Gly Gln Glu Asp  
       50                  55                  60  
 Ser Pro Ala Lys Gly Leu Ser Val Arg Leu Glu Phe Asp Tyr Ser Glu  
 15 65                  70                  75                  80  
 Asp Lys Ser Ser Trp Asp Asn Gln Gln Glu Asn Pro Pro Pro Thr Lys  
           85                  90                  95  
 Lys Ile Gly Lys Lys Pro Val Ala Lys Met Pro Leu Arg Arg Pro Lys  
          100                 105                 110  
 20 Met Lys Lys Thr Pro Glu Lys Leu Asp Asn Thr Pro Ala Ser Pro Pro  
      115                 120                 125  
 Arg Ser Pro Ala Glu Pro Asn Asp Ile Pro Ile Ala Lys Gly Thr Tyr  
      130                 135                 140  
 Thr Phe Asp Ile Asp Lys Trp Asp Asp Pro Asn Phe Asn Pro Phe Ser  
 25 145                 150                 155                 160  
 Ser Thr Ser Lys Met Gln Glu Ser Pro Lys Leu Pro Gln Gln Ser Tyr  
          165                 170                 175  
 Asn Phe Asp Pro Asp Thr Cys Asp Glu Ser Val Asp Pro Phe Lys Thr  
      180                 185                 190  
 30 Ser Ser Lys Pro Pro Ala His Leu Leu Asn Pro Gln Pro Ser Phe Glu  
      195                 200                 205  
 Ile Pro Ala Ser Ala Ile Gly Ser Gln Trp Ser Gly Pro Gly  
      210                 215                 220

35           <210> 1022  
             <211> 249  
             <212> PRT  
             <213> Homo sapiens

40           <400> 1022  
 Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Ile Xaa Xaa Ile  
   1                  5                  10                  15  
 Cys Xaa Gly Xaa Gln Trp Xaa Xaa Arg Xaa Asn Xaa Xaa Xaa Xaa Xaa  
      20                 25                 30  
 45 His Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Gly Xaa Xaa Met Xaa  
      35                 40                 45  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Met Xaa Xaa Cys Xaa Leu Xaa Xaa  
      50                 55                 60  
 Trp Gln Xaa Val Trp Xaa Arg Gln Ala Glu Ser Ala Cys Leu Leu Ile  
 50 65                 70                 75                 80  
 His Xaa Cys Met Asn Xaa Pro Ala Leu Xaa Xaa Tyr Ser Xaa Arg Xaa  
          85                 90                 95  
 Cys Ser Phe Arg Asn Ala Gly Leu Val Gly Gly Leu Xaa Xaa Xaa Xaa  
      100                 105                 110  
 55 Xaa Ala Ser Asn Leu Xaa Asn Val Xaa Xaa Ala Pro Xaa Gln Xaa Xaa  
      115                 120                 125  
 Xaa Arg Val His Leu Xaa Gly Xaa Val Xaa Xaa Leu Leu Leu Leu Arg  
      130                 135                 140  
 Leu Gly Xaa Thr Xaa Xaa Cys Glu His Thr Phe Thr His Xaa Xaa Ile  
 60 145                 150                 155                 160  
 Leu Ala Glu Xaa Leu Xaa Arg Thr Gly Pro Ile Xaa Xaa Ile Ser Ser  
          165                 170                 175  
 Ile Xaa Gly Xaa Pro Arg Xaa Leu Phe His Arg Xaa Leu Xaa Xaa Xaa

180 185 190  
 Xaa Arg Leu Ala Xaa Phe Leu Xaa Lys Pro Ser Leu Val Xaa Xaa Pro  
 195 200 205  
 Leu Xaa Gly Xaa Xaa Xaa Leu Xaa Phe Leu Gly Asp Xaa Pro Leu Tyr  
 5 210 215 220  
 Xaa Xaa Xaa Xaa Gln Trp Xaa Leu Phe Xaa Xaa Phe Xaa Pro Ile Phe  
 225 230 235 240  
 Xaa Pro Xaa Ile Phe Xaa His Leu Tyr  
 245  
 10  
 <210> 1023  
 <211> 231  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 1023  
 Leu Gln Arg Leu Phe Glu Glu Phe Arg Asp Ser Asp Asp Val Leu Gly  
 1 5 10 15  
 His Ile Met Lys Asn Ile Thr Ala Lys Arg Ser Arg Ala Arg Ile Val  
 20 20 25 30  
 Asp Lys Leu Leu Ala Leu Gly Leu Val Ala Glu Arg Arg Glu Leu Tyr  
 35 40 45  
 Lys Lys Arg Gln Lys Lys Leu Ala Ser Ser Ile Leu Pro Asn Gly Ala  
 50 55 60  
 25 Glu Ser Leu Lys Asp Phe Cys Gln Glu Asp Leu Glu Glu Glu Glu Asn  
 65 70 75 80  
 Leu Pro Glu Glu Asp Ser Glu Glu Glu Glu Glu Gly Gly Ser Glu Ala  
 85 90 95  
 Glu Gln Val Gln Gly Ser Leu Val Leu Ser Asn Glu Asn Leu Gly Gln  
 100 105 110  
 30 Ser Leu His Gln Glu Gly Phe Ser Ile Pro Leu Leu Trp Leu Gln Asn  
 115 120 125  
 Cys Leu Ile Arg Ala Ala Asp Arg Glu Glu Asp Gly Cys Ser Gln  
 130 135 140  
 35 Ala Val Pro Leu Val Pro Leu Thr Glu Glu Asn Glu Glu Ala Met Glu  
 145 150 155 160  
 Asn Glu Gln Phe Gln Gln Leu Leu Arg Lys Leu Gly Val Arg Pro Pro  
 165 170 175  
 Ala Ser Gly Gln Glu Thr Phe Trp Arg Ile Pro Ala Lys Leu Ser Pro  
 180 185 190  
 40 Thr Gln Leu Arg Arg Ala Ala Ala Ser Phe Glu Ser Thr Arg Gly Gly  
 195 200 205  
 Thr Glu Thr Cys Ser Gln Asn Cys Ser Leu Lys Xaa Leu Glu Ser Lys  
 210 215 220  
 45 Ala Leu Met Lys Ser Thr Cys  
 225 230  
 <210> 1024  
 <211> 116  
 50 <212> PRT  
 <213> Homo sapiens  
 <400> 1024  
 Ile Arg Glu Xaa Ala Trp Asp Ser Thr Ala Leu Ser Ser Xaa Arg Ser  
 1 5 10 15  
 Phe Trp Val Leu Tyr Asp Pro Ser Asn Ser Asp Leu Asn Xaa Pro Xaa  
 20 25 30  
 Lys Asn Val Xaa Ile Ser Thr Pro Arg Ala Phe Leu Ala Phe Xaa Val  
 35 40 45  
 60 Ile Leu Asn Xaa Ser Leu Xaa Ser Gly Xaa Ser Val Leu Xaa Leu Gly  
 50 55 60  
 Phe Leu Gly Thr Ser Pro Thr Xaa Gly Gly Ser Cys Ser Leu Pro Leu  
 65 70 75 80

Asn Xaa Xaa Xaa Leu Val Pro Arg Xaa Xaa Xaa Pro Thr Asn Leu Xaa  
                     85                    90                    95  
 Val Phe Trp Xaa Gly Phe Pro Leu Xaa Gly Xaa Phe Tyr Xaa Thr Xaa  
                     100                    105                    110  
 5 Gly Xaa Xaa Ser  
                     115  
                     <210> 1025  
                     <211> 110  
 10                   <212> PRT  
                     <213> Homo sapiens  
                     <400> 1025  
 Tyr Gln Thr Gln Ser Lys Xaa Ile His His Xaa Xaa Tyr Tyr Xaa Pro  
 15     1                    5                    10                    15  
 Thr Leu Xaa Gln Met Gln Glu Trp Ala Xaa Ile Trp Xaa Leu Xaa Asp  
                     20                    25                    30  
 Asp His Arg Lys Gln Asn Glu Asp Arg Gly Xaa Trp Xaa Xaa Xaa Lys  
                     35                    40                    45  
 20 Xaa Val Gln Asn Ser Arg Leu Ser Cys His Lys Ala Pro His Xaa Xaa  
                     50                    55                    60  
 Leu Arg Pro Thr Ser Xaa Xaa Lys Pro Lys Glu Gln Thr Asn Lys Arg  
                     65                    70                    75                    80  
 Gly Pro Gly Xaa Phe Xaa Tyr Phe Thr His Ser Xaa Tyr Leu Leu Arg  
 25                   85                    90                    95  
 Ser Ser Asn Asn Gln Xaa Lys Trp Phe Leu Lys Lys Xaa Asn  
                     100                    105                    110  
                     <210> 1026  
 30                   <211> 93  
                     <212> PRT  
                     <213> Homo sapiens  
                     <400> 1026  
 Asn Xaa Glu Ser Xaa Pro Asp Pro Phe Tyr Trp Ser Val Pro Leu Ala  
 35     1                    5                    10                    15  
 Xaa Xaa Trp Arg Trp Val Ala Xaa Pro Xaa Gly Glu Leu Tyr Asp Met  
                     20                    25                    30  
 Thr Gly Gly Ser Phe Val Xaa Leu Leu Xaa Xaa Thr Xaa Cys Leu Cys  
 40                   35                    40                    45  
 Pro His Phe Val Ser Tyr Asp His Pro Xaa Xaa Thr Arg Xaa Arg Pro  
                     50                    55                    60  
 Ile Pro Ala Phe Xaa Ile Gly Leu Glu Xaa Ser Thr Xaa Xaa Asp Glu  
                     65                    70                    75                    80  
 45 Xaa Val Cys Phe Val Phe Gly Ile Lys His Val Arg Leu  
                     85                    90  
                     <210> 1027  
                     <211> 205  
 50                   <212> PRT  
                     <213> Homo sapiens  
                     <400> 1027  
 Xaa Leu Xaa Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Phe  
 55     1                    5                    10                    15  
 Glu Thr Ile Val Glu Gln Ala Pro Leu Ala Ile Glu Asp Leu Leu Asn  
                     20                    25                    30  
 Glu Leu Asp Thr Gln Asp Glu Glu Val Ala Ser Asp Ser Asp Glu Ser  
                     35                    40                    45  
 60 Ser Glu Gly Gly Glu Arg Gly Asp Ala Leu Ser Gln Lys Arg Ser Glu  
                     50                    55                    60  
 Lys Pro Pro Ala Gly Ser Ile Cys Arg Ala Glu Pro Glu Ala Gly Glu  
                     65                    70                    75                    80

		<b>&lt;400&gt; 1029</b>															
	Trp	Ala	His	Leu	Ser	Ser	Ala	Ala	Leu	Pro	Ser	Arg	Leu	Ala	Gln	Glu	
	1				5					10					15		
55	Phe	Trp	Ser		Xaa	Pro	Glu	Ser	Thr	Xaa	Gln	Pro	Gly	Gln	Pro	Xaa	
				20					25					30			
	Pro	Ala	Xaa	Gln	Ala	Arg	Pro	Gly	Leu	Pro	Pro	Cys	Leu	Ser	Leu	Ala	
			35					40					45				
	Arg	Pro	His	His	Ser	Leu	Arg	Phe	Phe	Phe	Phe	Ser	Gly	Ser	Trp	Thr	
60		50					55					60					
	Leu	Ala	Ala	Phe	Ala	Arg	Ala	Leu	Val	Arg	Gly	Arg	Arg	Cys	Xaa	Pro	
	65					70					75					80	
	Xaa	Leu	Ala	Ser	Xaa	Phe	Leu	Ala	Thr	Gly	Xaa	Trp	Ala	Asp	Leu	Gly	

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<210> 1031  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1031

Phe Glu Thr Ile Val Glu Gln Ala Pro Leu Ala Ile Glu Asp Leu Leu  
 1 5 10 15  
 Asn Glu Leu Asp Thr Gln Asp Glu Glu Val Ala Ser Asp Ser Asp Glu  
 20 25 30  
 Ser Ser Glu Gly Gly Glu Arg Gly Asp Ala Leu Ser Gln Lys Arg Ser  
 35 40 45  
 Glu Lys Pro Pro Ala Gly Ser Ile Cys Arg Ala Glu Pro Glu Ala Gly  
 50 55 60  
 Glu Glu Gln Ala Gly Asp Asp Arg Asp Ser Gly Gly Pro Val Leu Gln  
 65 70 75 80  
 Phe Asp Tyr Glu Ala Val Ala Asn Arg Leu Phe Glu Met Ala Ser Arg  
 85 90 95  
 Gln Ser Thr Pro Ser Gln Asn Arg Lys Arg Leu Tyr Lys Val Ile Arg  
 100 105 110  
 Lys Leu Gln Asp Leu Ala Gly Gly Ile Phe Pro Glu Asp Glu Ile Pro  
 115 120 125  
 Glu Lys Ala Cys Arg Arg Leu Leu Glu Gly Arg Arg Gln Lys Lys Thr  
 130 135 140  
 Lys Lys Gln Lys Arg Leu Leu Arg Leu Gln Gln Glu Arg Gly Lys Gly  
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 Glu Lys Glu Pro Pro Ser Pro Gly Met Glu Arg Lys Arg Ser Arg Arg  
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 Arg Gly Val Gly Ala Arg Pro Arg Gly Ala Gly Arg Gly Trp  
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<210> 1032  
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 <212> PRT  
 <213> Homo sapiens

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<400> 1032

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 20 25 30  
 Gly Pro Ala Gln Leu Cys Leu Xaa Ala His Gln Pro Leu Pro Ala Pro  
 35 40 45  
 Arg Gly Arg Ala Pro Thr Pro Leu Leu Leu Leu Leu Phe Leu Ser Met  
 50 55 60  
 Pro Gly Leu Gly Gly Ser Phe Ser Pro Phe Pro Leu Ser Cys Cys Asn  
 65 70 75 80  
 Leu Ser Arg Arg Phe Cys Phe Phe Val Phe Phe Cys Arg Leu Pro Ser  
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 Ser Arg Arg Leu Gln Ala Phe Ser Gly Ile Ser Ser Ser Gly Lys Met  
 100 105 110  
 Pro Pro Ala Arg Ser Cys Ser Phe Arg Ile Thr Leu  
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<210> 1033  
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 <212> PRT  
 <213> Homo sapiens

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<400> 1033

Leu Leu Ala Arg Ala Leu Val Arg Gly Arg Arg Cys Xaa Pro Xaa Leu  
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 Ala Arg Ser Ala Val Pro Xaa Cys Ser Pro Ala Ser Ala Arg Ala Ser  
 35 40 45  
 Gly Ser Gly Pro Tyr Thr Pro Pro Pro Ala Pro Leu Pro Leu His Ala  
 5 50 55 60  
 Arg Ala Arg Gly Leu Leu Leu Thr Phe Pro Ser Leu Leu Leu Gln Pro  
 65 70 75 80  
 Glu Gln Thr Leu Leu Leu Arg Leu Leu Leu Pro Pro Pro Phe Lys  
 85 90 95  
 10 Gln Ala Pro Ala Gly Leu Leu Trp Asp Leu Ile Phe Arg Glu Asn Ala  
 100 105 110  
 Ser Cys Gln Val Leu Gln Leu Pro Asp His Phe Val Glu Thr Leu Ser  
 115 120 125  
 Val Leu Arg Arg Gly Ala Leu Ala Ala Gly His Phe Lys Gln Ser Val  
 15 130 135 140  
 Ser Asn Cys Leu Val Val Lys Leu Glu Asn Gly Ala Ala Thr Val Pro  
 145 150 155 160  
 Val Val Thr Cys Leu Leu Leu Thr Ser Leu Arg Phe Ser Pro Ala Asp  
 165 170 175  
 20 Gly Ala Cys Gly Arg Leu Leu Arg Pro Leu Leu Gly Gln Arg Val Ser  
 180 185 190  
 Thr Leu Thr Thr Leu Arg Gly Leu Ile Thr Val Arg Arg His Leu Leu  
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 Ile Leu Cys Val Gln Phe Ile Gln Glu Val Phe Asn Gly Lys Arg Gly  
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 Leu Leu His Asn Arg Leu Lys  
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 <212> PRT  
 <213> Homo sapiens

<400> 1034  
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 Pro Ala Xaa Gln Ala Arg Pro Gly Leu Pro Pro Cys Leu Ser Leu Ala  
 40 35 40 45  
 Arg Pro His His Ser Leu Arg Phe Phe Phe Phe Ser Gly Ser Trp Thr  
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 Leu Ala Ala Phe Ala Arg Ala Leu Val Arg Gly Arg Gly Val Leu Leu  
 65 70 75 80  
 45 Leu Leu Ala Ser Pro Ser Leu Ala Thr Ala Pro Gly Leu Ile Ser Glu  
 85 90 95  
 Gln Gly Pro Leu Xaa Cys Ala Trp Leu Phe Thr Lys Pro Xaa Ala Arg  
 100 105 110  
 Ala Ser Gly Val Gly Pro Leu Thr Pro Leu Pro Pro Gly Tyr Xaa Phe  
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 Xaa Phe Phe Ser Leu  
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55 <210> 1035  
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 <212> PRT  
 <213> Homo sapiens

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 Phe Leu Leu Leu Leu Arg Leu Leu Asp Ile Gly Arg Leu Cys Ser Gly  
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 5 Thr Gly Gln Gly Pro Arg Cys Pro Pro Ser Ser Gly Glu Pro Leu Phe  
       50                  55                  60  
 Gly His Gly Pro Trp Ala Asp Leu Gly Ala Gly Pro Ala Xaa Leu Cys  
   65                  70                  75                  80  
 10 Leu Ala Val His Gln Thr Xaa Cys Pro Arg Leu Gly Gly Arg Ala Pro  
                   85                  90                  95  
 Asn Thr Pro Ser Ser Trp Val Pro Xaa Ser Ser Ser Cys Pro Gly Ala  
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 <213> Homo sapiens

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                   20                  25                  30  
 Arg Gly Ala Arg Gln Lys Lys Glu Asp Thr Ser Ala Pro Asp Gln Cys  
                   35                  40                  45  
 Pro Ser Lys Gly Gly Gln Cys Pro Gly Ala Gly Glu Glu Glu Glu Thr  
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 30 Gln Gly Val Met Trp Pro Gly Gln Gly Gln Ala Gly Arg Glu Ala Arg  
   65                  70                  75                  80  
 Pro Arg Leu Xaa Arg Gly Xaa Arg Leu Thr Gly Leu Xaa Cys Arg Leu  
                   85                  90                  95  
 Arg Xaa Val Ala Pro Glu Leu Leu Cys Gln Ala Gly Gly Lys Gly Gly  
                   100                  105                  110  
 35 Thr Gly Glu Met Gly Pro Ser Leu Gly Ala Ser Ile Pro Gly Thr Gly  
                   115                  120                  125  
 Pro Phe Pro Arg Ala Ser Ala Cys Gly Cys Asp Asp Leu Gly Pro Glu  
                   130                  135                  140  
 40 Gly Gln Thr Pro Lys Thr Glu Thr Leu Pro Ala Ala Gly Leu Ala Ala  
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 Pro Ala Val Gly Gly Ser Glu Asn Lys Met Pro Arg Ser Pro Cys Gln  
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 Gly Ser Val

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<210> 1037  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

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 55 Gly Pro Ser Ser Pro Ala Ser Val Thr Val Thr Val Gly Asp Glu Gly  
                   20                  25                  30  
 Ala Asp Thr Pro Val Gly Ala Thr Pro Leu Ile Gly Asp Glu Ser Glu  
                   35                  40                  45  
 60 Asn Leu Glu Gly Asp Gly Asp Leu Arg Gly Gly Arg Ile Leu Leu Gly  
   50                  55                  60  
 His Ala Thr Lys Ser Phe Pro Ser Ser Pro Ser Lys Gly Gly Ser Cys  
   65                  70                  75                  80  
 Pro Ser Arg Ala Lys Met Ser Met Thr Gly Ala Gly Lys Ser Pro Pro

85 90 95  
 Ser Val Gln Ser Leu Ala Met Arg Leu Leu Ser Met Pro Gly Ala Gln  
 100 105 110  
 5 Gly Ala Ala Ala Gly Ser Glu Pro Pro Ala Thr Thr Ser Pro  
 115 120 125  
 Glu Gly Gln Pro Lys Val His Arg Ala Arg Lys Thr Met Ser Lys Pro  
 130 135 140  
 Gly Asn Gly Gln Val Ser Gly Met Gly Glu Met Gly  
 145 150 155  
 10 <210> 1038  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens  
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 20 25 30  
 Ala Arg Trp Thr Leu Gly Cys Pro Ser Gly Leu Val Val Ala Gly Gly  
 35 40 45  
 Gly Ser Asp Pro Ala Ala Ala Ala Pro Trp Ala Pro Gly Ile Leu Ser  
 50 55 60  
 25 Ser Leu Ile Ala Lys Leu Trp Thr Asp Gly Gly Asp Phe Pro Ala Pro  
 65 70 75 80  
 Val Ile Asp Ile Leu Ala Arg Leu Gly Gln Glu Pro Pro Leu Leu Gly  
 85 90 95  
 30 Glu Glu Gly Asn Asp Phe Val Ala Trp Pro Ser Arg Ile Arg Pro Pro  
 100 105 110  
 Arg Arg Ser Pro Ser Pro Ser Arg Phe Ser Asp Ser Ser Pro Met Ser  
 115 120 125  
 Gly Val Ala Pro Thr Gly Val Ser Ala Pro Ser Ser Pro Thr Val Thr  
 130 135 140  
 35 Val Thr Glu Ala Gly Asp Glu Gly Pro Ala Gly Ser Arg Glu Ser Gly  
 145 150 155 160  
 Leu Ala Leu Gly Arg Val Ser Ser Leu  
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 40 <210> 1039  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens  
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 Xaa Phe Phe Thr Val Xaa Leu Lys Gly Phe Tyr Ser Ile Tyr Ser Xaa  
 20 25 30  
 50 Pro Ile Phe Lys Xaa Arg Xaa Cys Cys Val Ser Lys Ile Xaa Leu Xaa  
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 Xaa Gly Trp  
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 <210> 1040  
 <211> 70  
 <212> PRT  
 60 <213> Homo sapiens  
 <400> 1040  
 Gly Ser Phe Gln Ser Arg Ala Asn Ser Tyr Ala Val Cys Pro Glu Ser

[illegible]

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5	Xaa	Leu	Ala	Ala	Ala	Ala	Asp	Xaa	Xaa	Asp	Gln	Leu	Leu	Val	Gly	Leu
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	Ser	Phe	Ser	Leu	Pro	Ser	Phe	Cys	Ser	Leu	Ser	Phe	Ser	Ser	Phe	Thr
				115				120					125			
	Ala	Gly	Ile	Leu	Pro	Leu	Lys	Val	Leu	Gln	Ala	His	Gly	Leu	Pro	Gly
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	Glu	Gly	Xaa	Ala	Arg	Ser	Xaa	Lys	Gly	Ser	Cys	Pro	Phe	Gln	Ala	Phe
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25	Xaa	Xaa	Thr	Pro	Xaa	Ser	Ser	Phe	Leu	Xaa	Phe	Ser	Xaa	Gln	Leu	Phe
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	Ile	Arg	Leu	Gln	Leu	His	Ser	Xaa	Arg	Leu	Gln	Lys	Leu	Val	Ile	Leu
	65					70					75					80
	Xaa	Ser	Ser	Cys	Cys	Leu	Asn	Phe	Ser	Ser	Ser	Cys	Thr	Xaa	Ser	Xaa
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	Pro	Gly	Arg	Cys	Ser	Gly	Xaa	Xaa	Gly	Ser	Ala	Ala	Gly	Trp	Ser	Leu
				100					105					110		
	Leu	Leu	Ala	Ala	Phe	Phe	Leu	Gln	Pro	Phe	Ile	Phe	Phe	Leu	His	Gly
				115				120					125			
35	Trp	His	Thr	Pro	Ala	Glu	Gly	Ala	Pro	Gly	Ser	Arg	Ser	Ser	Trp	Arg
		130					135					140				
	Gly	Thr	Leu	Val	Ile	Cys	His	Ser	Pro	Ser	Val	Tyr	Leu	Trp	Ile	Leu
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		<212>		PRT												
		<213>		Homo sapiens												
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 <212> PRT  
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 20 25 30  
 Ala His Arg Trp Trp Xaa Xaa Pro Gly Gly Thr His Thr Gly Val Leu  
 35 40 45  
 Ile Gly Arg Thr Ala Thr Val Xaa Glu Xaa Gly Val Arg Val Ile Pro  
 15 50 55 60  
 Lys Lys Trp Arg Ser Ser Glu Thr Xaa Phe Gly Val Xaa Gly Trp Xaa  
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 Glu Xaa Asn Xaa Ile Lys Xaa Asn Xaa Leu Ser Met Gly Ile Phe Gly  
 85 90 95  
 20 Thr His Pro Val Cys Gln Gly  
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<210> 1047  
 <211> 178  
 25 <212> PRT  
 <213> Homo sapiens

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 Glu Gln Asn Leu Asn Met Gln Leu Phe Ser Glu Ile His Asn Leu Gln  
 20 25 30  
 Asn Lys Phe Arg Asp Leu Ser Pro Arg Tyr Asp Ser Leu Val Gln  
 35 35 40 45  
 Ser Gln Ala Arg Glu Leu Ser Leu Gln Arg Gln Gln Ile Lys Asp Gly  
 50 55 60  
 His Gly Ile Cys Val Ile Ser Arg Gln His Met Asn Thr Met Ile Lys  
 65 70 75 80  
 Ala Phe Glu Glu Leu Leu Gln Ala Ser Asp Val Asp Tyr Cys Val Ala  
 40 85 90 95  
 Glu Gly Phe Gln Glu Gln Leu Asn Gln Cys Ala Glu Leu Leu Glu Lys  
 100 105 110  
 Leu Glu Lys Leu Phe Leu Asn Gly Lys Ser Val Gly Val Glu Met Asn  
 115 120 125  
 45 Thr Gln Asn Glu Leu Met Glu Arg Ile Glu Glu Asp Asn Leu Thr Tyr  
 130 135 140  
 Gln His Leu Leu Pro Glu Ser Pro Glu Pro Ser Ala Ser His Ala Leu  
 145 150 155 160  
 Ser Asp Tyr Glu Thr Ser Glu Lys Ser Phe Phe Ser Arg Asp Gln Lys  
 50 165 170 175  
 Pro Arg

<210> 1048  
 55 <211> 141  
 <212> PRT  
 <213> Homo sapiens

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 Lys Gly Ser Thr Pro Ser Thr Ile Glu Gln Val Cys Glu Gln Cys Glu  
 20 25 30

His Gly Gln Ala Asp Pro Gly Arg Gly Leu Gln Arg Leu Lys Leu Leu  
                   35                  40                  45  
 Trp Arg Val Ser Leu Pro Glu Asp Gly Gln Cys Pro Leu His Cys Glu  
           50                  55                  60  
 5 Gln Ile Gly Glu Met Lys Ala Glu Val Thr Lys Leu His Lys Lys Leu  
    65                  70                  75                  80  
 Phe Glu Gln Glu Lys Lys Leu Gln Asn Thr Met Lys Leu Leu Gln Leu  
                   85                  90                  95  
 10 Ser Lys Arg Gln Glu Lys Val Ile Phe Asp Gln Leu Val Val Thr His  
       100                  105                  110  
 Lys Ile Leu Arg Lys Ala Arg Gly Asn Leu Glu Leu Arg Pro Gly Gly  
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 Ala His Pro Gly Thr Cys Ser Pro Ser Arg Pro Gly Ser  
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 Val Val Ala Asn Asp Gln Xaa Gly His Thr Xaa Ser Ala Ser Cys Arg  
 25                  20                  25                  30  
 Thr Ala Thr Val Xaa Arg Xaa Gly Asn Pro Cys His Phe Gln Lys Ser  
           35                  40                  45  
 Gly Gly Val Ser Glu Thr Glu Phe Xaa Xaa His Trp Pro Gly Arg Asn  
       50                  55                  60  
 30 Gln Xaa Asp Gln Met Xaa Tyr Pro Phe His Gly Xaa Ile Cys Xaa Ile  
    65                  70                  75                  80  
 Xaa Phe Val Xaa Leu Lys Gly Xaa Leu Arg Asp Gly His Arg Leu Gly  
                   85                  90                  95  
 Lys Pro Xaa Xaa Xaa Leu Xaa Leu Gly Leu Phe Xaa Pro Leu Ala Xaa  
 35                  100                  105                  110  
 Val Leu Glu Pro Val Leu Lys Arg Xaa Xaa Phe Xaa Pro Xaa Leu Xaa  
       115                  120                  125  
 Ala Xaa Gln Thr Xaa Phe His  
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 Asn Arg Glu Ala Lys Lys Ser Arg Leu Pro Ile Leu Ile Lys Pro Ser  
 50                  20                  25                  30  
 Arg Ser Leu Gly Asn Met Tyr Arg Leu Pro Ala Thr Gln Glu Val Val  
           35                  40                  45  
 Thr Gln Leu Gln Ser Gln Ile Leu Glu Leu Gln Gly Glu Leu Lys Glu  
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 55 Phe Lys Thr Cys Asn Lys Gln Leu His Gln Lys Leu Ile Leu Ala Glu  
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 Ala Val Met Glu Gly Arg Pro Thr Pro Asp Lys Thr Leu Leu Asn Ala  
                   85                  90                  95  
 Gln Pro Pro Val Gly Ala Ala Tyr Gln Asp Ser Pro Gly Glu Gln Lys  
       100                  105                  110  
 60 Gly Ile Lys Thr Thr Ser Ser Val Trp Arg Asp Lys Glu Met Asp Ser  
       115                  120                  125  
 Asp Gln Gln Arg Ser Tyr Glu Ile Asp Ser Glu Ile Cys Pro Pro Asp  
                                   400

130 135 140  
 Asp Leu Ala Ser Leu Pro Ser Cys Lys Glu Asn Pro Glu Asp Val Leu  
 145 150 155 160  
 Ser Pro Thr Ser Val Ala Thr Tyr Leu Ser Ser Lys Ser Gln Pro Ser  
 5 165 170 175  
 Ala Lys Val Ser Val Met Gly Thr Asp Gln Ser Glu Ser Ile Asn Thr  
 180 185 190  
 Ser Asn Glu Thr Glu Tyr Leu Lys Gln Lys Xaa His Asp Leu Gly Asn  
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 10 Trp Asn Leu Xaa Arg Leu Pro Xaa Ile Ser  
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 20 25 30  
 Lys Lys Leu Phe Glu Gln Glu Lys Lys Leu Gln Asn Xaa Met Lys Leu  
 35 40 45  
 25 Leu Gln Leu Ser Lys Arg Gln Glu Lys Val Ile Phe Asp Gln Leu Val  
 50 55 60  
 Val Thr His Lys Ile Leu Arg Lys Ala Arg Gly Asn Leu Glu Leu Arg  
 65 70 75 80  
 Pro Gly Gly Ala His Pro Gly Thr Cys Ser Pro Ser Arg Pro Gly Ser  
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 35 <213> Homo sapiens  
  
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 20 25 30  
 Xaa Thr Ser Ala Phe Ile Ser Pro Ile Cys Ser Gln Xaa Xaa Gly His  
 35 40 45  
 Trp Pro Ser Xaa Gly Ser Glu Thr Leu Xaa Xaa Lys Leu Xaa Pro Ala  
 50 55 60  
 45 Val Xaa Pro Xaa Xaa Arg Val Ser Trp Ala Gly Ser His Xaa Leu Gln  
 65 70 75 80  
 Thr Cys Leu Xaa Xaa Ala Xaa Xaa Xaa Ala Leu Trp Phe Gln Xaa Leu  
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 Ala Lys Gly Ala Glu Ile Lys Thr Asn Glu Val Val Leu Ala Val  
 401

35 40 45  
 Glu Phe His Pro Thr Asp Ala Asn Thr Ile Ile Thr Cys Gly Lys Ser  
 50 55 60  
 His Ile Phe Phe Trp Thr Trp Ser Gly Asn Ser Leu Thr Arg Lys Gln  
 65 70 75 80  
 Gly Ile Phe Gly Lys Tyr Glu Lys Pro Lys Phe Val Gln Cys Leu Ala  
 85 90 95  
 Phe Leu Gly Asn Gly Asp Val Leu Thr Gly Asp Ser Gly Gly Val Met  
 100 105 110  
 10 Leu Ile Trp Ser Lys Thr Thr Val Glu Pro Thr Pro Gly Lys Gly Pro  
 115 120 125  
 Lys Gly Val Tyr Gln Ile Ser Lys Gln Ile Lys Ala His Asp Gly Ser  
 130 135 140  
 Val Phe Thr Leu Cys Gln Met Arg Asn Gly Met Leu Leu Thr Gly Gly  
 145 150 155 160  
 15 Gly Lys Asp Arg Lys Ile Ile Leu Trp Asp His Asp Leu Asn Pro Glu  
 165 170 175  
 Arg Glu Ile Glu Gly Pro Asp Gln Tyr Gly Thr Ile Arg Ala Val Ala  
 180 185 190  
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 195 200 205  
 Ile Leu Arg Xaa Asn His Phe Asn Asp Gly Leu  
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 35 Lys Lys Ile Cys Pro Pro Leu Lys Ile Xaa Arg Xaa Ile Ser Tyr Gly  
 35 40 45  
 Glu Lys Xaa Ser Glu Ile Leu Pro Phe Gly Xaa His Leu Leu Lys Thr  
 50 55 60  
 Xaa Lys Ile Val Xaa Phe Lys Xaa Xaa Xaa Asp Ser Lys His Pro Ile  
 65 70 75 80  
 40 Phe Leu Gln Tyr Val Cys Ser Val His Thr Tyr Arg Ser Ala Pro Val  
 85 90 95  
 Ser Ile Arg His Ile Tyr Leu Ser Val Ser Asn Asp Tyr Tyr Ile Ile  
 100 105 110  
 45 Arg Ser Ala Cys Ala Ile Leu Pro Ala Arg Asn Ile Leu Thr  
 115 120 125  
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 50 <212> PRT  
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 Lys Xaa Ile Gly Asn Pro Ser Leu Trp Xaa Xaa Pro Val Lys Asn Xaa  
 20 25 30  
 Gln Asn Ser Xaa Phe Gln Xaa Xaa Xaa Arg Phe Gln Ala Pro His Leu  
 35 40 45  
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 50 55 60  
 Tyr Gln Ala Tyr Ile Ser Val Cys  
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 10 His Asp Leu Asn Pro Glu Arg Glu Ile Glu Val Pro Asp Gln Tyr Gly  
           20                   25                   30  
 Thr Ile Arg Ala Val Ala Glu Gly Lys Ala Asp Gln Phe Leu Val Gly  
           35                   40                   45  
 15 Thr Ser Arg Asn Phe Ile Leu Arg Gly Thr Phe Asn Asp Gly Phe Gln  
           50                   55                   60  
 Ile Glu Val Gln Gly His Thr Asp Glu Leu Trp Gly Leu Ala Thr His  
 65                   70                   75                   80  
 Pro Phe Lys Asp Leu Leu Thr Cys Ala Gln Asp Arg Gln Val Cys  
           85                   90                   95  
 20 Leu Trp Asn Ser Met Glu His Xaa Leu Glu Trp Thr Arg Leu Val Asp  
           100                   105                   110  
 Glu Pro Gly His Cys Ala Asp Phe His Pro Ser Gly Thr Val Val Ala  
           115                   120                   125  
 25 Ile Gly Thr His Ser Gly Arg Trp Phe Val Leu Asp Ala Glu Thr Arg  
           130                   135                   140  
 Asp Leu Val Ser Ile His Thr Asp Gly Asn Glu Gln Leu Ser Val Met  
 145                   150                   155                   160  
 Arg Tyr Ser Ile Asp Gly Thr Phe Leu Ala Val Gly Ser His Asp Asn  
           165                   170                   175  
 30 Phe Ile Tyr Leu Tyr Val Val Ser Glu Asn Gly Arg Lys Xaa Ser Arg  
           180                   185                   190  
 Tyr Gly Arg Xaa Thr Gly His Ser Ser Tyr Ile Thr His Xaa  
           195                   200                   205  
  
 35           <210> 1057  
           <211> 70  
           <212> PRT  
           <213> Homo sapiens  
  
           <400> 1057  
 Glu Asp Met Xaa His Val Glu Xaa Leu Ser Glu Ile Ser Met Xaa Ile  
 1                   5                   10                   15  
 Gly Xaa Xaa Xaa Leu Pro Phe Gly Xaa Gln Leu Leu Lys Thr Leu Lys  
           20                   25                   30  
 45 Ile Val Leu Phe Lys Arg Arg Glu Ile Pro Ser Asn Pro Ser Phe Phe  
           35                   40                   45  
 Ser Met Tyr Val Leu Thr Tyr Leu Ser Glu Arg Ala Ser Lys Tyr Gln  
           50                   55                   60  
 Ala Tyr Ile Ser Val Cys  
 50 65                   70  
  
           <210> 1058  
           <211> 99  
           <212> PRT  
 55           <213> Homo sapiens  
  
           <400> 1058  
 Tyr Leu Leu Ala Arg Ser Asp Lys Tyr Val Arg Thr Tyr Ile Leu Lys  
 1                   5                   10                   15  
 60 Lys Asp Gly Leu Leu Gly Ile Ser Leu Leu Leu Lys Arg Thr Ile Leu  
           20                   25                   30  
 Arg Val Phe Asn Ser Cys Xaa Pro Lys Gly Arg Xaa Xaa Asp Pro Ile  
           35                   40                   45

Xaa Ile Glu Ile Ser Leu Ser Xaa Ser Thr Trp Xaa Ile Ser Ser Tyr  
 50 55 60  
 Leu Lys Lys His Thr Val Phe Ser Leu Xaa Pro Leu Asn Thr Pro Thr  
 65 70 75 80  
 5 Pro Phe His Tyr Xaa Gly Xaa Lys Xaa Met Val Xaa Asn Xaa Pro Trp  
 85 90 95  
 Glu Val Thr

10 <210> 1059  
 <211> 219  
 <212> PRT  
 <213> Homo sapiens

15 <400> 1059  
 Phe Leu Gln Pro Leu Gln Pro His Val Arg Val Trp Asp Ser Val Thr  
 1 5 10 15  
 Leu Ser Thr Leu Gln Ile Ile Gly Leu Gly Thr Phe Glu Arg Gly Val  
 20 20 25 30  
 Gly Cys Leu Asp Phe Ser Lys Ala Asp Ser Gly Val His Leu Cys Val  
 35 40 45  
 Ile Asp Asp Ser Asn Glu His Met Leu Thr Val Trp Asp Trp Gln Arg  
 50 55 60  
 Lys Ala Lys Gly Ala Glu Ile Lys Thr Thr Asn Glu Val Val Leu Ala  
 25 65 70 75 80  
 Val Glu Phe His Pro Thr Asp Ala Asn Thr Ile Ile Thr Cys Gly Lys  
 85 90 95  
 Ser His Ile Phe Phe Trp Thr Trp Ser Gly Asn Ser Leu Thr Arg Lys  
 100 105 110  
 30 Gln Gly Ile Phe Gly Lys Tyr Glu Lys Pro Lys Phe Val Gln Cys Leu  
 115 120 125  
 Ala Phe Leu Gly Asn Gly Asp Val Leu Thr Gly Asp Ser Gly Gly Val  
 130 135 140  
 Met Leu Ile Trp Ser Lys Thr Thr Val Glu Pro Thr Pro Gly Lys Gly  
 35 145 150 155 160  
 Pro Lys Gly Val Tyr Gln Ile Ser Lys Gln Ile Lys Ala His Asp Gly  
 165 170 175  
 Ser Val Phe Thr Leu Cys Gln Met Arg Asn Gly Met Leu Leu Thr Gly  
 180 185 190  
 40 Gly Xaa Lys Asp Arg Lys Ile Ile Leu Trp Asp His Asp Leu Asn Pro  
 195 200 205  
 Glu Arg Arg Asn Arg Xaa Ser Trp Ile Ser Met  
 210 215

45 <210> 1060  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

50 <400> 1060  
 Leu Leu His His Gln Ile Ser Met Cys Tyr Thr Pro Cys Lys Lys Tyr  
 1 5 10 15  
 Thr Asp Met Asn Arg Gln Phe Leu Glu Lys Lys Glu His Phe Phe Lys  
 20 25 30  
 55 Tyr Leu Gly Asn Thr Ala Leu Ser Asp Gln Gln Gly Val Tyr Leu Arg  
 35 40 45  
 Thr Ser Val Thr Phe Gly Val Ala Met Tyr Asn Glu Ile Tyr Asn His  
 50 55 60  
 Asp Thr Leu Arg Trp

60 65  
 <210> 1061  
 <211> 86

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1061

5 Arg Gly Xaa Trp Lys Pro Leu Cys Val Ser Leu Asp Lys Lys Ile Cys  
 1 5 10 15  
 Thr Xaa Val Glu Asn Thr Gln Cys Arg Ser Xaa Cys Gly Xaa Xaa Ile  
 20 25 30  
 Xaa Ile Ser Phe Pro Phe Gly Leu Pro Leu Leu Lys Xaa Leu Lys Ile  
 10 35 40 45  
 Val Xaa Phe Gln Lys Lys Arg Asp Ser Lys Xaa Pro Ile Phe Leu Gln  
 50 55 60  
 Tyr Val Cys Ser Cys Thr Tyr Leu Ser Glu Arg Ala Ser Lys Tyr Gln  
 65 70 75 80  
 15 Ala Tyr Ile Ser Val Cys  
 85

&lt;210&gt; 1062

&lt;211&gt; 200

20 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1062

25 Leu Ala Arg Ser Ala Asp Arg Arg Ala Ser Thr Asp Leu Thr Arg Lys  
 1 5 10 15  
 Met Lys Pro Asp Glu Thr Pro Met Phe Asp Pro Ser Leu Leu Lys Glu  
 20 25 30  
 Val Asp Trp Ser Gln Asn Thr Ala Thr Phe Ser Pro Ala Ile Ser Pro  
 35 40 45  
 30 Thr His Pro Gly Glu Gly Leu Val Leu Arg Pro Leu Cys Thr Ala Asp  
 50 55 60  
 Leu Asn Arg Gly Phe Phe Lys Val Leu Gly Gln Leu Thr Glu Thr Gly  
 65 70 75 80  
 Val Val Ser Pro Glu Gln Phe Met Lys Ser Phe Glu His Met Lys Lys  
 85 90 95  
 35 Ser Gly Asp Tyr Tyr Val Thr Val Val Glu Asp Val Thr Leu Gly Gln  
 100 105 110  
 Ile Val Ala Thr Ala Thr Leu Ile Ile Glu His Lys Phe Ile His Ser  
 115 120 125  
 40 Cys Ala Lys Arg Gly Arg Val Glu Asp Val Val Val Ser Asp Glu Cys  
 130 135 140  
 Arg Gly Lys Gln Leu Gly Lys Leu Leu Leu Ser Thr Leu Thr Leu Leu  
 145 150 155 160  
 Ser Lys Lys Leu Asn Cys Tyr Lys Ile Thr Leu Glu Cys Leu Pro Gln  
 165 170 175  
 45 Asn Val Gly Phe Tyr Lys Lys Phe Gly Tyr Thr Val Ser Glu Glu Asn  
 180 185 190  
 Tyr Met Cys Arg Arg Phe Leu Lys  
 195 200

50

&lt;210&gt; 1063

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

55

&lt;400&gt; 1063

Tyr Val Gly Asn Asn Thr Pro Leu Ser Val Leu Arg Cys Phe Phe Glu  
 1 5 10 15  
 Thr Lys Ile Phe Asn Phe Met His Val Ile Asn Ser Leu Ile Gln Xaa  
 20 25 30  
 Tyr Phe Phe Xaa Met Ser His Pro Asp Xaa Asp Xaa Tyr Phe Leu Leu  
 35 40 45  
 Pro Ile Leu Leu Thr Pro Lys Lys Gly Ser Gln Leu Leu Glu Lys Tyr

50 55 60  
 His Ala Gly Lys Asp Gln Val Lys Xaa Phe Ser Leu Xaa Lys Asn Ile  
 65 70 75 80  
 Pro Xaa Xaa Ile His Trp Lys Leu Asn Pro Xaa Gly Pro Pro Xaa Gln  
 85 90 95  
 5 Glu Ser Leu Lys Ala Phe Ser Trp Gly Phe Gln Gly Phe Pro  
 100 105 110  
  
 <210> 1064  
 10 <211> 266  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 1064  
 15 Val Ala Ala Ser Leu Leu Ala Pro Leu Leu Pro Glu Gly Ile Lys Glu  
 1 5 10 15  
 Glu Glu Glu Arg Trp Arg Arg Lys Val Ile Cys Lys Glu Glu Pro Val  
 20 25 30  
 Ser Glu Val Lys Glu Thr Ser Thr Thr Val Glu Glu Ala Thr Thr Ile  
 35 40 45  
 Val Lys Pro Gln Glu Ile Met Leu Asp Asn Ile Glu Asp Pro Ser Gln  
 50 55 60  
 Glu Asp Leu Cys Ser Val Val Gln Ser Gly Glu Ser Glu Glu Glu Glu  
 65 70 75 80  
 25 Glu Gln Asp Thr Leu Glu Leu Glu Leu Val Leu Glu Arg Lys Lys Ala  
 85 90 95  
 Glu Leu Arg Ala Leu Glu Glu Gly Asp Gly Ser Val Ser Gly Ser Ser  
 100 105 110  
 Pro Arg Ser Asp Ile Ser Gln Pro Ala Ser Gln Asp Gly Met Arg Arg  
 115 120 125  
 30 Leu Met Ser Lys Arg Gly Lys Trp Lys Met Phe Val Arg Ala Thr Ser  
 130 135 140  
 Pro Glu Ser Thr Ser Arg Ser Ser Ser Lys Thr Gly Arg Asp Thr Pro  
 145 150 155 160  
 35 Glu Asn Gly Glu Thr Ala Ile Gly Ala Glu Asn Ser Glu Lys Ile Asp  
 165 170 175  
 Glu Asn Ser Asp Lys Glu Met Glu Val Glu Glu Ser Ser Glu Lys Ile  
 180 185 190  
 Lys Val Gln Thr Thr Pro Lys Val Glu Glu Glu Gln Asp Leu Lys Phe  
 195 200 205  
 40 Gln Ile Gly Glu Leu Ala Asn Thr Leu Pro Ser Lys Phe Arg Val Ser  
 210 215 220  
 Ser Ile Asn Arg Gln Ser Ile Phe Asn Phe His Val Leu Leu Phe Gln  
 225 230 235 240  
 45 Thr Gly Thr Arg Ile Ala Thr Gly Gly Lys Gly Leu Leu Met Thr Leu  
 245 250 255  
 Asn Glu Asn Phe Arg Met Gln Gln Asn Asn  
 260 265  
  
 50 <210> 1065  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens  
  
 55 <400> 1065  
 Asp Leu Pro Met His Asn Arg Val Ser Ser Phe Ile Asn Glu Gly Thr  
 1 5 10 15  
 Gln Ser Pro Arg Thr Leu Ile Ser Leu Pro Lys Lys Arg Thr Thr Lys  
 20 25 30  
 60 Phe Val Lys Gly Asp Ser Ser Pro Leu Gly Pro Trp Asn Ser His Phe  
 35 40 45  
 Ile Phe Leu Ile Ser Asn Thr Val Lys Ala Lys Glu Arg Glu Arg Ile  
 50 55 60

Trp Glu Leu Lys Asn Lys Arg Ala Lys Ile Ser Asn Asn Glu Lys Lys  
 65 70 75 80  
 Ile Lys Lys Ser Gln Ile Tyr Lys Glu Met Phe Ser Ser Asp Leu Leu  
 85 90 95  
 5 Ala Glu Asp Ser Asn Leu Val Leu His Ser His Leu Gln Pro Arg Ser  
 100 105 110  
 Phe Pro

10 <210> 1066  
 <211> 276  
 <212> PRT  
 <213> Homo sapiens

15 <400> 1066  
 Val Ala Ala Ser Leu Leu Ala Pro Leu Leu Pro Glu Gly Ile Lys Glu  
 1 5 10 15  
 Glu Glu Glu Arg Trp Arg Arg Lys Val Ile Cys Lys Glu Glu Pro Val  
 20 20 25 30  
 Ser Glu Val Lys Glu Thr Ser Thr Thr Val Glu Glu Ala Thr Thr Ile  
 35 40 45  
 Val Lys Pro Gln Glu Ile Met Leu Asp Asn Ile Glu Asp Pro Ser Gln  
 50 55 60  
 Glu Asp Leu Cys Ser Val Val Gln Ser Gly Glu Ser Glu Glu Glu Glu  
 25 65 70 75 80  
 Glu Gln Asp Thr Leu Glu Leu Glu Leu Val Leu Glu Arg Lys Lys Ala  
 85 90 95  
 Glu Leu Arg Ala Leu Glu Glu Gly Asp Gly Ser Val Ser Gly Ser Ser  
 100 105 110  
 30 Pro Arg Ser Asp Ile Ser Gln Pro Ala Ser Gln Asp Gly Met Arg Arg  
 115 120 125  
 Leu Met Ser Lys Arg Gly Lys Trp Lys Met Phe Val Arg Ala Thr Ser  
 130 135 140  
 Pro Glu Ser Thr Ser Arg Ser Ser Ser Lys Thr Gly Arg Asp Thr Pro  
 35 145 150 155 160  
 Glu Asn Gly Glu Thr Ala Ile Gly Ala Glu Asn Ser Glu Lys Ile Asp  
 165 170 175  
 Glu Asn Ser Asp Lys Glu Met Glu Val Glu Glu Ser Ser Glu Lys Ile  
 180 185 190  
 40 Lys Val Gln Thr Thr Pro Lys Xaa Glu Glu Gln Asp Leu Lys Phe  
 195 200 205  
 Gln Ile Gly Glu Leu Ala Asn Thr Leu Pro Ser Lys Phe Arg Val Ser  
 210 215 220  
 Ser Ile Asn Arg Gln Xaa Ile Phe Asn Phe His Val Leu Leu Phe Gln  
 45 225 230 235 240  
 Thr Gly Thr Arg Ile Ala Thr Gly Xaa Lys Gly Xaa Phe Met Xaa Thr  
 245 250 255  
 Thr Leu Thr Lys Thr Leu Gly Cys Pro Xaa Thr Thr Xaa Pro Phe Glu  
 260 265 270  
 50 Ile Xaa Pro Ser  
 275

<210> 1067  
 <211> 114  
 55 <212> PRT  
 <213> Homo sapiens

<400> 1067  
 Asp Leu Pro Met His Asn Arg Val Ser Ser Phe Ile Asn Glu Gly Thr  
 1 5 10 15  
 Gln Ser Pro Arg Thr Leu Ile Ser Leu Pro Lys Lys Arg Thr Thr Lys  
 20 25 30  
 Phe Val Lys Gly Asp Ser Ser Pro Leu Gly Pro Trp Asn Ser His Phe

35 40 45  
 Ile Phe Leu Ile Ser Asn Thr Val Lys Ala Lys Glu Arg Glu Arg Ile  
 50 55 60  
 Trp Glu Leu Lys Asn Lys Arg Ala Lys Ile Ser Asn Asn Glu Lys Lys  
 5 65 70 75 80  
 Ile Lys Lys Ser Gln Ile Tyr Lys Glu Met Phe Ser Ser Asp Leu Leu  
 85 90 95  
 Ala Glu Asp Ser Asn Leu Val Leu His Ser His Leu Gln Pro Arg Ser  
 100 105 110  
 10 Phe Pro

<210> 1068  
 <211> 87  
 15 <212> PRT  
 <213> Homo sapiens

<400> 1068  
 Arg Thr Arg Leu Leu Ser Ser Ala Ser Arg Ser Asp Glu Asn Ile Ser  
 20 1 5 10 15  
 Leu Tyr Ile Trp Leu Phe Leu Ile Phe Phe Ser Leu Phe Glu Ile Phe  
 20 25 30  
 Ala Leu Leu Phe Phe Ser Ser Gln Ile Leu Ser Leu Ser Leu Ala Phe  
 35 40 45  
 25 Thr Val Phe Asp Ile Lys Asn Met Lys Cys Glu Phe His Gly Pro Arg  
 50 55 60  
 Gly Glu Glu Ser Pro Phe Thr Asn Phe Val Val Leu Phe Phe Gly Arg  
 65 70 75 80  
 Glu Ile Ser Val Leu Gly Asp  
 30 85

<210> 1069  
 <211> 265  
 35 <212> PRT  
 <213> Homo sapiens

<400> 1069  
 Val Thr Lys Leu Ser Val Lys Asp Arg Leu Gly Phe Val Ser Lys Pro  
 40 1 5 10 15  
 Ser Val Ser Ala Thr Glu Lys Val Leu Ser Thr Ser Thr Gly Leu Thr  
 20 25 30  
 Lys Thr Val Tyr Asn Pro Ala Ala Leu Lys Ala Ala Gln Lys Thr Leu  
 35 40 45  
 Leu Val Ser Thr Ser Ala Val Asp Asn Asn Glu Ala Gln Lys Lys Lys  
 50 55 60  
 45 Gln Glu Ala Leu Lys Leu Gln Gln Asp Val Arg Lys Arg Lys Gln Glu  
 65 70 75 80  
 Ile Leu Glu Lys His Ile Glu Thr Gln Lys Met Leu Ile Ser Lys Leu  
 85 90 95  
 50 Glu Lys Asn Lys Thr Met Lys Ser Glu Asp Lys Ala Glu Ile Met Lys  
 100 105 110  
 Thr Leu Glu Val Leu Thr Lys Asn Ile Thr Lys Leu Lys Asp Glu Val  
 115 120 125  
 Lys Ala Ala Ser Pro Gly Arg Cys Leu Pro Lys Ser Ile Lys Thr Lys  
 55 130 135 140  
 Thr Gln Met Gln Lys Glu Leu Leu Asp Thr Glu Leu Asp Leu Tyr Lys  
 145 150 155 160  
 Lys Met Gln Ala Gly Glu Glu Val Thr Glu Leu Arg Arg Lys Tyr Thr  
 165 170 175  
 60 Glu Leu Gln Leu Glu Ala Ala Lys Arg Gly Ile Leu Ser Ser Gly Arg  
 180 185 190  
 Gly Arg Gly Ile His Ser Arg Xaa Arg Gly Ala Val His Gly Arg Ser  
 195 200 205

Arg Gly Arg Arg Pro Arg Pro Ser Val Pro Gly Met Leu Trp Trp Ile  
     210                    215                    220  
 Pro Ser Lys Ala Leu Glu Ile Ser Ala Leu Pro Gly Ala Ile Xaa Xaa  
 225                    230                    235                    240  
 5 Ile Phe Phe Leu Xaa Ala Gln Ile Xaa Glu Ile Glu Xaa Gly Lys Ile  
                     245                    250                    255  
 Gly Asp Xaa His Phe Met Pro Asn Tyr  
                     260                    265

10           <210> 1070  
             <211> 27  
             <212> PRT  
             <213> Homo sapiens

15           <400> 1070  
 Val Leu Met His Pro Asp Val Ile Ile Lys Trp Asn Gly Leu Phe Lys  
   1                    5                    10                    15  
 Lys Lys Lys Gly Lys Lys Arg Glu Lys Gln Cys  
                     20                    25

20           <210> 1071  
             <211> 63  
             <212> PRT  
             <213> Homo sapiens

25           <400> 1071  
 Gln Leu Phe Thr Glu Val Lys Cys Lys His Gln Ser Phe Lys Ile Lys  
   1                    5                    10                    15  
 Xaa Arg Xaa Glu Val Ser Ser Phe Leu Ala Ile Xaa Glu Ile His Leu  
 30                      20                    25                    30  
 His Pro Phe Tyr Gln Lys Leu Phe Leu Gln Ile Cys Lys Ser Xaa Leu  
           35                    40                    45  
 Asp Asn Leu Met Lys His Arg Xaa Arg Ser Ser Tyr Xaa Asp Gln  
   50                    55                    60

35           <210> 1072  
             <211> 190  
             <212> PRT  
             <213> Homo sapiens

40           <400> 1072  
 Asn Thr Ser Leu Val Ile Asp Glu Thr Leu Leu Glu Gln Gly Gln Leu  
   1                    5                    10                    15  
 Asp Thr Pro Gly Val His Asn Val Thr Ala Leu Ser Asn Leu Ile Thr  
 45                      20                    25                    30  
 Trp Gln Lys Val Asp Tyr Asp Phe Ser Tyr His Gln Met Glu Phe Pro  
           35                    40                    45  
 Cys Asn Ile Asn Val Phe Ile Thr Ser Glu Gly Arg Ser Leu Leu Pro  
   50                    55                    60  
 50 Ala Asp Cys Gln Ile His Leu Gln Pro Gln Leu Ile Pro Pro Asn Met  
   65                    70                    75                    80  
 Glu Glu Tyr Met Asn Ser Leu Leu Ser Ala Val Leu Pro Ser Val Leu  
                     85                    90                    95  
 Asn Lys Phe Arg Ile Tyr Leu Thr Leu Leu Arg Phe Leu Glu Tyr Ser  
 55                      100                    105                    110  
 Ile Ser Asp Glu Ile Thr Lys Ala Val Glu Asp Asp Phe Val Glu Met  
           115                    120                    125  
 Arg Lys Asn Asp Pro Gln Ser Ile Thr Ala Asp Asp Leu His Gln Leu  
   130                    135                    140  
 60 Leu Val Val Ala Arg Cys Leu Ser Leu Ser Ala Gly Gln Thr Thr Leu  
   145                    150                    155                    160  
 Ser Arg Glu Arg Trp Leu Arg Ala Lys Gln Leu Glu Ser Leu Arg Arg  
                     165                    170                    175

Thr Arg Leu Gln Gln Gln Lys Cys Val Asn Gly Asn Glu Leu  
 180 185 190

5 <210> 1073  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

10 <400> 1073  
 Leu Leu Ile Trp Asp Val Leu Phe Ile Gly Lys Val Leu Ser Arg Glu  
 1 5 10 15  
 Leu Phe Cys Lys Thr Lys Gln Cys Met Tyr Phe Ser Leu Val Asn Tyr  
 20 25 30  
 Asn Leu His Trp His Lys Lys His Met Val Thr Asn Val Leu Cys Ser  
 35 40 45  
 15 Arg Thr Ile Lys Glu Asn Val Phe Tyr Pro His Lys Ser Ser Glu Ala  
 50 55 60  
 Phe Ile Leu Phe Leu Lys Val  
 65 70

20 <210> 1074  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

25 <400> 1074  
 Leu Ala Asp Leu Thr Tyr Phe Gly Thr Thr Asp Asp Pro Xaa Lys Asn  
 1 5 10 15  
 Ala Gln Asn Xaa Ile Xaa Ser Lys His Leu Met Thr Phe Xaa Lys Ile  
 20 25 30  
 30 Lys Leu Xaa Lys Xaa Xaa Met Xaa Phe Xaa Val Pro Ile Leu Phe His  
 35 40 45  
 Ile Xaa Ala Gln Leu Cys Xaa Pro Xaa Phe Pro Leu His Gly Ser Gln  
 50 55 60  
 35 Met Pro Trp Asp Trp Glu Lys  
 65 70

40 <210> 1075  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

45 <400> 1075  
 Cys Ser Glu Lys Ala Ala Pro His Lys Ala Glu Gly Leu Glu Glu Ala  
 1 5 10 15  
 Asp Thr Gly Ala Ser Gly Cys His Ser His Pro Glu Glu Gln Pro Thr  
 20 25 30  
 Ser Ile Ser Pro Ser Arg His Gly Ala Leu Ala Glu Leu Cys Pro Pro  
 35 40 45  
 50 Gly Gly Ser His Arg Met Ala Leu Gly Thr Ala Ala Ala Leu Gly Ser  
 50 55 60  
 Asn Val Ile Arg Asn Glu Gln Leu Pro Leu Gln Tyr Leu Ala Asp Val  
 65 70 75 80  
 Asp Thr Ser Asp Glu Glu Ser Ile Arg Ala His Val Met Ala Ser His  
 85 90 95  
 55 His Ser Lys Arg Arg Gly Arg Ala Ser Ser Glu Ser Gln Gly Leu Gly  
 100 105 110  
 Ala Gly Val Arg Thr Glu Ala Asp Val Xaa Glu Glu Ala Leu Arg Arg  
 115 120 125  
 60 Lys Leu Glu Glu Leu Thr Ser Asn Val Ser Asp Gln Glu Thr Ser Ser  
 130 135 140  
 Glu Glu Glu Glu Ala Lys Asp Glu Lys Ala Glu Pro Asn Arg Asp Lys  
 145 150 155 160



Ser Val Gly Pro Leu Pro Gln Ala Asp Pro Glu Val Gly Thr Xaa Ala  
 165 170 175  
 Ile Lys Pro Thr Asp Arg Lys Lys Ala Pro Arg Thr Leu Gly Thr Pro  
 180 185 190  
 5 Ser Val Asn Arg Thr Thr Asp Glu Glu Leu Ser Xaa Leu Xaa Asp Arg  
 195 200 205  
 Xaa Ala Ile Asp Arg Leu  
 210  
 10 <210> 1076  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens  
 15 <400> 1076  
 Pro Ala Thr Ser Val Thr Arg Arg Pro Arg Pro Arg Arg Arg Lys Pro  
 1 5 10 15  
 Arg Thr Lys Arg Gln Ser Pro Thr Gly Thr Asn Gln Leu Gly Leu Ser  
 20 20 25 30  
 Pro Arg Arg Thr Arg Arg Trp Ala Arg Xaa Pro Ser Asn Gln Gln Thr  
 35 40 45  
 Gly Lys Lys Pro Pro Gly Pro Trp Gly Pro Arg Gln Ser Thr Gly Pro  
 50 55 60  
 Gln Met Arg Ser Cys Gln Xaa Trp Xaa Thr Xaa Trp Gln Leu Thr Gly  
 65 70 75 80  
 25 Phe Lys Ser Xaa Thr Gly Lys Xaa Ser Xaa Val Phe Xaa Thr Phe Glu  
 85 90 95  
 Xaa Lys Asp Cys Asn Pro Leu Arg Ala Pro Arg Ala Ser Thr Gly  
 100 105 110  
 30 <210> 1077  
 <211> 236  
 <212> PRT  
 <213> Homo sapiens  
 35 <400> 1077  
 Ala Phe Leu Ala Ser Leu Glu Arg Gly Arg Arg Ile Ile Asp Arg Thr  
 1 5 10 15  
 Leu Arg Thr Leu Gly Pro Ser Asp Met Phe Pro Ala Glu Val Ala Trp  
 40 20 25 30  
 Ser Leu Ser Leu Cys Gly Asp Leu Gly Leu Pro Leu Asp Met Val Glu  
 35 40 45  
 Leu Met Leu Glu Glu Lys Gly Val Gln Leu Asp Ser Ala Gly Leu Glu  
 50 55 60  
 Arg Leu Ala Gln Glu Glu Ala Gln His Arg Ala Arg Gln Ala Glu Pro  
 65 70 75 80  
 Val Gln Lys Gln Gly Leu Trp Leu Asp Val His Ala Leu Gly Glu Leu  
 85 90 95  
 Gln Arg Gln Gly Val Pro Pro Thr Asp Asp Ser Pro Lys Tyr Asn Tyr  
 100 105 110  
 50 Ser Leu Arg Pro Ser Gly Ser Tyr Glu Phe Gly Thr Cys Glu Ala Gln  
 115 120 125  
 Val Leu Gln Leu Tyr Thr Glu Asp Gly Thr Ala Val Ala Ser Val Gly  
 130 135 140  
 55 Lys Gly Gln Arg Cys Gly Leu Leu Leu Asp Arg Thr Asn Phe Tyr Ala  
 145 150 155 160  
 Glu Gln Gly Gly Gln Ala Ser Asp Arg Gly Tyr Leu Val Arg Ala Gly  
 165 170 175  
 Gln Glu Asp Val Leu Phe Pro Val Ala Arg Ala Gln Val Cys Gly Gly  
 180 185 190  
 60 Phe Ile Leu His Glu Ala Ile Xaa Pro Glu Cys Leu Arg Leu Gly Asp  
 195 200 205  
 Gln Val Gln Leu His Val Asp Xaa Ala Trp Arg Leu Ser Cys Met Ala  
 411

	210		215		220
	Lys His Thr Gly Thr His Leu Ala Glu Leu Gly Thr				
	225		230		235

5           <210> 1078  
             <211> 125  
             <212> PRT  
             <213> Homo sapiens

10           <400> 1078  
             Thr Pro Leu Asp Trp Ser Gly Trp Pro Lys Arg Arg Pro Ser Thr Gly  
             1                           5                           10                           15  
             His Gly Arg Leu Ser Gln Phe Arg Ser Arg Asp Cys Gly Leu Met Ser  
                          20                           25                           30  
 15           Met Arg Leu Gly Ser Cys Ser Ala Lys Glu Cys Pro Gln Leu Thr Thr  
                          35                           40                           45  
             Ala Pro Ser Thr Thr Thr Pro Cys Asp Pro Ala Glu Val Met Ser Ser  
                          50                           55                           60  
             Ala Pro Val Arg Pro Arg Cys Cys Asn Cys Ile Gln Arg Thr Gly Gln  
 20           65                           70                           75                           80  
             Gln Trp Pro Pro Trp Gly Lys Ala Ser Ala Val Ala Ser Ser Trp Thr  
                          85                           90                           95  
             Gly Pro Thr Ser Thr Gln Asn Arg Gly Ala Arg Leu Gln Thr Val Ala  
                          100                           105                           110  
 25           Thr Trp Cys Gly Gln Gly Lys Arg Thr Cys Cys Ser Gln  
                          115                           120                           125

            <210> 1079  
             <211> 180  
             <212> PRT  
             <213> Homo sapiens

30           <400> 1079  
             Asn Leu His Arg Pro Gly Pro Gly Leu Leu Gly Thr Ala Arg Pro Leu  
             1                           5                           10                           15  
             Ala Leu Pro Ala Pro Gly Ser His Gly Leu Lys Pro Gly Pro Pro Val  
                          20                           25                           30  
             Leu Arg Arg Ser Trp Ser Cys Pro Arg Gly Gly His Ser Ala Gly Leu  
                          35                           40                           45  
 40           Ser Pro Arg Arg Pro Leu Leu Ser Arg Pro Leu Tyr Thr Val Ala Thr  
                          50                           55                           60  
             Pro Gly Pro His Arg Cys Arg Thr His Asn Phe Arg Trp Val Ala Gly  
             65                           70                           75                           80  
             Ser Ser Cys Thr Trp Gly Cys Arg Gln Leu Gly Ala Leu Leu Gly Ala  
                          85                           90                           95  
 45           Ala Ala Pro Gln Ala His Gly His Gln Ala Thr Ile Pro Ala Ser Glu  
                          100                           105                           110  
             Leu Ala Gln Pro Ala Val Pro Gly Ala Gly Pro Pro Leu Gly Pro Thr  
                          115                           120                           125  
 50           Ala Pro Val Gln Arg Ser Leu Ala Gly Pro Leu Ser Pro Pro Ala Ser  
                          130                           135                           140  
             Ala Leu Pro Cys Pro Arg Gly Val Pro Gly Leu His Thr Val Thr Arg  
             145                           150                           155                           160  
             Thr Arg Pro Leu Gln Gly Thr Tyr Leu Lys Ala Pro Gly Ser Ser  
                          165                           170                           175  
 55           Glu Ser Asp Gln  
                          180

60           <210> 1080  
             <211> 137  
             <212> PRT  
             <213> Homo sapiens

<400> 1080  
 Thr Arg Ala Pro Xaa Ala Thr Xaa Trp Gly Phe Xaa Ile Gln Ala Pro  
 1 5 10 15  
 Gln Gly Pro Met Xaa Lys Xaa Phe Leu Leu Cys Pro Phe Gln Gly Xaa  
 20 25 30  
 Pro Arg Val Pro Ile Ala Pro Pro Phe His Asn Xaa Arg Ala Trp Gly  
 35 40 45  
 Thr Gly Lys Cys Ser Lys Pro Pro Ile Gly Gly Pro Arg Ala Trp Gly  
 50 55 60  
 Xaa Xaa Lys Trp Trp Ala Gln Gly Pro Gly Lys His Leu Xaa Asp Xaa  
 65 70 75 80  
 Gly Lys Leu Ala Leu Gln Tyr Ser Pro Lys Pro Met Xaa Ser Ser Gln  
 85 90 95  
 Leu Leu Thr Gln Val Arg Pro Arg Asp Pro Thr Trp Thr Lys Gly Asn  
 100 105 110  
 Ala Arg Ser Pro Glu Gly Ala Ser Arg Thr Phe Pro His Ala Glu Ala  
 115 120 125  
 Arg Thr Arg Gly Trp Arg Pro Ser Ser  
 130 135  
 <210> 1081  
 <211> 235  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1081  
 Ala Leu Asp Cys Asn Ser Glu Glu Asn Asn Phe Leu Thr Arg Glu Asn  
 1 5 10 15  
 Gly Glu Pro Asp Ala Phe Asp Glu Leu Phe Asp Ala Asp Gly Asp Gly  
 20 25 30  
 Glu Ser Tyr Thr Glu Glu Ala Asp Asp Gly Glu Thr Gly Glu Thr Arg  
 35 40 45  
 Asp Glu Lys Glu Asn Leu Ala Thr Leu Phe Gly Asp Met Glu Asp Leu  
 50 55 60  
 Thr Asp Glu Glu Glu Val Pro Ala Ser Gln Ser Thr Glu Asn Arg Val  
 65 70 75 80  
 Leu Pro Ala Pro Ala Pro Arg Arg Glu Lys Thr Asn Glu Glu Leu Gln  
 85 90 95  
 Glu Glu Leu Arg Asn Leu Gln Glu Gln Met Lys Ala Leu Gln Glu Gln  
 100 105 110  
 Leu Lys Val Thr Thr Ile Lys Gln Thr Ala Ser Pro Ala Arg Leu Gln  
 115 120 125  
 Lys Ser Pro Val Glu Lys Ser Pro Arg Pro Pro Leu Lys Glu Arg Arg  
 130 135 140  
 Val Gln Arg Ile Gln Glu Ser Thr Cys Phe Ser Ala Glu Leu Asp Val  
 145 150 155 160  
 Pro Ala Leu Pro Arg Thr Lys Arg Val Ala Arg Thr Pro Lys Ala Ser  
 165 170 175  
 Pro Pro Asp Pro Lys Ser Ser Ser Ser Arg Met Thr Ser Ala Pro Ser  
 180 185 190  
 Gln Pro Leu Gln Thr Ile Ser Arg Asn Lys Pro Ser Gly Ile Leu Glu  
 195 200 205  
 Val Lys Leu Xaa Gly Thr Pro Arg Lys Xaa Leu Gly Lys Arg Leu Xaa  
 210 215 220  
 Pro Ile Cys Val Glu Thr Phe Xaa Trp Ser Trp  
 225 230 235  
 <210> 1082  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1082

Val Glu Asn Gln Val Ile Ile Val Phe Ser Lys Leu Ser Val Asp Asp  
 1 5 10 15  
 Cys Ile Thr Ser Phe Thr Glu Val Phe Ala Gln Lys Leu Glu Gly Lys  
 20 25 30  
 5 Gln Arg Ala Met Phe Leu Tyr Leu Leu Val Ile Glu Cys Ser Leu Leu  
 35 40 45  
 Tyr His Asn Lys Ile Leu Val Phe Ile Arg Thr Pro Arg Gly Lys Arg  
 50 55 60  
 Ile Trp Leu Asn Ser His Ser Arg  
 65 70  
 10  
 <210> 1083  
 <211> 52  
 <212> PRT  
 15 <213> Homo sapiens  
 <400> 1083  
 Gly Thr Lys Asn Ser Pro Glu Thr Lys Xaa Xaa Ala Arg Xaa Leu Xaa  
 1 5 10 15  
 20 Ala Leu Pro Thr Lys Met Xaa Asn Gly Asp Gly Asn Val Lys Gly Lys  
 20 25 30  
 Xaa Leu Gly Pro Lys Asp Arg Arg Xaa Lys Phe Trp Phe Xaa Lys Xaa  
 35 40 45  
 Arg Arg Pro Cys  
 25 50  
 <210> 1084  
 <211> 242  
 <212> PRT  
 30 <213> Homo sapiens  
 <400> 1084  
 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn  
 1 5 10 15  
 35 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr  
 20 25 30  
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu  
 35 40 45  
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr  
 40 50 55 60  
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys  
 65 70 75 80  
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser  
 85 90 95  
 45 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu  
 100 105 110  
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu  
 115 120 125  
 Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln  
 50 130 135 140  
 Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu  
 145 150 155 160  
 Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser  
 165 170 175  
 55 Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe  
 180 185 190  
 Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln His Ser  
 195 200 205  
 Ser Ala Ala Ala Ala Ala Thr Gly Arg Xaa Arg Xaa Pro Arg Ala Gly  
 60 210 215 220  
 Xaa Asp Ala Pro Gln Pro Gly Asp Pro Val Pro Leu Ala Arg Ala Pro  
 225 230 235 240  
 Thr Arg

5 <210> 1085  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<400> 1085  
 10 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn  
 1 5 10 15  
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr  
 20 25 30  
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu  
 35 40 45  
 15 Ala Leu Lys Asn Glu His Asn Tyr Ile Leu Gln Ser Leu Leu Xaa Thr  
 50 55 60  
 Xaa Xaa Cys Leu Lys Lys Asp Asp Glu Ser Asn Phe Gly Gly Gly Glu  
 65 70 75 80  
 20 Ile Lys His Asp Arg Lys Ser Leu Xaa Met Phe Gly Ala Xaa Leu Xaa  
 85 90 95  
 Xaa Ala Gln Val Met Met Xaa Phe Ser Asn Tyr  
 100 105

25 <210> 1086  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 1086  
 30 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn  
 1 5 10 15  
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr  
 20 25 30  
 35 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu  
 35 40 45  
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr  
 50 55 60  
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys  
 65 70 75 80  
 40 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser  
 85 90 95  
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu  
 100 105 110  
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu  
 115 120 125  
 45 Asn Gln Trp Leu Pro Asp Glu Leu Ala His Thr His Xaa Asn Cys Arg  
 130 135 140  
 Lys Met Thr Ile Cys Gly Leu Thr Gly Gly Gly Glu Lys Thr Ser  
 145 150 155

50 <210> 1087  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

55 <400> 1087  
 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn  
 1 5 10 15  
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr  
 20 25 30  
 60 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu  
 35 40 45  
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr

50                      55                      60  
 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys  
 65                      70                      75                      80  
 Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser  
 5                      85                      90                      95  
 Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu  
 100                      105                      110  
 Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Pro Ser Val Pro Gly  
 115                      120                      125  
 10 Glu Ser Met Ala  
 130

<210> 1088  
 <211> 198  
 15 <212> PRT  
 <213> Homo sapiens

<400> 1088  
 Gln Gly Leu Glu Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser  
 20 1                      5                      10                      15  
 Leu Leu Glu Thr Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu  
 20                      25                      30  
 Val Glu Glu Lys Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu  
 35                      40                      45  
 25 Leu Gly Leu Ser Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu  
 50                      55                      60  
 Asn Ala Val Glu Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg  
 65                      70                      75                      80  
 Leu Cys Gln Glu Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln  
 85                      90                      95  
 30 Gln Lys Leu Gln Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu  
 100                      105                      110  
 Lys Lys His Leu Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp  
 115                      120                      125  
 35 Ile Ser Pro Ser Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu  
 130                      135                      140  
 Asp Asp Leu Phe Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln  
 145                      150                      155                      160  
 Gln Gln His Ser Ser Ala Ala Ala Ala Thr Gly Arg Xaa Arg Xaa  
 165                      170                      175  
 40 Pro Arg Ala Gly Xaa Asp Ala Pro Gln Pro Gly Asp Pro Val Pro Leu  
 180                      185                      190  
 Ala Arg Ala Pro Thr Arg  
 195

45 <210> 1089  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

50 <400> 1089  
 Gln Arg Glu Arg Ala Arg Pro Ser Gly Ala Arg Arg Met Tyr Asp Asn  
 1                      5                      10                      15  
 Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr  
 20                      25                      30  
 Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu  
 35                      40                      45  
 Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr  
 50                      55                      60  
 60 Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys  
 65                      70                      75                      80  
 Ser Asn Met Ile Pro Glu Val Thr Gly Asp Val Gly Ala Arg Pro Glu  
 85                      90                      95

44

<210> 1090  
 <211> 646  
 <212> PRT  
 5 <213> Homo sapiens

<400> 1090  
 Ser Pro Arg Arg Glu Thr Gly Lys Glu Ser Arg Lys Ser Gln Ser Pro  
 1 5 10 15  
 10 Ser Pro Lys Asn Glu Ser Ala Arg Gly Arg Lys Lys Ser Arg Ser Gln  
 20 25 30  
 Ser Pro Lys Lys Asp Ile Ala Arg Glu Arg Arg Gln Ser Gln Ser Arg  
 35 40 45  
 15 Ser Pro Lys Arg Asp Thr Thr Arg Glu Ser Arg Arg Ser Glu Ser Leu  
 50 55 60  
 Ser Pro Arg Arg Glu Thr Ser Arg Glu Asn Lys Arg Ser Gln Pro Arg  
 65 70 75 80  
 Val Lys Asp Ser Ser Pro Gly Glu Lys Ser Arg Ser Gln Ser Arg Glu  
 85 90 95  
 20 Arg Glu Ser Asp Arg Asp Gly Gln Arg Arg Glu Arg Glu Arg Arg Thr  
 100 105 110  
 Arg Lys Trp Ser Arg Ser Arg Ser His Ser Arg Ser Pro Ser Arg Cys  
 115 120 125  
 25 Arg Thr Lys Ser Lys Ser Ser Ser Phe Gly Arg Ile Asp Arg Asp Ser  
 130 135 140  
 Tyr Ser Pro Arg Trp Lys Gly Arg Trp Ala Asn Asp Gly Trp Arg Cys  
 145 150 155 160  
 Pro Pro Gly Asn Asp Arg Tyr Arg Lys Asn Asp Pro Xaa Lys Pro Asn  
 165 170 175  
 30 Glu Asn Thr Xaa Lys Glu Lys Asn Asp Ile His Leu Asp Ala Asp Asp  
 180 185 190  
 Pro Asn Ser Ala Asp Lys His Arg Asn Asp Cys Pro Asn Trp Ile Thr  
 195 200 205  
 35 Glu Lys Ile Asn Ser Gly Pro Asp Pro Arg Thr Arg Asn Pro Glu Lys  
 210 215 220  
 Leu Lys Glu Ser His Trp Glu Glu Asn Arg Asn Glu Asn Ser Gly Asn  
 225 230 235 240  
 Ser Trp Asn Lys Asn Phe Gly Ser Gly Trp Val Ser Asn Arg Gly Arg  
 245 250 255  
 40 Gly Arg Gly Asn Arg Gly Arg Gly Thr Tyr Arg Ser Ser Phe Ala Tyr  
 260 265 270  
 Lys Asp Gln Asn Glu Asn Arg Trp Gln Asn Arg Lys Pro Leu Ser Gly  
 275 280 285  
 45 Asn Ser Asn Ser Ser Gly Ser Glu Ser Phe Lys Phe Val Glu Gln Gln  
 290 295 300  
 Ser Tyr Lys Arg Lys Ser Glu Gln Glu Phe Ser Phe Asp Thr Pro Ala  
 305 310 315 320  
 Asp Arg Ser Gly Trp Thr Ser Ala Ser Ser Trp Ala Val Arg Lys Thr  
 325 330 335  
 50 Leu Pro Ala Asp Val Gln Asn Tyr Tyr Ser Arg Arg Gly Arg Asn Ser  
 340 345 350  
 Ser Gly Pro Gln Ser Gly Trp Met Lys Gln Glu Glu Glu Thr Ser Gly  
 355 360 365  
 55 Gln Asp Ser Ser Leu Lys Asp Gln Thr Asn Gln Gln Val Asp Gly Ser  
 370 375 380  
 Gln Leu Pro Ile Asn Met Met Gln Pro Gln Met Asn Val Met Gln Gln  
 385 390 395 400  
 Gln Met Asn Ala Gln His Gln Pro Met Asn Ile Phe Pro Tyr Pro Val  
 405 410 415  
 60 Gly Val His Ala Pro Leu Met Asn Ile Gln Arg Asn Pro Phe Asn Ile  
 420 425 430  
 His Pro Gln Leu Pro Leu His Leu His Thr Gly Val Pro Leu Met Gln  
 435 440 445

Val Ala Thr Pro Thr Ser Val Ser Gln Gly Leu Pro Pro Pro Pro  
 450 455 460  
 Pro Pro Pro Pro Ser Gln Gln Val Asn Tyr Ile Ala Ser Gln Pro Asp  
 465 470 475 480  
 5 Gly Lys Gln Leu Gln Gly Ile Pro Ser Ser Ser His Val Ser Asn Asn  
 485 490 495  
 Met Ser Thr Pro Val Leu Pro Ala Pro Thr Ala Ala Pro Gly Asn Thr  
 500 505 510  
 10 Gly Met Val Gln Gly Pro Ser Ser Gly Asn Thr Ser Ser Ser Ser His  
 515 520 525  
 Ser Lys Ala Ser Asn Ala Ala Val Lys Leu Ala Glu Ser Lys Val Ser  
 530 535 540  
 Val Ala Val Glu Ala Ser Ala Asp Ser Ser Lys Thr Asp Lys Lys Leu  
 545 550 555 560  
 15 Gln Ile Gln Glu Lys Ala Ala Gln Glu Val Lys Leu Ala Ile Lys Pro  
 565 570 575  
 Phe Tyr Gln Asn Lys Asp Ile Thr Lys Glu Glu Tyr Lys Glu Ile Val  
 580 585 590  
 20 Arg Lys Ala Val Asp Lys Val Cys His Ser Lys Ser Gly Glu Val Asn  
 595 600 605  
 Ser Thr Lys Val Ala Asn Leu Val Lys Ala Tyr Val Asp Lys Tyr Lys  
 610 615 620  
 Tyr Ser Arg Lys Gly Ser Gln Lys Lys Thr Leu Glu Glu Pro Val Ser  
 625 630 635 640  
 25 Thr Glu Lys Asn Ile Gly  
 645

<210> 1091  
 <211> 155  
 30 <212> PRT  
 <213> Homo sapiens

<400> 1091  
 Arg Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu Glu Asn  
 35 1 5 10 15  
 Arg Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly Ser Gly  
 20 25 30  
 Trp Val Ser Asn Arg Gly Arg Gly Arg Gly Asn Arg Gly Arg Gly Thr  
 35 40 45  
 40 Tyr Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg Trp Gln  
 50 55 60  
 Asn Arg Lys Pro Leu Ser Gly Asn Ser Asn Ser Ser Gly Ser Glu Ser  
 65 70 75 80  
 45 Phe Lys Phe Val Glu Gln Gln Ser Tyr Lys Arg Lys Ser Glu Gln Glu  
 85 90 95  
 Phe Ser Phe Asp Thr Pro Ala Asp Arg Ser Gly Trp Thr Ser Ala Ser  
 100 105 110  
 Ser Trp Ala Val Arg Lys Thr Leu Pro Ala Asp Val Gln Asn Tyr Tyr  
 115 120 125  
 50 Ser Arg Arg Gly Arg Asn Ser Ser Gly Pro Gln Ser Gly Trp Met Lys  
 130 135 140  
 Gln Glu Glu Glu Thr Ser Gly Arg Ile Leu Ala  
 145 150 155

55 <210> 1092  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

60 <400> 1092  
 Val Lys Ser Val Cys His Ser Lys Ala Ser Asn Ala Ala Val Lys Leu  
 1 5 10 15  
 Ala Glu Ser Lys Val Ser Val Ala Val Glu Ala Ser Ala Asp Ser Ser



20 25 30  
 Lys Thr Asp Lys Lys Leu Gln Ile Gln Glu Lys Ala Ala Gln Glu Val  
 35 40 45  
 Lys Leu Ala Ile Lys Pro Phe Tyr Gln Asn Lys Asp Ile Thr Lys Glu  
 5 50 55 60  
 Glu Tyr Lys Glu Ile Val Arg Lys Ala Val Asp Lys Val Cys His Ser  
 65 70 75 80  
 Lys Ser Gly Glu Val Asn Ser Thr Lys Val Ala Asn Leu Val Lys Ala  
 85 90 95  
 10 Tyr Val Asp Lys Tyr Lys Tyr Ser Arg Lys Gly Ser Gln Lys Lys Thr  
 100 105 110  
 Leu Glu Glu Pro Val Ser Thr Glu Lys Asn Ile Gly  
 115 120  
 15 <210> 1093  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens  
 20 <400> 1093  
 Ser Pro Arg Arg Glu Thr Gly Lys Glu Ser Arg Lys Ser Gln Ser Pro  
 1 5 10 15  
 Ser Pro Lys Asn Glu Ser Ala Arg Gly Arg Lys Lys Ser Arg Ser Gln  
 20 25 30  
 25 Ser Pro Lys Lys Asp Ile Ala Arg Glu Arg Arg Gln Ser Gln Ser Arg  
 35 40 45  
 Ser Pro Lys Arg Asp Thr Thr Arg Glu Ser Arg Arg Ser Glu Ser Leu  
 50 55 60  
 Ser Pro Arg Arg Glu Thr Ser Arg Glu Asn Lys Arg Ser Gln Pro Arg  
 30 65 70 75 80  
 Val Lys Asp Ser Ser Pro Gly Glu Lys Ser Arg Ser Gln Ser Arg Glu  
 85 90 95  
 Arg Glu Ser Asp Arg Asp Gly Gln Arg Arg Glu Arg Glu Arg Arg Thr  
 100 105 110  
 35 Arg Lys Trp Ser Arg Ser Arg Ser His Ser Arg Ser Pro Ser Arg Cys  
 115 120 125  
 Arg Thr Lys Ser Lys Ser Ser Ser Phe Gly Arg Ile Asp Arg Asp Ser  
 130 135 140  
 Tyr Ser Pro Arg Trp Lys Gly Arg Trp Ala Asn Asp Gly Trp Arg Cys  
 40 145 150 155 160  
 Pro Pro Gly Asn Asp Arg Tyr Arg Lys Asn Asp Pro Xaa Lys Pro Asn  
 165 170 175  
 Glu Asn Thr Xaa Lys Glu Lys Asn Asp Ile His Leu Asp Ala Asp Asp  
 180 185 190  
 45 Pro Asn Ser Cys Gly Lys His  
 195  
 50 <210> 1094  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1094  
 Asn Asp Ile His Leu Asp Ala Asp Asp Pro Asn Ser Ala Asp Lys His  
 55 1 5 10 15  
 Arg Asn Asp Cys Pro Asn Trp Ile Thr Glu Lys Ile Asn Ser Gly Pro  
 20 25 30  
 Asp Pro Arg Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu  
 35 40 45  
 60 Glu Asn Arg Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly  
 50 55 60  
 Ser Gly Trp Val Ser Asn Arg Gly Arg Gly Arg Gly Asn Arg Gly Arg  
 65 70 75 80

Gly Thr Tyr Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg  
 85 90 95  
 Trp Gln Asn Arg Lys Pro Leu Ser Gly Asn Ser Asn Ser Ser Gly Ser  
 100 105 110  
 5 Glu Ser Phe Lys Phe Val Glu Gln Gln Ser Tyr Lys Arg Lys Ser Glu  
 115 120 125  
 Gln Glu Phe Ser Phe Asp Thr Pro Ala Asp Arg Ser Gly Trp Thr Ser  
 130 135 140  
 10 Ala Ser Ser Trp Ala Val Arg Lys Thr Leu Pro Ala Asp Val Gln Asn  
 145 150 155 160  
 Tyr Tyr Ser Arg Arg Gly Arg Asn Ser Ser Gly Pro Gln Ser Gly Trp  
 165 170 175  
 Met Lys Gln Glu Glu Glu Thr Ser Gly Gln Asp Ser Ser Leu Lys Asp  
 180 185 190  
 15 Gln Thr Asn Gln Gln Val Asp Gly Ser Gln Leu Pro Ile Asn Met Met  
 195 200 205  
 Gln Pro Ala Asn Glu Cys Asn Ala Ala Gln Met Asn Ala His Thr Ser  
 210 215 220  
 Leu  
 20 225

&lt;210&gt; 1095

&lt;211&gt; 246

&lt;212&gt; PRT

25 &lt;213&gt; Homo sapiens

&lt;400&gt; 1095

Thr Leu Gly Leu Lys Thr Ser Gly Gln Asp Ser Ser Leu Lys Asp Gln  
 1 5 10 15  
 30 Thr Asn Gln Gln Val Asp Gly Ser Gln Leu Pro Ile Asn Met Met Gln  
 20 25 30  
 Pro Gln Met Asn Val Met Gln Gln Met Asn Ala Gln His Gln Pro  
 35 40 45  
 Met Asn Ile Phe Pro Tyr Pro Val Gly Val His Ala Pro Leu Met Asn  
 50 55 60  
 35 Ile Gln Arg Asn Pro Phe Asn Ile His Pro Gln Leu Pro Leu His Leu  
 65 70 75 80  
 His Thr Gly Val Pro Leu Met Gln Val Ala Thr Pro Thr Ser Val Ser  
 85 90 95  
 40 Gln Gly Leu Pro Pro Pro Pro Pro Pro Pro Ser Gln Gln Val  
 100 105 110  
 Asn Tyr Ile Ala Ser Gln Pro Asp Gly Lys Gln Leu Gln Gly Ile Pro  
 115 120 125  
 Ser Ser Ser His Val Ser Asn Asn Met Ser Thr Pro Val Leu Pro Ala  
 130 135 140  
 45 Pro Thr Ala Ala Pro Gly Asn Thr Gly Met Val Gln Gly Pro Ser Ser  
 145 150 155 160  
 Gly Asn Thr Ser Ser Ser His Ser Lys Ala Ser Asn Ala Ala Val  
 165 170 175  
 50 Lys Leu Ala Glu Ser Lys Val Ser Val Ala Val Glu Ala Ser Ala Asp  
 180 185 190  
 Ser Ser Lys Thr Asp Lys Lys Leu Gln Ile Gln Glu Lys Ala Ala Gln  
 195 200 205  
 55 Glu Val Lys Leu Ala Ile Lys Pro Phe Tyr Gln Asn Lys Asp Ile Thr  
 210 215 220  
 Lys Glu Glu Tyr Lys Glu Ile Val Arg Lys Ala Val Xaa Lys Val Gly  
 225 230 235 240  
 Ile Xaa Arg Val Glu Lys  
 245

60

&lt;210&gt; 1096

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1096

5      Lys Lys Val Phe Leu Pro Thr Ser Leu Cys Ile Ser Tyr Gly Gln Trp  
       1                      5                      10                      15  
 Met Glu Glu Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln  
                     20                      25                      30  
 Glu Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu  
                     35                      40                      45  
 10    Met Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr  
                     50                      55                      60  
 Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu Ser Val  
                     65                      70                      75                      80  
 Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys  
                     85                      90                      95  
 15    Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys  
                     100                      105                      110  
 Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn  
                     115                      120                      125  
 20    Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly  
                     130                      135                      140  
 Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His  
                     145                      150                      155                      160  
 Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp  
                     165                      170                      175  
 25    Gly Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser Val Thr  
                     180                      185                      190  
 Gly Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys Xaa Thr  
                     195                      200                      205  
 30    Ala Leu Phe Gly Cys Arg  
                     210

&lt;210&gt; 1097

&lt;211&gt; 214

35      &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1097

40      Lys Lys Val Phe Leu Pro Thr Ser Leu Cys Ile Ser Tyr Gly Gln Trp  
       1                      5                      10                      15  
 Met Glu Glu Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln  
                     20                      25                      30  
 Glu Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu  
                     35                      40                      45  
 45    Met Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr  
                     50                      55                      60  
 Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu Ser Val  
                     65                      70                      75                      80  
 Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys  
                     85                      90                      95  
 50    Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys  
                     100                      105                      110  
 Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn  
                     115                      120                      125  
 55    Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly  
                     130                      135                      140  
 Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His  
                     145                      150                      155                      160  
 Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp  
                     165                      170                      175  
 60    Gly Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser Val Thr  
                     180                      185                      190  
 Gly Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys Xaa Thr

195 200 205  
Ala Leu Phe Gly Cys Arg  
210

5 <210> 1098  
<211> 178  
<212> PRT  
<213> Homo sapiens

10 <400> 1098  
Met Met Gly Leu Leu Gly Gln Ser Leu Xaa Gln Ile Xaa Gln Ser Ile  
1 5 10 15  
His Phe Met Arg Glu Trp Ala Xaa Ser Xaa Ala Pro Val Thr Pro Val  
20 25 30  
15 Pro Val Val Glu Ser Xaa Gln Leu Asn Gly Gly Gly Asp Val Ala Met  
35 40 45  
Leu Glu Leu Thr Xaa Gln Asn Phe Thr Pro Asn Leu Arg Val Trp Phe  
50 55 60  
20 Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser Met Leu  
65 70 75 80  
Cys Val Val Pro Asp Ile Xaa Ala Phe Arg Glu Gly Trp Arg Trp Val  
85 90 95  
Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp Gly Ile  
100 105 110  
25 Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro Gly Pro  
115 120 125  
Arg Pro His Cys Ser Ala Ala Gly Ala Ile Leu Arg Ala Asn Ser Ser  
130 135 140  
Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser Tyr Thr  
30 145 150 155 160  
Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala Thr Val  
165 170 175  
Val Ser

35 <210> 1099  
<211> 218  
<212> PRT  
<213> Homo sapiens

40 <400> 1099  
Thr Val Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn  
1 5 10 15  
Glu Lys Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser  
45 20 25 30  
Gly Trp Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu  
35 40 45  
Gln Glu Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln  
50 55 60  
Glu Met Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys  
65 70 75 80  
Thr Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu Ser  
85 90 95  
Val Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser  
55 100 105 110  
Lys Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu  
115 120 125  
Lys Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe  
130 135 140  
60 Asn Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu  
145 150 155 160  
Gly Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile  
165 170 175

His Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Pro  
 180 185 190  
 Arg Trp Leu His Pro Leu Trp Thr Asn Ser Gln Thr Cys Val Leu Ser  
 195 200 205  
 5 Tyr Trp His Gly Leu Pro Lys Ile Asp Asn  
 210 215  
 <210> 1100  
 <211> 201  
 10 <212> PRT  
 <213> Homo sapiens  
 <400> 1100  
 Val Val Gln Ala Gly Val Phe Gly Arg Ala Trp Glu His Lys Ser Leu  
 1 5 10 15  
 Phe His His Val Ser Arg Thr Ser His Ser Gly Pro Gly Leu Val Ala  
 20 25 30  
 Lys Met Val Lys Pro Lys Tyr Lys Gly Arg Ser Thr Ile Asn Pro Ser  
 35 40 45  
 20 Lys Ala Ser Thr Asn Pro Asp Arg Val Gln Gly Ala Gly Gly Gln Asn  
 50 55 60  
 Met Arg Asp Arg Ala Thr Ile Arg Arg Leu Asn Met Tyr Arg Gln Lys  
 65 70 75 80  
 Glu Arg Arg Asn Ser Arg Gly Lys Ile Ile Lys Pro Leu Gln Tyr Gln  
 85 90 95  
 25 Ser Thr Val Ala Ser Gly Thr Val Ala Arg Val Glu Pro Asn Ile Lys  
 100 105 110  
 Trp Phe Gly Asn Thr Arg Val Ile Lys Gln Ser Ser Leu Gln Lys Phe  
 115 120 125  
 30 Gln Glu Glu Met Asp Thr Val Met Lys Asp Pro Tyr Lys Val Val Met  
 130 135 140  
 Lys Gln Ser Lys Leu Pro Met Ser Leu Leu His Asp Arg Ile Arg Pro  
 145 150 155 160  
 His Asn Leu Lys Gly His Ile Leu Asp Thr Glu Ser Phe Glu Thr Thr  
 165 170 175  
 35 Phe Gly Pro Xaa Ser Gln Lys Glu Thr Asp Gln Thr Tyr Phe Ala Ser  
 180 185 190  
 Asp Met Gln Ser Leu Ile Glu Asn Ala  
 195 200  
 40 <210> 1101  
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 <213> Homo sapiens  
 45 <400> 1101  
 Ala Gly Xaa Phe Gly Arg Ala Trp Glu His Lys Ser Leu Phe His His  
 1 5 10 15  
 Val Ser Arg Thr Ser His Ser Gly Pro Gly Leu Val Ala Lys Met Val  
 20 25 30  
 Lys Pro Lys Tyr Lys Gly Arg Ser Thr Ile Asn Pro Ser Lys Ala Ser  
 35 40 45  
 Thr Asn Pro Asp Arg Val Gln Gly Ala Gly Gly Gln Asn Met Arg Asp  
 50 55 60  
 55 Arg Ala Thr Ile Arg Arg Leu Asn Met Tyr Arg Gln Lys Glu Arg Arg  
 65 70 75 80  
 Asn Ser Arg Gly Lys Ile Ile Lys Pro Leu Gln Tyr Gln Ser Thr Val  
 85 90 95  
 Ala Ser Gly Thr Val Ala Arg Val Glu Pro Asn Ile Lys Trp Phe Gly  
 100 105 110  
 60 Asn Thr Arg Val Ile Lys Gln Ser Ser Leu Gln Lys Phe Gln Glu Glu  
 115 120 125  
 Met Asp Thr Val Met Lys Asp Pro Tyr Lys Val Val Met Lys Gln Ser

130 135 140  
 Lys Leu Pro Met Ser Leu Leu His Asp Arg Ile Arg Pro His Asn Leu  
 145 150 155 160  
 Lys Val His Ile Leu Asp Thr Glu Ser Phe Glu Thr Thr Phe Gly Pro  
 165 170 175  
 5 Lys Ser Gln Arg Lys Arg Pro Asn Leu Phe Ala Ser Asp Met Gln Ser  
 180 185 190  
 Leu Ile Glu Asn Ala Glu Met Ser Thr Glu Ser Tyr Asp Pro Gly Gln  
 195 200 205  
 10 Gly Ser  
 210  
 <210> 1102  
 <211> 232  
 15 <212> PRT  
 <213> Homo sapiens  
 <400> 1102  
 Arg Val Gln Ile Pro Ser Phe Lys Glu Asp Xaa Arg Gly Pro Xaa Xaa  
 20 1 5 10 15  
 Val Arg Leu Pro Gln Xaa Cys Gly Arg Phe Phe His Glu Ser Xaa Asp  
 20 25 30  
 Phe Gly Lys Ile Gln Xaa Xaa Pro Gln Phe Phe Gly Asn Asp Leu Val  
 35 40 45  
 25 Xaa Val Xaa Val Ser Asp Leu Glu Lys Glu Leu Glu Ser Phe Phe Leu  
 50 55 60  
 Met Lys Arg Arg Arg Asn Arg Ser Thr Lys Glu Met Met Arg Glu Glu  
 65 70 75 80  
 Ser Ser Ser Glu Pro Glu Glu Glu Asn Val Gly Asn Asp Thr Lys Ala  
 85 90 95  
 30 Val Ile Lys Ala Leu Asp Glu Lys Ile Val Lys Tyr Gln Lys Phe Leu  
 100 105 110  
 Asp Lys Ala Lys Ala Lys Lys Phe Ser Ala Val Arg Ile Ser Lys Gly  
 115 120 125  
 35 Leu Ser Glu Lys Ile Phe Ala Lys Pro Glu Glu Gln Arg Lys Thr Leu  
 130 135 140  
 Glu Glu Asp Val Asp Asp Arg Xaa Pro Ser Lys Lys Gly Lys Lys Arg  
 145 150 155 160  
 Lys Ala Gln Arg Glu Glu Glu Gln Glu His Ser Asn Lys Ala Pro Arg  
 165 170 175  
 40 Ala Leu Thr Ser Lys Glu Arg Arg Arg Ala Val Arg Gln Gln Arg Pro  
 180 185 190  
 Lys Lys Val Gly Val Arg Tyr Tyr Glu Thr His Asn Val Lys Asn Arg  
 195 200 205  
 45 Asn Arg Asn Lys Lys Lys Thr Asn Asp Ser Glu Gly Gln Lys His Lys  
 210 215 220  
 Arg Lys Lys Phe Arg Gln Lys Gln  
 225 230  
 50 <210> 1103  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1103  
 Trp Ala Thr Lys Arg Trp Val Ala Val Leu Ser Gln Asp Tyr Pro Thr  
 1 5 10 15  
 Leu Ala Phe His Ala Ser Leu Thr Asn Pro Phe Gly Lys Gly Ala Phe  
 20 25 30  
 60 Ile Gln Leu Leu Arg Gln Phe Gly Lys Leu His Thr Asp Lys Lys Gln  
 35 40 45  
 Ile Ser Val Gly Phe Ile Gly Tyr Pro Asn Val Gly Lys Ser Ser Val  
 50 55 60

Ile Asn Thr Leu Arg Ser Lys Lys Val Cys Asn Val Ala Pro Ile Ala  
 65 70 75 80  
 Gly Glu Thr Lys Val Trp Gln Tyr Ile Thr Leu Met Arg Arg Ile Phe  
 85 90 95  
 5 Leu Ile Asp Cys Pro Gly Val Val Tyr Pro Ser Glu Asp Ser Glu Thr  
 100 105 110  
 Asp Ile Val Leu Lys Gly Val Val Gln Val Glu Lys Ile Lys Ser Pro  
 115 120 125  
 10 Glu Asp His Ile Gly Ala Val Leu Glu Arg Ala Lys Pro Glu Tyr Ile  
 130 135 140  
 Ser Lys Thr Tyr Lys Ile Asp Ser Trp Glu Asn Ala Glu Asp Phe Leu  
 145 150 155 160  
 Glu Lys Leu Ala Phe Arg Thr Gly Lys Leu Leu Lys Gly Gly Glu Pro  
 165 170 175  
 15 Asp Leu Gln Thr Val Gly Lys Met Val Leu Asn Asp Trp Gln Lys Gly  
 180 185 190  
 Arg Ile Xaa Phe Phe Val Lys Pro Pro Asn Ala Glu Pro Leu Trp Ala  
 195 200 205  
 Pro Thr  
 20 210

&lt;210&gt; 1104

&lt;211&gt; 210

&lt;212&gt; PRT

25 &lt;213&gt; Homo sapiens

&lt;400&gt; 1104

Val Gln Ala Gly Val Phe Gly Arg Ala Trp Glu His Lys Ser Leu Phe  
 1 5 10 15  
 30 His His Val Ser Arg Thr Ser His Ser Gly Pro Gly Leu Val Ala Lys  
 20 25 30  
 Met Val Lys Pro Lys Tyr Lys Gly Arg Ser Thr Ile Asn Pro Ser Lys  
 35 40 45  
 Ala Ser Thr Asn Pro Asp Arg Val Gln Gly Ala Gly Gly Gln Asn Met  
 50 55 60  
 35 Arg Asp Arg Ala Thr Ile Arg Arg Leu Asn Met Tyr Arg Gln Lys Glu  
 65 70 75 80  
 Arg Arg Asn Ser Arg Gly Lys Ile Ile Lys Pro Leu Gln Tyr Gln Ser  
 85 90 95  
 40 Thr Val Ala Ser Gly Thr Val Ala Arg Val Glu Pro Asn Ile Lys Trp  
 100 105 110  
 Phe Gly Asn Thr Arg Val Ile Lys Gln Ser Ser Leu Gln Lys Phe Gln  
 115 120 125  
 Glu Glu Met Asp Thr Val Met Lys Asp Pro Tyr Lys Val Val Met Lys  
 130 135 140  
 45 Gln Ser Lys Leu Pro Met Ser Leu Leu His Asp Arg Ile Arg Pro His  
 145 150 155 160  
 Asn Leu Lys Val His Ile Leu Asp Thr Glu Ser Phe Glu Thr Thr Phe  
 165 170 175  
 50 Gly Pro Lys Ser Arg Xaa Asn Asp Gln Thr Tyr Leu Gln Val Ile Cys  
 180 185 190  
 Ser Leu Leu Ser Lys Met Leu Lys Cys Pro Leu Arg Ala Met Thr Arg  
 195 200 205  
 Ala Arg  
 55 210

&lt;210&gt; 1105

&lt;211&gt; 368

&lt;212&gt; PRT

60 &lt;213&gt; Homo sapiens

&lt;400&gt; 1105

Glu Ile Asp Gln Val Val Pro Ala Ala Gln Ser Ser Pro Ile Asn Cys

	1		5		10		15									
	Glu	Lys	Arg	Glu	Asn	Leu	Leu	Pro	Phe	Val	Gly	Leu	Asn	Asn	Leu	Gly
				20					25					30		
5	Asn	Thr	Cys	Tyr	Leu	Asn	Ser	Ile	Leu	Gln	Val	Leu	Tyr	Phe	Cys	Pro
			35					40					45			
	Gly	Phe	Lys	Ser	Gly	Val	Lys	His	Leu	Phe	Asn	Ile	Ile	Ser	Arg	Lys
		50					55					60				
	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Ala	Asn	Gln	Lys	Asp	Lys	Gly	Asn	Cys
	65					70					75				80	
10	Lys	Glu	Asp	Ser	Leu	Ala	Ser	Tyr	Glu	Leu	Ile	Cys	Ser	Leu	Gln	Ser
				85						90					95	
	Leu	Ile	Ile	Ser	Val	Glu	Gln	Leu	Gln	Ala	Ser	Phe	Leu	Leu	Asn	Pro
				100					105						110	
	Glu	Lys	Tyr	Thr	Asp	Glu	Leu	Ala	Thr	Gln	Pro	Arg	Arg	Leu	Leu	Asn
15			115					120					125			
	Thr	Leu	Arg	Glu	Leu	Asn	Pro	Met	Tyr	Glu	Gly	Tyr	Leu	Gln	His	Asp
		130					135					140				
	Ala	Gln	Glu	Val	Leu	Gln	Cys	Ile	Leu	Gly	Asn	Ile	Gln	Glu	Thr	Cys
	145					150					155				160	
20	Gln	Leu	Leu	Lys	Lys	Glu	Glu	Val	Lys	Asn	Val	Ala	Glu	Leu	Pro	Thr
				165						170					175	
	Lys	Val	Glu	Glu	Ile	Pro	His	Pro	Lys	Glu	Glu	Met	Asn	Gly	Ile	Asn
			180						185					190		
25	Ser	Ile	Glu	Met	Asp	Ser	Met	Arg	His	Ser	Glu	Asp	Phe	Lys	Glu	Lys
		195						200					205			
	Leu	Pro	Lys	Gly	Asn	Gly	Lys	Arg	Lys	Ser	Asp	Thr	Glu	Phe	Gly	Asn
		210				215						220				
	Met	Lys	Lys	Lys	Val	Lys	Leu	Ser	Lys	Glu	His	Gln	Ser	Leu	Glu	Glu
	225					230					235				240	
30	Asn	Gln	Arg	Gln	Thr	Arg	Ser	Lys	Arg	Lys	Ala	Thr	Ser	Asp	Thr	Leu
				245						250					255	
	Glu	Ser	Pro	Pro	Lys	Ile	Ile	Pro	Lys	Tyr	Ile	Ser	Glu	Asn	Glu	Ser
			260						265					270		
35	Pro	Arg	Pro	Ser	Gln	Lys	Lys	Ser	Arg	Val	Lys	Ile	Asn	Trp	Leu	Lys
		275					280						285			
	Ser	Ala	Thr	Lys	Gln	Pro	Ser	Ile	Leu	Ser	Lys	Phe	Cys	Ser	Leu	Gly
		290					295					300				
	Lys	Ile	Thr	Thr	Asn	Gln	Gly	Val	Lys	Gly	Gln	Ser	Lys	Glu	Asn	Glu
	305					310					315				320	
40	Cys	Asp	Pro	Glu	Glu	Asp	Leu	Gly	Lys	Cys	Glu	Ser	Asp	Asn	Thr	Thr
				325						330					335	
	Asn	Gly	Cys	Gly	Leu	Glu	Ser	Pro	Gly	Asn	Thr	Val	Thr	Pro	Val	Asn
			340						345					350		
45	Val	Asn	Glu	Val	Lys	Pro	Ile	Asn	Lys	Gly	Glu	Glu	Gln	Ile	Gly	Phe
		355					360						365			

&lt;210&gt; 1106

&lt;211&gt; 218

&lt;212&gt; PRT

50 &lt;213&gt; Homo sapiens

&lt;400&gt; 1106

	Glu	Ile	Asp	Gln	Val	Val	Pro	Ala	Ala	Gln	Ser	Ser	Pro	Ile	Asn	Cys
	1			5					10					15		
55	Glu	Lys	Arg	Glu	Asn	Leu	Leu	Pro	Phe	Val	Gly	Leu	Asn	Asn	Leu	Gly
				20					25					30		
	Asn	Thr	Cys	Tyr	Leu	Asn	Ser	Ile	Leu	Gln	Val	Leu	Tyr	Phe	Cys	Pro
			35					40					45			
	Gly	Phe	Lys	Ser	Gly	Val	Lys	His	Leu	Phe	Asn	Ile	Ile	Ser	Arg	Lys
60		50					55					60				
	Lys	Glu	Ala	Leu	Lys	Asp	Glu	Ala	Asn	Gln	Lys	Asp	Lys	Gly	Asn	Cys
	65					70					75				80	
	Lys	Glu	Asp	Ser	Leu	Ala	Ser	Tyr	Glu	Leu	Ile	Cys	Ser	Leu	Gln	Ser



85 90 95  
 Leu Ile Ile Ser Val Glu Gln Leu Gln Ala Ser Phe Leu Leu Asn Pro  
 100 105 110  
 Glu Lys Tyr Thr Asp Glu Leu Ala Thr Gln Pro Arg Arg Leu Leu Asn  
 115 120 125  
 5 Thr Leu Arg Glu Leu Asn Pro Met Tyr Glu Gly Tyr Leu Gln His Asp  
 130 135 140  
 Ala Gln Glu Val Leu Gln Cys Ile Leu Gly Asn Ile Gln Glu Thr Cys  
 145 150 155 160  
 10 Gln Leu Leu Lys Lys Glu Glu Val Lys Asn Val Ala Glu Phe Leu Leu  
 165 170 175  
 Arg Xaa Lys Lys Ser Ser Ser Glu Glu Glu Met Asn Gly Leu Gln His  
 180 185 190  
 Xaa Asp Gly Xaa Met Xaa Leu Leu Xaa Thr Phe Lys Arg Thr Pro Lys  
 195 200 205  
 15 Gly Met Gly Lys Glu Lys Val Pro Trp Ile  
 210 215  
  
 <210> 1107  
 20 <211> 121  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 1107  
 25 Leu Asn Tyr Pro Lys Arg Arg His Leu Asn Thr Trp Ile Tyr Thr Ser  
 1 5 10 15  
 Leu Leu Cys Leu Leu Phe Lys Ile Lys Cys Ser Tyr Leu Tyr Ser Pro  
 20 25 30  
 Tyr Phe Gly Val Ile Ile Tyr Met Met Phe Ile Val Pro Val Val Phe  
 35 40 45  
 30 His Pro Arg Ser Arg Ile Ser Phe Ser Thr Phe Ser Phe Ile Arg Val  
 50 55 60  
 Met Lys Leu Asn Pro Trp Ala Met Ser Glu Ala Gln Ser Leu Glu Cys  
 65 70 75 80  
 35 Val Tyr Ser Gln Trp Cys Met Tyr Ile Leu Cys Leu Asp Ser Leu Arg  
 85 90 95  
 Ser Val Ser Glu Asn Leu Asp Ser Ser Leu Leu His Lys Asn Phe Ile  
 100 105 110  
 40 Cys Ile Tyr Glu Asp Asp Ser Val Pro  
 115 120  
  
 <210> 1108  
 <211> 211  
 <212> PRT  
 45 <213> Homo sapiens  
  
 <400> 1108  
 Glu Thr Cys Gln Leu Leu Lys Lys Glu Glu Val Lys Asn Val Ala Glu  
 1 5 10 15  
 50 Leu Pro Thr Lys Val Glu Glu Ile Pro His Pro Lys Glu Glu Met Asn  
 20 25 30  
 Gly Ile Asn Ser Ile Glu Met Asp Ser Met Arg His Ser Glu Asp Phe  
 35 40 45  
 Lys Glu Lys Leu Pro Lys Gly Asn Gly Lys Arg Lys Ser Asp Thr Glu  
 50 55 60  
 55 Phe Gly Asn Met Lys Lys Lys Val Lys Leu Ser Lys Glu His Gln Ser  
 65 70 75 80  
 Leu Glu Glu Asn Gln Arg Gln Thr Arg Ser Lys Arg Lys Ala Thr Ser  
 85 90 95  
 60 Asp Thr Leu Glu Ser Pro Pro Lys Ile Ile Pro Lys Tyr Ile Ser Glu  
 100 105 110  
 Asn Glu Ser Pro Arg Pro Ser Gln Lys Lys Ser Arg Val Lys Ile Asn  
 115 120 125

Trp Leu Lys Ser Ala Thr Lys Gln Pro Ser Ile Leu Ser Lys Phe Cys  
 130 135 140  
 Ser Leu Gly Lys Ile Thr Asn Gln Gly Val Lys Gly Gln Ser Lys  
 145 150 155 160  
 5 Glu Asn Glu Cys Asp Pro Glu Glu Asp Leu Gly Lys Cys Glu Ser Asp  
 165 170 175  
 Asn Thr Thr Asn Gly Cys Gly Leu Glu Ser Pro Gly Asn Thr Val Thr  
 180 185 190  
 10 Pro Val Asn Val Asn Glu Val Lys Pro Ile Asn Lys Gly Glu Glu Gln  
 195 200 205  
 Ile Gly Phe  
 210  
 <210> 1109  
 15 <211> 187  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1109  
 20 Asn Val Ala Glu Leu Pro Thr Lys Val Glu Glu Ile Pro His Pro Lys  
 1 5 10 15  
 Glu Glu Met Asn Gly Ile Asn Ser Ile Glu Met Asp Ser Met Arg His  
 20 25 30  
 Ser Glu Asp Phe Lys Glu Lys Leu Pro Lys Gly Asn Gly Lys Arg Lys  
 35 40 45  
 25 Ser Asp Thr Glu Phe Gly Asn Met Lys Lys Lys Val Lys Leu Ser Lys  
 50 55 60  
 Glu His Gln Ser Leu Glu Glu Asn Gln Arg Gln Thr Arg Ser Lys Arg  
 65 70 75 80  
 30 Lys Ala Thr Ser Asp Thr Leu Glu Ser Pro Pro Lys Ile Ile Pro Lys  
 85 90 95  
 Tyr Ile Ser Glu Asn Glu Ser Pro Arg Pro Ser Gln Lys Lys Ser Arg  
 100 105 110  
 Val Lys Ile Asn Trp Leu Lys Ser Ala Thr Lys Gln Pro Ser Ile Leu  
 115 120 125  
 35 Ser Lys Phe Cys Ser Leu Gly Lys Ile Thr Thr Asn Gln Gly Val Lys  
 130 135 140  
 Gly Gln Ser Lys Glu Asn Glu Cys Asp Pro Glu Glu Asp Leu Gly Lys  
 145 150 155 160  
 40 Cys Glu Ser Asp Asn Thr Thr Asn Gly Cys Gly Leu Glu Ser Pro Gly  
 165 170 175  
 Asn Thr Val Thr Pro Val Asn Val Asn Glu Ser  
 180 185  
 45 <210> 1110  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1110  
 50 Ile Pro Thr Glu Val Ala Ile Glu Ser Thr Pro Met Ile Leu Glu Ser  
 1 5 10 15  
 Ser Ile Met Ser Ser His Val Met Lys Gly Ile Asn Leu Ser Ser Gly  
 20 25 30  
 55 Asp Gln Asn Leu Ala Pro Glu Ile Gly Ile Gln Glu Ile Ala Leu His  
 35 40 45  
 Ser Gly Glu Glu Pro His Ala Glu Glu His Leu Lys Gly Asp Phe Tyr  
 50 55 60  
 Glu Ser Glu His Gly Ile Asn Ile Asp Leu Asn Ile Asn Asn His Leu  
 65 70 75 80  
 60 Ile Ala Lys Glu Met Glu His Asn Thr Val Cys Ala Ala Gly Thr Ser  
 85 90 95  
 Pro Val Gly Glu Ile Gly Glu Glu Lys Ile Leu Pro Thr Ser Glu Thr

100 105 110  
 Lys Gln Cys Thr Val Leu Asp Thr Tyr Pro Gly Val Ser Glu Ala Asp  
 115 120 125  
 Ala Gly Glu Thr Leu Ser Ser Thr Gly Pro Phe Ala Leu Glu Pro Asp  
 130 135 140  
 5 Ala Thr Gly Thr Ser Lys Gly Ile Glu Phe Thr Thr Ala Ser Thr Leu  
 145 150 155 160  
 Ser Leu Val Asn Lys Tyr Asp Val Asp Leu Ser Leu Thr Thr Gln Asp  
 165 170 175  
 10 Thr Glu His Asp Met Val Ile Ser Thr Ser Pro Ser Gly Gly Ser Glu  
 180 185 190  
 Ala Asp Ile Glu Gly Pro Leu Pro Ala Lys Asp Ile His Leu Asp Leu  
 195 200 205  
 Pro Ser Asn Asn Asn Leu Val Ser Lys Asp Thr Glu Glu Pro Leu Pro  
 210 215 220  
 15 Val Lys Glu Ser Asp Gln Thr Leu Ala Ala Leu Leu Ser Pro Lys Glu  
 225 230 235 240  
 Ser Ser Gly Gly Glu Lys Glu Val Pro Pro Pro Lys Glu Thr Leu  
 245 250 255  
 20 Pro Asp Ser Gly Phe Ser Ala Asn Ile Glu Asp Ile Asn Glu Ala Asp  
 260 265 270  
 Leu Val Arg Pro Leu Leu Pro Lys Asp Met Glu Arg Leu Thr Ser Leu  
 275 280 285  
 Lys Ser Trp His Leu Lys Asp Leu Tyr Leu Gln Val Met Phe Gly Pro  
 290 295 300  
 25 Trp Thr Arg Ser Ala Gly Gln Pro Xaa Leu  
 305 310  
  
 <210> 1111  
 30 <211> 218  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 1111  
 35 Pro Val Gly Glu Ile Gly Glu Glu Lys Ile Leu Pro Thr Ser Glu Thr  
 1 5 10 15  
 Lys Gln Cys Thr Val Leu Asp Thr Tyr Pro Gly Val Ser Glu Ala Asp  
 20 25 30  
 40 Ala Gly Glu Thr Leu Ser Ser Thr Gly Pro Phe Ala Leu Glu Pro Asp  
 35 40 45  
 Ala Thr Gly Thr Ser Lys Gly Ile Glu Phe Thr Thr Ala Ser Thr Leu  
 50 55 60  
 Ser Leu Val Asn Lys Tyr Asp Val Asp Leu Ser Leu Thr Thr Gln Asp  
 65 70 75 80  
 45 Thr Glu His Asp Met Val Ile Ser Thr Ser Pro Ser Gly Gly Ser Glu  
 85 90 95  
 Ala Asp Ile Glu Gly Pro Leu Pro Ala Lys Asp Ile His Leu Asp Leu  
 100 105 110  
 Pro Ser Asn Asn Asn Leu Val Ser Lys Asp Thr Glu Glu Pro Leu Pro  
 115 120 125  
 50 Val Lys Glu Ser Asp Gln Thr Leu Ala Ala Leu Leu Ser Pro Lys Glu  
 130 135 140  
 Ser Ser Gly Gly Glu Lys Glu Val Pro Pro Pro Pro Lys Glu Thr Leu  
 145 150 155 160  
 55 Pro Asp Ser Gly Phe Ser Ala Asn Ile Glu Asp Ile Asn Glu Ala Asp  
 165 170 175  
 Leu Val Arg Pro Leu Leu Pro Lys Asp Met Glu Arg Leu Thr Ser Leu  
 180 185 190  
 Lys Ser Trp His Leu Lys Asp Leu Tyr Leu Gln Val Met Phe Gly Pro  
 195 200 205  
 60 Trp Thr Arg Ser Ala Gly Gln Pro Xaa Leu  
 210 215

<210> 1112  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1112  
 Ile Pro Thr Glu Val Ala Ile Glu Ser Thr Pro Met Ile Leu Glu Ser  
 1 5 10 15  
 Ser Ile Met Ser Ser His Val Met Lys Gly Ile Asn Leu Ser Ser Gly  
 10 20 25 30  
 Asp Gln Asn Leu Ala Pro Glu Ile Gly Ile Gln Glu Ile Ala Leu His  
 35 40 45  
 Ser Gly Glu Glu Pro His Ala Glu Glu His Leu Lys Gly Asp Phe Tyr  
 50 55 60  
 15 Glu Ser Glu His Gly Ile Asn Ile Asp Leu Asn Ile Asn Asn His Leu  
 65 70 75 80  
 Ile Ala Lys Glu Met Glu His Asn Thr Val Cys Ala Ala Gly Thr Ser  
 85 90 95  
 Pro Val Gly Glu Ile Gly Glu Glu Lys Ile Leu Pro Thr Ser Glu Thr  
 100 105 110  
 20 Lys Gln Arg Thr Val Leu Asp Thr Tyr Pro Gly Val Ser Glu Ala Asp  
 115 120 125  
 Ala Gly Glu Thr Leu Ser Ser Thr Gly Pro Phe Ala Leu Glu Pro Asp  
 130 135 140  
 25 Ala Thr Gly Thr Ser Lys Gly Ile Glu Phe Thr Thr Ala Ser Thr Leu  
 145 150 155 160  
 Ser Leu Ser

30

<210> 1113  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

35

<400> 1113  
 Ser Gly Cys Gly Ala Pro Ala Ala Gly Ala Gly Pro Arg Gly Ala Glu  
 1 5 10 15  
 Leu Gly Ser Gly Ala Gln Ala Val Pro Arg Gly Ala Met Lys Gly Lys  
 20 25 30  
 40 Glu Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly Gly Ser Pro  
 35 40 45  
 Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln Gly Asn Arg Leu  
 50 55 60  
 Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Ala Cys Tyr Gly Arg Ala  
 45 65 70 75 80  
 Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr Asn Arg Ala Leu  
 85 90 95  
 Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu Ala Asp Cys Arg  
 100 105 110  
 50 Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala His Phe Phe Leu  
 115 120 125  
 Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu Ala Ile Ala Asn  
 130 135 140  
 Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg Leu Asn Phe Gly  
 55 145 150 155 160  
 Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Xaa Lys Arg Trp Asn  
 165 170 175  
 Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu Leu Xaa Phe Tyr  
 180 185 190  
 60 Xaa Phe Xaa Leu Ile Ala Xaa Asp Arg Glu Arg Lys Xaa Lys Xaa Cys  
 195 200 205  
 Gln Gly Asn His Glu Gly Tyr Glu Asp Asp Lys Pro Arg Pro Gly Pro  
 210 215 220

Ser Arg Leu Ala Leu Arg Pro Ser Thr Thr Ser Thr Trp Arg Thr Trp  
 225 230 235 240  
 Thr Ser Phe Phe Phe Gln Val Asp Glu Arg Gly Arg Ser Glu Thr Ser  
 245 250 255  
 5 Pro Thr Tyr Leu Cys Gly Lys Ile Ser Phe Glu Pro Met Arg Glu Pro  
 260 265 270  
 Cys Ile Thr Pro Ser Gly Ile Thr Tyr Asp Arg Lys Asp Ile Glu Glu  
 275 280 285  
 His Leu Gln Arg Val Gly His Phe Asp Pro Val Thr Arg Ser Pro Leu  
 290 295 300  
 10 Thr Gln Glu Gln Leu Ile Pro Asn Leu Ala Met Lys Glu Val Ile Asp  
 305 310 315 320  
 Ala Phe Ile Ser Glu Asn Gly Trp Val Glu Asp Tyr  
 325 330

15

<210> 1114  
 <211> 259  
 <212> PRT  
 <213> Homo sapiens

20

<400> 1114  
 Val Thr Gln Glu Phe Thr Gln Tyr Trp Ala Gln Arg Glu Ala Asp Phe  
 1 5 10 15  
 Lys Glu Thr Leu Leu Gln Glu Arg Glu Ile Leu Glu Glu Asn Ala Glu  
 20 25 30  
 25 Arg Arg Leu Ala Ile Phe Lys Asp Leu Val Gly Lys Cys Asp Thr Arg  
 35 40 45  
 Glu Glu Ala Ala Lys Asp Ile Cys Ala Thr Lys Val Glu Thr Glu Glu  
 50 55 60  
 30 Ala Thr Ala Cys Leu Glu Leu Lys Phe Asn Gln Ile Lys Ala Glu Leu  
 65 70 75 80  
 Ala Lys Thr Lys Gly Glu Leu Ile Lys Thr Lys Glu Glu Leu Lys Lys  
 85 90 95  
 Arg Glu Asn Glu Ser Asp Ser Leu Ile Gln Glu Leu Glu Thr Ser Asn  
 100 105 110  
 35 Lys Lys Ile Ile Thr Gln Asn Gln Arg Ile Lys Glu Leu Ile Asn Ile  
 115 120 125  
 Ile Asp Gln Lys Glu Asp Thr Ile Asn Glu Phe Gln Asn Leu Lys Ser  
 130 135 140  
 40 His Met Glu Asn Thr Phe Lys Cys Asn Asp Lys Ala Asp Thr Ser Ser  
 145 150 155 160  
 Leu Ile Ile Asn Asn Lys Leu Ile Cys Asn Glu Thr Val Glu Val Pro  
 165 170 175  
 Lys Asp Ser Lys Ser Lys Ile Cys Ser Glu Arg Lys Arg Val Asn Glu  
 180 185 190  
 45 Asn Glu Leu Gln Gln Asp Glu Pro Pro Ala Lys Lys Gly Ser Ile His  
 195 200 205  
 Cys Ser Ser Ala Ser Leu Lys Thr Lys Arg Lys Val Glu Glu Val Arg  
 210 215 220  
 50 Pro Glu His Cys Arg Lys Leu Lys Thr Xaa Arg Val Leu Gln Gly Lys  
 225 230 235 240  
 Ile Met Lys Gly Leu Glu Ser Ile Phe Ser Ser Leu Phe Glu Asn Asp  
 245 250 255  
 Leu Lys Lys

55

<210> 1115  
 <211> 204  
 <212> PRT  
 <213> Homo sapiens

60

<400> 1115  
 Arg Ile Ser Asn Ser Arg Xaa Pro Ile Gly Lys Ile Leu Ser Xaa Leu  
 431

1 5 10 15  
 Val Leu Lys Pro Ile Trp Glu Glu Cys Lys Glu Ile Val Lys Ala Ser  
 20 25 30  
 Ser Lys Lys Ser His Gln Ile Glu Glu Leu Glu Gln Gln Ile Glu Lys  
 35 40 45  
 5 Leu Gln Ala Glu Val Lys Gly Tyr Lys Asp Glu Asn Asn Arg Leu Lys  
 50 55 60  
 Glu Lys Glu His Lys Asn Gln Asp Asp Leu Leu Lys Glu Lys Glu Thr  
 65 70 75 80  
 10 Leu Ile Gln Gln Leu Lys Glu Glu Leu Gln Glu Lys Asn Val Thr Leu  
 85 90 95  
 Asp Val Gln Ile Gln His Val Val Glu Gly Lys Arg Ala Leu Ser Glu  
 100 105 110  
 Leu Thr Gln Gly Val Thr Cys Tyr Lys Ala Lys Ile Lys Glu Leu Glu  
 115 120 125  
 Thr Ile Leu Glu Thr Gln Lys Val Glu Cys Ser His Ser Ala Lys Leu  
 130 135 140  
 Glu Gln Asp Ile Leu Glu Lys Glu Ser Ile Ile Leu Lys Leu Glu Arg  
 145 150 155 160  
 20 Asn Leu Lys Glu Phe Gln Glu His Leu Gln Asp Ser Val Lys Asn Thr  
 165 170 175  
 Lys Asp Leu Asn Val Lys Glu Leu Lys Leu Lys Glu Glu Ile Thr Gln  
 180 185 190  
 Leu Thr Asn Asn Leu Gln Asp Met Lys His Leu Leu  
 195 200  
 25

&lt;210&gt; 1116

&lt;211&gt; 92

&lt;212&gt; PRT

30 <213> Homo sapiens

&lt;400&gt; 1116

Val Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly Lys  
 1 5 10 15  
 35 Xaa Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His Gly  
 20 25 30  
 Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys His  
 35 40 45  
 Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln Asn  
 50 55 60  
 40 Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp Arg Leu  
 65 70 75 80  
 Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys  
 85 90  
 45

&lt;210&gt; 1117

&lt;211&gt; 224

&lt;212&gt; PRT

50 <213> Homo sapiens

&lt;400&gt; 1117

Gly Asn Ser Ser Leu Asn Ser Thr Ser Asn Thr Lys Val Ser Ala Val  
 1 5 10 15  
 55 Pro Thr Asn Met Ala Ala Lys Lys Thr Ser Thr Pro Lys Ile Asn Phe  
 20 25 30  
 Val Gly Gly Asn Lys Leu Gln Ser Thr Gly Asn Lys Ala Glu Asp Thr  
 35 40 45  
 Lys Gly Thr Glu Cys Val Lys Ser Thr Pro Val Thr Ser Ala Val Gln  
 50 55 60  
 60 Ile Pro Glu Val Lys Gln Asp Thr Val Ser Glu Pro Val Thr Pro Ala  
 65 70 75 80  
 Ser Leu Ala Ala Leu Gln Ser Asp Val Gln Pro Val Gly His Asp Tyr  
 85 90 95

Val Glu Glu Val Arg Asn Asp Glu Gly Lys Val Ile Arg Phe His Cys  
 100 105 110  
 Lys Leu Cys Glu Cys Ser Phe Asn Asp Pro Asn Ala Lys Glu Met His  
 115 120 125  
 5 Leu Lys Gly Arg Arg His Arg Leu Gln Tyr Lys Lys Lys Val Asn Pro  
 130 135 140  
 Asp Leu Gln Val Glu Val Lys Pro Ser Ile Arg Xaa Arg Lys Ile Gln  
 145 150 155 160  
 Glu Glu Lys Met Arg Lys Gln Met Xaa Lys Glu Glu Tyr Trp Arg Xaa  
 165 170 175  
 10 Xaa Lys Glu Lys Gly Ala Leu Glu Asn Gly Asn Glu Thr Xaa Xaa Lys  
 180 185 190  
 Arg His Val Leu Glu Glu Asn Gly Xaa Arg Thr Thr Leu Phe Gly Met  
 195 200 205  
 15 Ile Ala Xaa Asn Ala Xaa Xaa Arg Xaa Ser His Xaa Pro Xaa Gly His  
 210 215 220

&lt;210&gt; 1118

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1118

Glu Arg Cys Gly Ala Ala Arg Phe Ala Cys Lys Cys Ile Thr Lys Arg  
 1 5 10 15  
 Gln Pro Arg Met Lys Lys Ala Ser Arg Ser Val Gly Ser Val Pro Lys  
 20 25 30  
 Val Ser Ala Ile Ser Lys Thr Gln Thr Ala Glu Lys Ile Lys Pro Glu  
 35 40 45  
 30 Asn Ser Ser Ser Ala Ser Thr Gly Gly Lys Leu Val Lys Pro Gly Thr  
 50 55 60  
 Ala Ala Ser Leu Ser Lys Thr Lys Ser Ser Asp Leu Leu Ala Gly  
 65 70 75 80  
 Met Ala Gly Gly Val Thr Val Thr Asn Gly Val Lys Gly Lys Lys Ser  
 85 90 95  
 35 Thr Cys Pro Ser Ala Ala Pro Ser Ala Ser Ala Pro Ala Met Thr Thr  
 100 105 110  
 Val Glu Asn Lys Ser Lys Ile Ser Thr Gly Thr Ala Ser Ser Thr Lys  
 115 120 125  
 40 Arg Ser Thr Ser Thr Gly Gln Gly Ala Asn Asp Met Ala Leu Ala Lys  
 130 135 140  
 Arg Ser Arg Ser Arg Thr Ala Thr Glu Cys Asp Val Arg Met Ser Lys  
 145 150 155 160  
 Ser

&lt;210&gt; 1119

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1119

Leu Ile Glu Ala Glu Gly Ile Glu Asp Ile Glu Lys Glu Asp Ile Glu  
 1 5 10 15  
 55 Ser Gln Glu Ile Glu Ala Gln Glu Gly Glu Asp Asp Thr Phe Leu Thr  
 20 25 30  
 Ala Gln Asp Gly Glu Glu Glu Glu Asn Glu Lys Asp Ile Ala Gly Ser  
 35 40 45  
 Gly Asp Gly Thr Gln Glu Val Ser Lys Pro Leu Pro Ser Glu Gly Ser  
 50 55 60  
 60 Leu Ala Glu Ala Asp His Thr Ala His Glu Glu Met Glu Ala His Thr  
 65 70 75 80  
 Thr Val Lys Glu Ala Glu Asp Asp Asn Ile Ser Val Thr Ile Gln Ala

				85					90					95		
	Glu	Asp	Ala	Ile	Thr	Leu	Asp	Phe	Asp	Gly	Asp	Asp	Leu	Leu	Glu	Thr
				100					105					110		
5	Gly	Lys	Asn	Val	Lys	Ile	Thr	Asp	Ser	Glu	Ala	Ser	Lys	Pro	Lys	Asp
			115					120					125			
	Gly	Gln	Asp	Ala	Ile	Ala	Gln	Ser	Pro	Glu	Lys	Glu	Ser	Lys	Asp	Tyr
			130				135					140				
	Glu	Met	Asn	Ala	Asn	His	Lys	Asp	Gly	Lys	Lys	Glu	Asp	Cys	Val	Lys
			145			150					155				160	
10	Gly	Asp	Pro	Val	Glu	Lys	Glu	Ala	Arg	Glu	Ser	Ser	Xaa	Lys	Ala	Glu
				165						170					175	
	Ser	Gly	Asp	Gln	Arg	Lys	Xaa	Tyr	Phe							
			180						185							
15				<210>		1120										
				<211>		236										
				<212>		PRT										
				<213>		Homo sapiens										
20				<400>		1120										
	Lys	Gln	Val	Ser	Gln	Lys	Met	Gly	Arg	Xaa	Ala	Ile	Xaa	Xaa	Ser	Pro
	1				5					10					15	
	Xaa	Lys	Glu	Ser	Lys	Asp	Tyr	Glu	Met	Asn	Ala	Xaa	His	Lys	Asp	Gly
			20					25					30			
25	Lys	Lys	Glu	Asp	Cys	Val	Lys	Gly	Asp	Pro	Val	Glu	Lys	Glu	Ala	Arg
			35					40				45				
	Glu	Ser	Ser	Lys	Lys	Ala	Glu	Ser	Gly	Asp	Lys	Glu	Lys	Asp	Thr	Leu
		50					55					60				
	Lys	Lys	Gly	Pro	Ser	Ser	Thr	Gly	Ala	Xaa	Gly	Gln	Ala	Lys	Ser	Ser
30		65				70				75					80	
	Ser	Lys	Glu	Ser	Lys	Asp	Ser	Lys	Thr	Ser	Ser	Lys	Asp	Xaa	Lys	Gly
				85					90					95		
	Ser	Xaa	Ser	Ser	Thr	Ser	Gly	Ser	Ser	Xaa	Ser	Ser	Thr	Lys	Asn	Xaa
			100					105						110		
35	Trp	Val	Ser	Gly	Leu	Ser	Ser	Asn	Thr	Lys	Ala	Ala	Asp	Leu	Lys	Asn
			115					120					125			
	Leu	Phe	Gly	Lys	Tyr	Gly	Lys	Val	Leu	Ser	Ala	Lys	Val	Val	Thr	Asn
		130				135						140				
	Ala	Arg	Ser	Pro	Gly	Ala	Lys	Cys	Tyr	Gly	Ile	Val	Thr	Met	Ser	Ser
40		145				150					155				160	
	Ser	Thr	Glu	Val	Ser	Arg	Cys	Ile	Ala	His	Xaa	His	Arg	Thr	Glu	Leu
				165					170						175	
	His	Gly	Gln	Leu	Ile	Ser	Val	Glu	Lys	Val	Lys	Gly	Asp	Pro	Ser	Lys
			180					185					190			
45	Lys	Glu	Met	Lys	Lys	Glu	Asn	Asp	Glu	Lys	Ser	Ser	Ser	Arg	Ser	Ser
	Gly	Asp	Lys	Lys	Asn	Thr	Ser	Asp	Arg	Ser	Ser	Lys	Thr	Gln	Ala	Ser
		210					215					220				
	Val	Lys	Lys	Glu	Glu	Lys	Arg	Ser	Ser	Glu	Lys	Xaa				
50		225				230					235					
				<210>		1121										
				<211>		205										
				<212>		PRT										
55				<213>		Homo sapiens										
				<400>		1121										
	Ser	Gly	Cys	Gly	Ala	Pro	Ala	Ala	Gly	Ala	Gly	Pro	Arg	Gly	Ala	Glu
	1				5					10					15	
60	Leu	Gly	Ser	Gly	Ala	Gln	Ala	Val	Pro	Arg	Gly	Ala	Met	Lys	Gly	Lys
			20					25					30			
	Glu	Glu	Lys	Glu	Gly	Gly	Ala	Arg	Leu	Gly	Ala	Gly	Gly	Gly	Ser	Pro
			35					40					45			



Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln Gly Asn Arg Leu  
 50 55 60  
 Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Cys Tyr Gly Arg Ala  
 65 70 75 80  
 5 Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr Asn Arg Ala Leu  
 85 90 95  
 Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu Ala Asp Cys Arg  
 100 105 110  
 Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala His Phe Phe Leu  
 115 120 125  
 10 Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu Ala Ile Ala Asn  
 130 135 140  
 Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg Leu Asn Phe Gly  
 145 150 155 160  
 15 Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Xaa Lys Arg Trp Asn  
 165 170 175  
 Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu Leu Xaa Phe Tyr  
 180 185 190  
 Xaa Phe Xaa Leu Ile Ala Xaa Asp Arg Xaa Lys Glu Thr  
 195 200 205  
 20

&lt;210&gt; 1122

&lt;211&gt; 136

&lt;212&gt; PRT

25 <213> Homo sapiens

&lt;400&gt; 1122

Phe Pro Arg Lys Arg Glu Arg Lys Xaa Lys Xaa Cys Gln Gly Asn His  
 1 5 10 15  
 30 Glu Gly Tyr Glu Asp Asp Lys Pro Arg Pro Gly Pro Ser Arg Leu Ala  
 20 25 30  
 Leu Arg Pro Ser Thr Thr Ser Thr Trp Arg Thr Trp Thr Ser Phe Phe  
 35 40 45  
 Phe Gln Val Asp Glu Arg Gly Arg Ser Glu Thr Ser Pro Thr Tyr Leu  
 50 55 60  
 35 Cys Gly Lys Ile Ser Phe Glu Pro Met Arg Glu Pro Cys Ile Thr Pro  
 65 70 75 80  
 Ser Gly Ile Thr Tyr Asp Arg Lys Asp Ile Glu Glu His Leu Gln Arg  
 85 90 95  
 40 Val Gly His Phe Asp Pro Val Thr Arg Ser Pro Leu Thr Gln Glu Gln  
 100 105 110  
 Leu Ile Pro Asn Leu Ala Met Lys Glu Val Ile Asp Ala Phe Ile Ser  
 115 120 125  
 Glu Asn Gly Trp Val Glu Asp Tyr  
 130 135  
 45

&lt;210&gt; 1123

&lt;211&gt; 206

&lt;212&gt; PRT

50 <213> Homo sapiens

&lt;400&gt; 1123

Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu Asp Phe  
 1 5 10 15  
 55 Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu Val Glu  
 20 25 30  
 Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile Val Thr  
 35 40 45  
 Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp Lys Lys  
 50 55 60  
 60 Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu Lys Glu  
 65 70 75 80  
 Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr Glu Lys

85 90 95  
 Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu Lys Met  
 100 105 110  
 5 Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys Ala Tyr  
 115 120 125  
 Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr Ser Lys  
 130 135 140  
 Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Lys Pro Ser Ile  
 145 150 155 160  
 10 Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val Ser Lys  
 165 170 175  
 Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp Gln Ile  
 180 185 190  
 15 Asn Ala Glu Lys Lys Leu Ser Ala Gln Xaa Ile Trp Ser Ala  
 195 200 205  
  
 <210> 1124  
 <211> 94  
 <212> PRT  
 20 <213> Homo sapiens  
  
 <400> 1124  
 Gln Leu Asn Ser Thr Gln Arg Glu Leu Glu Leu Glu Asn Ser Ala Ile  
 1 5 10 15  
 25 Arg Lys Ser Cys Ala Glu Pro Ala Lys Gly Glu Glu Ala Phe Gln  
 20 25 30  
 Met Ser Glu Val Asp Glu Glu Ser Gly Leu Lys Asp Ser Glu Pro Glu  
 35 40 45  
 Arg Lys Arg Lys Lys Thr Glu Asp Ser Ser Ser Gly Lys Ser Val Ala  
 50 55 60  
 30 Ser Asp Val Pro Glu Glu Leu Asp Phe Leu Asp Leu Arg Leu Asp Ser  
 65 70 75 80  
 Ser Val Gln Phe Val Pro Ser Ser Thr Gln Val Lys Lys Gln  
 85 90  
 35  
 <210> 1125  
 <211> 237  
 <212> PRT  
 40 <213> Homo sapiens  
  
 <400> 1125  
 Arg Pro Gly Lys Arg Arg Cys Gly Val Gly Cys Phe Pro Glu Ala Gly  
 1 5 10 15  
 45 Leu Asn Gly Ser Arg Leu Ser His Arg Val Ser Ser Pro Pro Ser Pro  
 20 25 30  
 Asn Gln Glu Ile Ala Arg Glu Arg Cys Gly Ala Ala Arg Phe Ala Cys  
 35 40 45  
 Lys Cys Ile Thr Lys Arg Gln Pro Arg Met Lys Lys Ala Ser Arg Ser  
 50 55 60  
 Val Gly Ser Val Pro Lys Val Ser Ala Ile Ser Lys Thr Gln Thr Ala  
 65 70 75 80  
 Glu Lys Ile Lys Pro Glu Asn Ser Ser Ser Ala Ser Thr Gly Gly Lys  
 85 90 95  
 55 Leu Val Lys Pro Gly Thr Ala Ala Ser Leu Ser Lys Thr Lys Ser Ser  
 100 105 110  
 Asp Asp Leu Leu Ala Gly Met Ala Gly Gly Val Thr Val Thr Asn Gly  
 115 120 125  
 Val Lys Gly Lys Lys Ser Thr Cys Pro Ser Ala Ala Pro Ser Ala Ser  
 130 135 140  
 60 Ala Pro Ala Met Thr Thr Val Glu Asn Lys Ser Lys Ile Ser Thr Gly  
 145 150 155 160  
 Thr Xaa Ser Ser Thr Lys Arg Ser Thr Xaa Thr Gly Asn Lys Glu Ser  
 165 170 175

Ser Ser Thr Arg Glu Arg Leu Arg Glu Arg Thr Arg Leu Asn Gln Ser  
 180 185 190  
 Lys Lys Leu Pro Xaa Ala Gly Xaa Gly Ala Asn Asp Met Ala Phe Gly  
 195 200 205  
 5 Gln Thr Xaa Xaa Gln Leu Asn Xaa Phe Gln Asn Val Thr Phe Arg Xaa  
 210 215 220  
 Xaa Gln Xaa Leu Ser Gln Thr Ile Xaa Asn Pro Val Xaa  
 225 230 235  
  
 10 <210> 1126  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens  
  
 15 <400> 1126  
 Leu Asn Glu Ile Tyr Thr Lys Thr Asp Ser Lys Ser Ile Met Arg Met  
 1 5 10 15  
 Lys Ser Gly Gln Met Phe Ala Lys Glu Asp Leu Lys Arg Lys Lys Leu  
 20 20 25 30  
 Val Arg Asp Gly Ser Val Phe Leu Lys Asn Ala Ala Gly Arg Leu Lys  
 35 40 45  
 Glu Val Gln Ala Val Leu Leu Thr Asp Ile Leu Val Phe Leu Gln Glu  
 50 55 60  
 Lys Asp Gln Lys Tyr Ile Phe Ala Ser Leu Asp Gln Lys Ser Thr Val  
 65 70 75 80  
 25 Ile Ser Leu Lys Lys Leu Ile Val Arg Glu Val Ala His Glu Glu Lys  
 85 90 95  
 Gly Leu Phe Leu Ile Ser Met Gly Met Thr Asp Pro Glu Met Val Glu  
 100 105 110  
 30 Val His Ala Ser Ser Lys Glu Glu Arg Asn Ser Trp Ile Gln Ile Ile  
 115 120 125  
 Gln Asp Thr Ile Asn Thr Leu Asn Arg Asp Glu Asp Glu Gly Ile Pro  
 130 135 140  
 Ser Glu Asn Glu Glu Glu Lys Lys Met Leu Asp Thr Arg Pro Arg Glu  
 145 150 155 160  
 35 Leu Lys Glu His Phe Pro Glu Gly Gln Lys Ile Ser Leu Val Glu Arg  
 165 170 175  
 Arg Asn Asp Phe Pro Xaa Trp Leu Met His Pro Leu Ser Arg Asp Trp  
 180 185 190  
 40 Ser His Pro  
 195  
  
 <210> 1127  
 <211> 160  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 1127  
 Glu Glu Gly Arg Ala Leu His Asp Gly Ile Ala Ile Ala Tyr Ala Thr  
 1 5 10 15  
 Leu Glu Tyr Phe Ile Arg Asp Val Lys Ser Leu Thr Leu Phe Val Thr  
 20 25 30  
 His Tyr Pro Pro Val Cys Glu Leu Lys Asn Tyr Ser His Gln Val  
 35 40 45  
 55 Gly Asn Tyr His Met Gly Phe Leu Val Ser Glu Asp Glu Ser Lys Leu  
 50 55 60  
 Asp Pro Gly Thr Ala Glu Gln Val Pro Asp Phe Val Thr Phe Leu Tyr  
 65 70 75 80  
 Gln Ile Thr Arg Gly Ile Ala Ala Arg Ser Tyr Gly Leu Asn Val Ala  
 85 90 95  
 60 Lys Leu Ala Asp Val Pro Gly Glu Ile Leu Lys Lys Ala Ala His Lys  
 100 105 110  
 Ser Lys Glu Leu Glu Gly Leu Ile Asn Thr Lys Arg Lys Arg Leu Lys

115 120 125  
 Tyr Phe Ala Lys Leu Trp Thr Met His Asn Ala Gln Asp Leu Gln Lys  
 130 135 140  
 Trp Thr Glu Glu Phe Asn Met Glu Glu Thr Gln Thr Ser Leu Leu His  
 5 145 150 155 160  
  
 <210> 1128  
 <211> 82  
 <212> PRT  
 10 <213> Homo sapiens  
  
 <400> 1128  
 Ile Pro Ser Leu Gln Glu Glu Ala Lys Lys Gln Ile Glu Asp Leu Asn  
 1 5 10 15  
 15 Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys Glu Thr Glu  
 20 25 30  
 Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp Glu Val Glu  
 35 40 45  
 Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile Ser Asp Leu  
 20 50 55 60  
 Glu Asn Thr Gly Lys Lys Leu Gln Xaa Pro Lys Xaa Asp Met Gly Lys  
 65 70 75 80  
 Arg Asn  
  
 25  
 <210> 1129  
 <211> 414  
 <212> PRT  
 30 <213> Homo sapiens  
  
 <400> 1129  
 Ser Arg Thr Arg Thr Ser Asp Arg Leu Asn Arg Ile Ala Asn Gln Val  
 1 5 10 15  
 35 Ala Ile Gln Arg Lys Lys Gln Phe Val Glu Arg Ala His Ser Tyr Trp  
 20 25 30  
 Leu Leu Lys Arg Leu Ser Arg Asn Gly Ala Pro Leu Leu Arg Arg Leu  
 35 40 45  
 Gln Ser Ser Leu Gln Ser Gln Arg Ser Ser Gln Gln Arg Glu Asn Asp  
 50 55 60  
 40 Glu Glu Met Lys Ala Ala Lys Glu Lys Leu Lys Tyr Trp Gln Arg Leu  
 65 70 75 80  
 Arg His Asp Leu Glu Arg Ala Arg Leu Leu Ile Glu Leu Leu Arg Lys  
 85 90 95  
 Arg Glu Lys Leu Lys Arg Glu Gln Val Lys Val Glu Gln Val Ala Met  
 100 105 110  
 45 Glu Leu Arg Leu Thr Pro Leu Thr Val Leu Leu Arg Ser Val Leu Asp  
 115 120 125  
 Gln Leu Gln Asp Lys Asp Pro Ala Arg Ile Phe Ala Gln Pro Val Ser  
 130 135 140  
 50 Leu Lys Glu Val Pro Asp Tyr Leu Asp His Ile Lys His Pro Met Asp  
 145 150 155 160  
 Phe Ala Thr Met Arg Lys Arg Leu Glu Ala Gln Gly Tyr Lys Asn Leu  
 165 170 175  
 His Glu Phe Glu Glu Asp Phe Asp Leu Ile Ile Asp Asn Cys Met Lys  
 180 185 190  
 55 Tyr Asn Ala Arg Asp Thr Val Phe Tyr Arg Ala Ala Val Arg Leu Arg  
 195 200 205  
 Asp Gln Gly Gly Val Val Leu Arg Gln Ala Arg Arg Glu Val Asp Ser  
 210 215 220  
 60 Ile Gly Leu Glu Glu Ala Ser Gly Met His Leu Pro Glu Arg Pro Ala  
 225 230 235 240  
 Ala Ala Pro Arg Arg Pro Phe Ser Trp Glu Asp Val Asp Arg Leu Leu  
 245 250 255

Asp Pro Ala Asn Arg Ala His Leu Gly Leu Glu Glu Gln Leu Arg Glu  
 260 265 270  
 Leu Leu Asp Met Leu Asp Leu Thr Cys Ala Met Lys Ser Ser Gly Ser  
 275 280 285  
 5 Arg Ser Lys Arg Ala Lys Leu Leu Lys Lys Glu Ile Ala Leu Leu Arg  
 290 295 300  
 Asn Lys Leu Ser Gln Gln His Ser Gln Pro Leu Pro Thr Gly Pro Gly  
 305 310 315 320  
 Leu Glu Gly Phe Glu Glu Asp Gly Ala Ala Leu Gly Pro Gly Gly Gly  
 10 325 330 335  
 Arg Arg Ser Pro Ser Glu Val Gly Asp Ser Ser Ala Ala Lys Glu Lys  
 340 345 350  
 Val Ala Glu His Met Arg Arg Leu Xaa Xaa Trp Arg Arg Ser Xaa Xaa  
 355 360 365  
 15 Glu Lys Arg Leu Asp Ala Gly Leu His Gln Xaa Leu Leu Gly Cys Xaa  
 370 375 380  
 Glu Pro Thr Xaa Asn Pro Ala Gly Gly Leu Gly Gly Gly Arg Pro His  
 385 390 395 400  
 20 Pro Asp Asp Leu Gly Pro Ser Ser Ser Arg Phe Ser Phe Lys  
 405 410

&lt;210&gt; 1130

&lt;211&gt; 178

&lt;212&gt; PRT

25 &lt;213&gt; Homo sapiens

&lt;400&gt; 1130

Ile Val Glu Arg Glu Ser Gly His Tyr Val Glu Met His Ala Arg Tyr  
 1 5 10 15  
 30 Ile Gly Thr Thr Val Phe Val Arg Gln Val Gly Arg Tyr Leu Thr Leu  
 20 25 30  
 Ala Ile Arg Met Pro Glu Asp Leu Ala Met Ser Tyr Glu Glu Ser Gln  
 35 40 45  
 Asp Leu Gln Leu Cys Val Asn Gly Cys Pro Leu Ser Glu Arg Ile Asp  
 50 55 60  
 35 Asp Gly Gln Gly Gln Val Ser Ala Ile Leu Gly His Ser Leu Pro Arg  
 65 70 75 80  
 Thr Ser Leu Val Gln Ala Trp Pro Gly Tyr Thr Leu Glu Thr Ala Asn  
 85 90 95  
 40 Thr Gln Cys His Glu Lys Met Pro Val Lys Asp Ile Tyr Phe Gln Ser  
 100 105 110  
 Cys Val Phe Asp Leu Leu Thr Thr Gly Asp Ala Asn Phe Thr Ala Ala  
 115 120 125  
 Ala His Ser Ala Leu Glu Asp Val Glu Ala Leu His Pro Arg Lys Glu  
 130 135 140  
 45 Arg Trp His Ile Phe Pro Ser Ser Gly Asn Gly Thr Pro Arg Gly Gly  
 145 150 155 160  
 Ser Asp Leu Ser Val Ser Leu Gly Leu Thr Cys Leu Ile Leu Ile Val  
 165 170 175  
 50 Phe Leu

&lt;210&gt; 1131

&lt;211&gt; 118

55 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1131

Ala Gly Arg Arg His Arg Thr Gly Asn Arg Cys Pro Ser Leu Ala Ser  
 1 5 10 15  
 Ser His Gly Ile Glu Cys Trp Gln Ser Pro Val Cys Ser Gln Ala Arg  
 20 25 30  
 Pro Ala Pro Arg Arg Cys Glu Ala Gly Cys Val Pro Gly Trp Gln Thr

35 40 45  
 Pro Gly Pro Ala Arg His Arg Cys Val His Ser Gly Gly Ser Arg Ser  
 50 55 60  
 Arg Thr Ala Ala Gly Pro Gly Ser Pro Arg Arg Thr Trp Pro Gly Leu  
 65 70 75 80  
 Gln Ala Tyr Gly Trp Gln Gly Ser Gly Ser Asp Pro Pro Ala Ala Gln  
 85 90 95  
 Thr Leu Trp Ser Leu Tyr Ser Gly Arg Ala Ser Pro His Ser Gly His  
 100 105 110  
 10 Ser Pro Phe Pro Arg Tyr  
 115

<210> 1132  
 <211> 166  
 15 <212> PRT  
 <213> Homo sapiens

<400> 1132  
 Thr Asp Arg Gln Ile Thr Ala Ser Thr Gly Ser Pro Ile Ala Thr Ala  
 1 5 10 15  
 Gly Glu Asn Val Pro Ala Phe Leu Pro Trp Val Gln Gly Leu His Ile  
 20 25 30  
 Leu Gln Gly Thr Val Gly Cys Gly Ser Lys Val Gly Ile Thr Ser Gly  
 35 40 45  
 25 Glu Gln Val Glu Asp Thr Gly Leu Glu Ile Asp Val Leu His Trp His  
 50 55 60  
 Leu Leu Met Ala Leu Ser Val Gly Ser Leu Gln Cys Val Ala Arg Pro  
 65 70 75 80  
 Gly Leu His Gln Gly Gly Ala Arg Gln Ala Val Ser Gln Asp Gly Arg  
 85 90 95  
 30 His Leu Ala Leu Pro Val Ile Asp Ala Phe Thr Gln Gly Ala Ala Val  
 100 105 110  
 His Ala Gln Leu Gln Val Leu Ala Leu Val Gly His Gly Gln Val  
 115 120 125  
 35 Phe Arg His Thr Asp Gly Lys Gly Gln Val Ala Thr His Leu Pro His  
 130 135 140  
 Lys His Cys Gly Pro Tyr Ile Ala Gly Val His Leu His Ile Val Ala  
 145 150 155 160  
 Thr Leu Pro Phe His Asp  
 165  
 40

<210> 1133  
 <211> 365  
 <212> PRT  
 45 <213> Homo sapiens

<400> 1133  
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 1 5 10 15  
 50 Ala Pro Ala Arg Pro Arg Arg Arg Gln Phe Arg Leu Lys Lys Leu Ile  
 20 25 30  
 Asp Gln Glu Ile Lys Ser Gln Glu Glu Lys Glu Gln Glu Lys Glu Lys  
 35 40 45  
 Arg Val Thr Thr Leu Lys Glu Leu Thr Lys Leu Lys Ser Phe Ala  
 50 55 60  
 55 Leu Met Val Val Asp Glu Gln Gln Arg Leu Thr Ala Gln Leu Thr Leu  
 65 70 75 80  
 Gln Arg Gln Lys Ile Gln Glu Leu Thr Thr Asn Ala Lys Glu Thr His  
 85 90 95  
 60 Thr Lys Leu Ala Leu Ala Glu Ala Arg Val Gln Glu Glu Glu Gln Lys  
 100 105 110  
 Ala Thr Arg Leu Glu Lys Glu Leu Gln Thr Gln Thr Thr Lys Phe His  
 115 120 125

	Gln	Asp	Gln	Asp	Thr	Ile	Met	Ala	Lys	Leu	Thr	Asn	Glu	Asp	Ser	Gln
	130						135					140				
	Asn	Arg	Gln	Leu	Gln	Gln	Lys	Leu	Ala	Ala	Leu	Ser	Arg	Gln	Ile	Asp
	145				150						155					160
5	Glu	Leu	Glu	Glu	Thr	Asn	Arg	Ser	Leu	Arg	Lys	Ala	Glu	Glu	Glu	Leu
					165					170						175
	Gln	Asp	Ile	Lys	Glu	Lys	Ile	Ser	Lys	Gly	Glu	Tyr	Gly	Asn	Ala	Gly
				180					185					190		
10	Ile	Met	Ala	Glu	Val	Glu	Glu	Leu	Arg	Lys	Arg	Val	Leu	Asp	Met	Glu
			195					200					205			
	Gly	Lys	Asp	Glu	Glu	Leu	Ile	Lys	Met	Glu	Glu	Gln	Cys	Arg	Asp	Leu
	210					215						220				
	Asn	Lys	Arg	Leu	Glu	Arg	Glu	Thr	Leu	Gln	Ser	Lys	Asp	Phe	Lys	Leu
	225					230					235					240
15	Glu	Val	Glu	Lys	Leu	Ser	Lys	Arg	Ile	Met	Ala	Leu	Glu	Lys	Leu	Glu
					245					250					255	
	Asp	Ala	Phe	Asn	Lys	Ser	Lys	Gln	Glu	Cys	Tyr	Ser	Leu	Lys	Cys	Asn
				260					265					270		
20	Leu	Glu	Lys	Glu	Arg	Met	Thr	Thr	Lys	Gln	Leu	Ser	Gln	Glu	Leu	Glu
			275					280					285			
	Ser	Leu	Lys	Val	Arg	Ile	Lys	Glu	Leu	Glu	Ala	Ile	Glu	Ser	Arg	Leu
	290						295					300				
	Glu	Lys	Thr	Glu	Phe	Thr	Leu	Lys	Glu	Asp	Leu	Thr	Lys	Leu	Lys	Thr
	305					310					315					320
25	Leu	Thr	Val	Met	Phe	Val	Asp	Glu	Arg	Lys	Thr	Met	Ser	Glu	Lys	Leu
					325					330					335	
	Lys	Lys	Thr	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Leu	Gln	Val
				340					345					350		
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			355					360					365			
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	<211> 221															
	<212> PRT															
35	<213> Homo sapiens															
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				20					25					30		
	Ser	Glu	Gln	Ile	Val	Glu	Val	Gly	Glu	Glu	Leu	Ile	Asn	Glu	Tyr	Ala
				35				40					45			
45	Ser	Lys	Leu	Gly	Asp	Asp	Ile	Trp	Ile	Ile	Tyr	Glu	Gln	Val	Met	Ile
	50					55						60				
	Ala	Ala	Leu	Asp	Tyr	Gly	Arg	Asp	Asp	Leu	Ala	Leu	Phe	Cys	Leu	Gln
	65					70					75					80
	Glu	Leu	Arg	Arg	Gln	Phe	Pro	Gly	Ser	His	Arg	Val	Lys	Arg	Leu	Thr
					85					90					95	
50	Gly	Met	Arg	Phe	Glu	Ala	Met	Glu	Arg	Tyr	Asp	Asp	Ala	Ile	Gln	Leu
				100					105					110		
	Tyr	Asp	Arg	Ile	Leu	Gln	Glu	Asp	Pro	Thr	Asn	Thr	Ala	Ala	Arg	Lys
				115				120					125			
	Arg	Lys	Ile	Ala	Ile	Arg	Lys	Ala	Gln	Gly	Lys	Asn	Val	Glu	Ala	Ile
55							135					140				
	Arg	Glu	Leu	Asn	Glu	Tyr	Leu	Glu	Gln	Phe	Val	Gly	Asp	Gln	Glu	Ala
	145					150					155					160
	Trp	His	Glu	Leu	Ala	Glu	Leu	Tyr	Ile	Asn	Glu	His	Asp	Tyr	Ala	Lys
					165					170					175	
60	Ala	Ala	Phe	Cys	Leu	Glu	Glu	Leu	Met	Met	Thr	Asn	Pro	His	Asn	His
				180					185					190		
	Leu	Tyr	Cys	Gln	Gln	Tyr	Ala	Glu	Val	Lys	Tyr	Thr	Gln	Gly	Gly	Leu
				195				200						205		

Glu Thr Leu Glu Leu Ser Arg Lys Phe Leu His Arg His  
 210 215 220

5 <210> 1135  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

10 <400> 1135  
 Arg Glu Leu Glu Pro Ala Glu Phe Glu Thr Met Leu Leu Phe Cys Pro  
 1 5 10 15  
 Gly Cys Gly Asn Gly Leu Ile Val Glu Glu Gly Gln Arg Cys His Arg  
 20 25 30  
 Phe Ala Cys Asn Thr Cys Pro Tyr Val His Asn Ile Thr Arg Lys Val  
 35 40 45  
 15 Thr Asn Arg Lys Tyr Pro Lys Leu Lys Glu Val Asp Asp Val Leu Gly  
 50 55 60  
 Gly Ala Ala Ala Trp Glu Asn Val Asp Ser Thr Ala Glu Ser Cys Pro  
 65 70 75 80  
 20 Lys Cys Glu His Pro Arg Ala Tyr Phe Met Gln Leu Gln Thr Arg Ser  
 85 90 95  
 Ala Asp Glu Pro Met Thr Thr Phe Tyr Lys Cys Cys Asn Ala Gln Cys  
 100 105 110  
 Gly His Arg Trp Arg Asp  
 115  
 25

<210> 1136  
 <211> 126  
 <212> PRT  
 30 <213> Homo sapiens

<400> 1136  
 Gly Ser Trp Ala Ile Leu Ala Leu Ile Pro Pro Ala Val Ser Thr Leu  
 1 5 10 15  
 35 Ser Ile Ala Ala Leu Val Glu Gly Gly His Arg Leu Ile Cys Arg Ala  
 20 25 30  
 Gly Leu Lys Leu His Glu Val Ser Thr Arg Met Phe Ala Phe Gly Thr  
 35 40 45  
 Arg Leu Cys Ser Arg Val Asn Ile Leu Pro Gly Ser Cys Ser Thr Lys  
 50 55 60  
 40 His Ile Ile His Phe Phe Gln Phe Trp Val Leu Pro Ile Cys Tyr Leu  
 65 70 75 80  
 Ala Gly Asp Val Val His Val Gly Ala Arg Val Ala Gly Glu Ala Val  
 85 90 95  
 45 Ala Ala Leu Ser Leu Leu His Asp Gln Pro Val Pro Ala Ala Gly Ala  
 100 105 110  
 Glu Gln Gln His Gly Leu Glu Leu Arg Arg Leu Gln Leu Pro  
 115 120 125

50 <210> 1137  
 <211> 208  
 <212> PRT  
 <213> Homo sapiens

55 <400> 1137  
 Ser Leu Arg Phe Tyr Leu Ser Leu Gly Gln Leu Tyr Leu Ser Met Asn  
 1 5 10 15  
 Ile Asp Asp Lys Leu Glu Gly Leu Phe Leu Lys Cys Gly Gly Ile Asp  
 20 25 30  
 60 Glu Met Gln Ser Ser Arg Thr Met Val Val Met Gly Gly Val Ser Gly  
 35 40 45  
 Gln Ser Thr Val Ser Gly Glu Leu Gln Asp Ser Val Leu Gln Asp Arg  
 50 55 60



Ser Met Pro His Gln Glu Ile Leu Ala Ala Asp Glu Val Leu Gln Glu  
 65 70 75 80  
 Ser Glu Met Arg Gln Gln Asp Met Ile Ser His Asp Glu Leu Met Val  
 85 90 95  
 5 His Glu Glu Thr Val Lys Asn Asp Glu Glu Gln Met Glu Thr His Glu  
 100 105 110  
 Arg Leu Pro Gln Gly Leu Gln Tyr Ala Leu Asn Val Pro Ile Ser Val  
 115 120 125  
 10 Lys Gln Glu Ile Thr Phe Thr Asp Val Ser Glu Gln Leu Met Arg Asp  
 130 135 140  
 Lys Lys Gln Ile Arg Glu Pro Val Asp Leu Gln Lys Lys Lys Arg  
 145 150 155 160  
 Lys Gln Arg Ser Pro Ala Lys Ile Leu Thr Ile Asn Glu Asp Gly Ser  
 165 170 175  
 15 Leu Gly Leu Lys Thr Pro Lys Ser His Val Cys Glu His Cys Asn Ala  
 180 185 190  
 Ala Phe Arg Thr Asn Tyr Pro Tyr Arg Asp Met Ser Ser Tyr Arg  
 195 200 205  
  
 20 <210> 1138  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens  
  
 25 <400> 1138  
 Lys Arg Arg Leu Gln Gly Lys Glu Cys Cys Arg Val Glu Lys Glu Ile  
 1 5 10 15  
 Met Val Glu Phe Leu Pro Phe Ile Gly Phe Arg Asn Pro Gln Tyr His  
 20 25 30  
 30 Leu Asn His Leu Cys His Pro Ile Pro Pro Leu Asn Thr Leu Gly Lys  
 35 40 45  
 Arg Pro Ser Arg Gln Xaa Thr Cys Leu Asn Phe Gln Ala Xaa Asp Ser  
 50 55 60  
 Ser Leu Tyr Pro Arg Ala Gly Ala Glu Ser Arg Gly His Arg Xaa Gln  
 65 70 75 80  
 35 Ala Ala Ala Ala Pro Thr Phe Xaa Gly Ala Leu Arg Gly Gly Glu Gly  
 85 90 95  
 Gly Arg Gly Glu Asn Phe Cys Cys Gly Ser Phe Gly Asn Ser Ser His  
 100 105 110  
 40 Pro Xaa Ala Phe Leu Leu Phe Leu Pro  
 115 120  
  
 <210> 1139  
 <211> 178  
 45 <212> PRT  
 <213> Homo sapiens  
  
 <400> 1139  
 Arg Ser Lys Gly Cys Asp Cys Cys Gly Glu Lys Ser Gln Pro Gln Glu  
 1 5 10 15  
 Lys Ser Leu Ile Gly Leu Lys Asn Thr Glu Asn Asn Asp Val Glu Ile  
 20 25 30  
 Ser Glu Thr Lys Lys Ala Asp Val Gln Ala Pro Val Ser Pro Ser Glu  
 35 40 45  
 55 Thr Ser Gln Ala Asn Pro Tyr Ser Glu Gly Gln Phe Leu Asp Glu His  
 50 55 60  
 His Ser Val Asn Phe His Leu Gly Leu Lys Glu Asp Asn Asp Thr Ile  
 65 70 75 80  
 Asn Asp Ser Leu Ile Val Ser Glu Thr Lys Ser Lys Glu Asn Thr Met  
 85 90 95  
 60 Gln Glu Ser Leu Pro Ser Gly Ile Val Asn Phe Arg Glu Glu Ile Cys  
 100 105 110  
 Asp Met Asp Ser Ser Glu Ala Met Ser Leu Glu Ser Gln Glu Ser Pro

115 120 125  
 Asn Glu Asn Phe Lys Thr Val Gly Pro Cys Leu Gly Asp Ser Lys Asn  
 130 135 140  
 Val Ser Gln Glu Ser Leu Glu Thr Lys Glu Glu Lys Pro Glu Glu Thr  
 145 150 155 160  
 5 Pro Lys Met Glu Leu Ser Leu Glu Asn Val Leu Leu Lys Glu Met His  
 165 170 175  
 Val Lys  
  
 10 <210> 1140  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens  
  
 15 <400> 1140  
 Phe Leu Asn Leu Arg Gly Asp Ile Gly Ser His Trp Leu Gln Phe Lys  
 1 5 10 15  
 Leu Leu Thr Glu Ile Ser Ser Ala Val Phe Ile Leu Thr Asp Asn Ile  
 20 20 25 30  
 Ser Lys Lys Glu Tyr Lys Leu Leu Tyr Ser Met Lys Glu Ser Thr Thr  
 35 40 45  
 Lys Tyr Tyr Phe Ile Leu Ser Pro Tyr Arg Gly Lys Arg Asn Thr Asn  
 50 55 60  
 25 Leu Arg Phe Leu Asn Lys Leu Ile Pro Val Leu Lys Ile Asp His Ser  
 65 70 75 80  
 His Val Leu Val Lys Val Ser Ser Thr Asp Ser Asp Ser Phe Val Lys  
 85 90 95  
 Arg Ile Arg Ala Ile Val Gly Asn Val Leu Arg Ala Pro Cys Arg Arg  
 100 105 110  
 30 Val Ser Val Glu Asp Met Ala His Ala Ala Arg Lys Leu Gly Leu Lys  
 115 120 125  
 Val Asp Glu Asp Cys Glu Glu Cys Gln Lys Ala Lys Asp Arg Met Glu  
 130 135 140  
 35 Arg Ile Thr Arg Lys Ile Lys Asp Ser Asp Ala Tyr Xaa Lys Asp Gln  
 145 150 155 160  
 Leu Arg Leu Xaa Gly Asp Pro Trp Arg Lys Ala Ala Gln Val Glu Lys  
 165 170 175  
 Glu Phe Cys Asn Phe Ser Gly Pro Trp Pro Pro  
 180 185  
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 <210> 1141  
 <211> 145  
 <212> PRT  
 <213> Homo sapiens  
  
 45 <400> 1141  
 Lys Trp Xaa Val Pro Ile Arg His Glu Lys Pro Ser Lys Xaa Gln Arg  
 1 5 10 15  
 50 Phe Xaa Ser Xaa Xaa Gln Gln Val Leu Lys Xaa Glu Ser Asp Xaa Thr  
 20 25 30  
 Asp Gln Phe Lys Arg Cys Tyr Gln Glu Tyr Xaa Ser Pro Gln Gly Arg  
 35 40 45  
 Xaa Thr Ser Ser Ser Leu Xaa Cys Xaa Ser Ser Cys Gln Gly Ser Cys  
 50 55 60  
 55 Gly Val Gly Pro Leu Xaa Ser Cys Xaa Leu Ser Leu Ala Pro Gly Val  
 65 70 75 80  
 Gly Ala Ala Ser Leu Val Thr Ala Gly Pro Gly Gly Gln Val Val Pro  
 85 90 95  
 60 Gly Xaa Arg Trp Gly Ser Cys Pro Glu Glu Ala Glu Val Gly Leu Ala  
 100 105 110  
 Pro Ala Gln Pro Lys Gly Leu Gln Trp Thr Ser Ile Gln Asp Val Ser  
 115 120 125

Ala Arg Gly Val Gln Gly Thr Pro Met Ala Pro Tyr Leu Leu Thr Asp  
 130 135 140  
 Leu  
 145

5

<210> 1142  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

10

<400> 1142  
 Xaa His Phe Xaa Phe Leu Thr Leu Val Xaa Xaa Asn Xaa Xaa Thr Phe  
 1 5 10 15  
 Xaa Phe Cys Ser Ala Ser His Val Glu Trp Ala Pro Xaa Ile Phe Lys  
 20 25 30  
 Xaa Pro Lys His Lys Pro His Met Gly Ala Pro Phe Lys Lys Xaa Val  
 35 40 45  
 Gly His Xaa Xaa Thr Phe Leu Asn Leu Xaa Thr Gly Val Phe Leu Asp  
 50 55 60  
 Xaa Leu Lys  
 65

15

<210> 1143  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

25

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 Glu Asn Glu Val Lys Leu Leu Val Glu Arg Met Met Ala Leu Gln Thr  
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 Asp Ile Val Asp Leu Gln Arg Ser Pro Met Gly Arg Lys Gln Gly Gly  
 20 25 30  
 Thr Leu Asp Asp Leu Glu Glu Gln Ala Arg Glu Leu Tyr Arg Arg Leu  
 35 40 45  
 Arg Glu Lys Pro Arg Asp Gln Arg Thr Glu Gly Asp Ser Gln Glu Met  
 50 55 60  
 Val Arg Leu Leu Leu Gln Ala Ile Gln Ser Phe Glu Lys Lys Val Arg  
 65 70 75 80  
 Val Ile Tyr Thr Gln Leu Ser Lys Thr Val Val Cys Lys Gln Lys Ala  
 85 90 95  
 Leu Glu Leu Leu Pro Lys Val Glu Glu Val Val Ser Leu Met Asn Glu  
 100 105 110  
 Asp Glu Lys Thr Val Val Arg Leu Gln Glu Lys Arg Gln Lys Glu Leu  
 115 120 125  
 Trp Asn Leu Leu Lys Ile Ala Cys Thr Arg Ser Val Val Leu Ser Val  
 130 135 140  
 Glu Thr Pro Ile Ala  
 145

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<210> 1144  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

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 His Pro Arg Pro Ala Arg Cys Pro Leu Val Thr Pro Thr Pro Thr Glu  
 1 5 10 15  
 Leu Glu Arg Leu Arg Leu Arg Ser Arg Pro Val Tyr Gly Val Cys Pro  
 20 25 30  
 Val Tyr Glu Asp Val Pro Ala Arg Asn Glu Arg Ile Tyr Val Tyr Glu  
 35 40 45  
 Asn Lys Lys Glu Ala Phe Ala Ser Cys Gln Asp Asp Gln Arg Val Arg  
 50 55 60

60

445

Phe Lys Ala Phe Ser Pro Xaa Lys Thr Leu Lys Asn Leu Xaa Lys Glu  
 65 70 75 80  
 Phe Val Asn Ile Ser Xaa Ser Asn Lys Thr Ser Leu His Xaa Phe Cys  
 85 90 95  
 5 Glu Asn Asn Phe Thr Leu Phe Asn Asp Lys Leu Lys Xaa Val Gly Leu  
 100 105 110  
 Xaa Asn Lys Thr Ala Pro Xaa Ala Ser Asp Ser Ser Lys Ile  
 115 120 125  
  
 10 <210> 1145  
 <211> 152  
 <212> PRT  
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 15 <400> 1145  
 Arg Pro Ala Ala Pro Ala Ser Gly Glu Met Thr Met Asp Ala Leu Leu  
 1 5 10 15  
 Ala Arg Leu Lys Leu Leu Asn Pro Asp Asp Leu Arg Glu Glu Ile Val  
 20 25 30  
 Lys Ala Gly Leu Lys Cys Gly Pro Ile Thr Ser Thr Thr Arg Phe Ile  
 35 40 45  
 Phe Glu Lys Lys Leu Ala Gln Ala Leu Leu Glu Gln Gly Gly Arg Leu  
 50 55 60  
 Ser Ser Phe Tyr His His Glu Ala Gly Val Thr Ala Leu Ser Gln Asp  
 65 70 75 80  
 25 Pro Gln Arg Ile Leu Lys Pro Ala Glu Gly Asn Pro Thr Asp Gln Ala  
 85 90 95  
 Gly Phe Ser Glu Asp Arg Asp Phe Gly Tyr Ser Val Gly Leu Asn Pro  
 100 105 110  
 30 Pro Glu Glu Glu Ala Val Thr Ser Lys Thr Cys Ser Val Pro Pro Ser  
 115 120 125  
 Asp Thr Asp Thr Tyr Arg Ala Gly Ala Thr Ala Ser Lys Glu Pro Pro  
 130 135 140  
 Cys Leu Trp Gly Val Ser Ser Val  
 145 150  
  
 35 <210> 1146  
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 <212> PRT  
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 40 <400> 1146  
 Pro Arg Gly Ala Phe Met Gln Leu Ile Thr Val Ala Glu Gly Phe Ser  
 1 5 10 15  
 45 Gln Asp Leu Gly Cys Asp His Ile Leu Val Ile Asp Ser Gly Gly Leu  
 20 25 30  
 Ile Gly Gly Ala Leu Thr Ser Ala Gly Asp Arg Phe Glu Leu Glu Ala  
 35 40 45  
 Ser Leu Ala Thr Leu Leu Met Gly Leu Ser Asn Val Thr Val Ile Ser  
 50 55 60  
 Leu Ala Glu Thr Lys Asp Ile Pro Ala Ala Ile Leu His Ala Phe Leu  
 65 70 75 80  
 Arg Leu Glu Lys Thr Gly His Met Pro Asn Tyr Gln Phe Val Tyr Gln  
 85 90 95  
 55 Asn Leu His Asp Val Ser Val Pro Gly Pro Arg Pro Arg Asp Lys Arg  
 100 105 110  
 Gln Leu Leu Asp Pro Pro Gly Asp Leu Ser Arg Ala Ala Ala Gln Met  
 115 120 125  
 Glu Lys Gln Gly Asp Gly Phe Arg Ala Leu Ala Gly Leu Ala Phe Cys  
 130 135 140  
 60 Asp Pro Glu Asn Asn Thr Ser Gly Thr Ser Ser Leu Trp His Gly His  
 145 150 155 160  
 Leu His Gly Arg Ser Glu Leu Trp Pro Thr Val Lys Pro Tyr Leu Asn

165 170 175

5 <210> 1147  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

10 <400> 1147  
 Met Phe Leu Phe Trp Phe Asp Xaa Xaa Phe Leu Met Phe Ser Ser Arg  
 1 5 10 15  
 Ile Ser Ser Ile Gln Ile Trp Phe His Cys Arg Pro Lys Leu Thr Ala  
 20 25 30  
 Ala Met Glu Val Ser Val Pro Gln Ala Gly Cys Ala Arg Cys Val Val  
 35 40 45  
 15 Leu Arg Val Ala Glu Gly Gln Ala Cys Gln Cys Pro Glu Ala Val Ala  
 50 55 60  
 Leu Phe Leu His Leu Gly Cys Ser Pro Ala Gln Val Thr Arg Trp Ile  
 65 70 75 80  
 20 Gln Glu Leu Ser Leu Val Ser Gly Pro Arg Ala Gly Asn Arg Tyr Ile  
 85 90 95  
 Met Lys Val Leu Val Tyr Lys Leu Val Val Gly His Val Pro Arg Phe  
 100 105 110  
 Phe

25 <210> 1148  
 <211> 136  
 <212> PRT  
 <213> Homo sapiens

30 <400> 1148  
 Glu Asp Glu Gln Lys Thr Glu Gly Leu Glu Ser Pro Gln Thr Val Phe  
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 Lys Xaa Xaa Ser Asp Leu Thr Asp Gln Leu Gln Arg Cys Tyr Gln Glu  
 20 25 30  
 35 Tyr Xaa Ser Pro Gln Gly Arg Glu Thr Ser Ser Ser Leu Xaa Cys Xaa  
 35 40 45  
 Ser Ser Cys Gln Gly Ser Cys Gly Val Gly Pro Leu Tyr Ser Cys Ser  
 50 55 60  
 40 Xaa Ser Leu Ala Pro Gly Val Gly Ala Ala Ser Leu Val Thr Ala Gly  
 65 70 75 80  
 Pro Gly Gly Gln Val Val Pro Gly Xaa Arg Trp Gly Ser Cys Pro Xaa  
 85 90 95  
 45 Glu Ala Xaa Val Gly Leu Ala Pro Ala Gln Pro Lys Gly Leu Gln Trp  
 100 105 110  
 Thr Ser Ile Gln Asp Val Ser Ala Arg Gly Val Gln Gly Thr Pro Met  
 115 120 125  
 Xaa Pro Tyr Leu Leu Thr Asp Leu  
 130 135

50 <210> 1149  
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 <212> PRT  
 <213> Homo sapiens

55 <400> 1149  
 Glu Gly Phe Leu Trp Xaa Thr Pro Phe Leu Met Gly Xaa Pro Asn Gly  
 1 5 10 15  
 Gly Val Val Xaa Leu Xaa Pro Xaa Lys Arg Ala Gly Ala Pro Ile Arg  
 20 25 30  
 60 His Glu Lys Thr Ser Lys Arg Gln Arg Val Trp Ser Leu Leu Lys Gln  
 35 40 45  
 Cys Leu Lys Xaa Xaa Val Thr Ser Gln Thr Ser Phe Arg Asp Val Thr

447

[illegible]

	65				70				75					80			
	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met	Asp	His	Ile	Leu	Asn	Leu	
					85					90					95		
5	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser	Ala	Lys	Ile	Ile	Ser	Phe	
				100					105					110			
	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser	Leu	Gln	Ser	Arg	Ile	Glu	
			115					120					125				
	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln	Glu	Leu	Leu	Ser	Glu	Thr	
		130					135					140					
10	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala	Ser	Gln	Cys	Val	Leu	Asp	
	145					150					155					160	
	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Xaa	Tyr	Leu	Phe	Asp	Lys	Lys	
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        <211> 217
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        <213> Homo sapiens
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	1				5					10					15	
	Ser	Ala	Val	Leu	Pro	Pro	Thr	Cys	Ile	Gln	Leu	Leu	Asp	Ser	Ser	Asn
				20					25					30		
25	Trp	Lys	Glu	Arg	Leu	Ala	Cys	Met	Glu	Glu	Phe	Gln	Lys	Ala	Val	Glu
			35					40					45			
	Leu	Met	Asp	Arg	Thr	Glu	Met	Pro	Cys	Gln	Ala	Leu	Val	Arg	Met	Leu
		50					55					60				
	Ala	Lys	Lys	Pro	Gly	Trp	Lys	Glu	Thr	Asn	Phe	Gln	Val	Met	Gln	Met
30	65					70					75					80
	Lys	Leu	His	Ile	Val	Ala	Leu	Ile	Ala	Gln	Lys	Gly	Asn	Phe	Ser	Lys
					85					90					95	
	Thr	Ser	Ala	Gln	Val	Val	Leu	Asp	Gly	Leu	Val	Asp	Lys	Ile	Gly	Asp
				100					105					110		
35	Val	Lys	Cys	Gly	Asn	Asn	Ala	Lys	Glu	Ala	Met	Thr	Ala	Ile	Ala	Glu
			115					120					125			
	Ala	Cys	Met	Leu	Pro	Trp	Thr	Ala	Glu	Gln	Val	Val	Ser	Met	Ala	Phe
		130					135					140				
	Ser	Gln	Lys	Asn	Pro	Lys	Asn	Gln	Ser	Glu	Thr	Leu	Asn	Trp	Leu	Ser
40	145					150					155					160
	Asn	Ala	Ile	Lys	Glu	Phe	Gly	Phe	Ser	Gly	Leu	Asn	Val	Lys	Ala	Phe
					165					170					175	
	Ile	Asn	Asn	Val	Lys	Thr	Ala	Leu	Ala	Ala	Thr	Asn	Pro	Ala	Val	Arg
				180					185					190		
45	Thr	Ala	Ala	Ile	Thr	Leu	Leu	Gly	Val	Met	Tyr	Leu	Tyr	Val	Xaa	Pro
			195					200					205			
	Ser	Phe	Ala	Lys	Trp	Ser	Phe	Xaa	Gly							
		210					215									

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50          <210> 1154
           <211> 261
           <212> PRT
           <213> Homo sapiens
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Gly Leu Lys Val Leu Lys Gly Ile Leu Xaa Pro His Gly Asp Glu Ser  
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Ile Glu Gln Leu Lys Thr Gln Met Ser Ser Cys Val Ala Lys Trp Leu  
                20              25              30  
60 Gln Asp Glu Met Phe His Ser Asp Phe Gln His His Asn Lys Ala Leu  
            35              40              45  
Ala Val Met Val Asp His Leu Glu Ser Glu Lys Glu Gly Val Ile Gly  
   50              55              60

Cys Leu Asp Leu Ile Leu Lys Trp Leu Thr Leu Arg Phe Phe Asp Thr  
 65 70 75 80  
 Asn Thr Ser Val Leu Met Lys Ala Leu Glu Tyr Leu Lys Leu Leu Phe  
 85 90 95  
 5 Thr Leu Leu Ser Glu Glu Glu Tyr His Leu Thr Glu Asn Glu Ala Ser  
 100 105 110  
 Ser Phe Ile Pro Tyr Leu Val Val Lys Val Gly Glu Pro Lys Asp Val  
 115 120 125  
 Ile Arg Lys Asp Val Arg Ala Ile Leu Asn Arg Met Cys Leu Val Tyr  
 130 135 140  
 10 Pro Ala Ser Lys Met Phe Pro Phe Ile Met Glu Gly Thr Lys Ser Lys  
 145 150 155 160  
 Asn Ser Lys Gln Arg Ala Glu Cys Leu Glu Glu Leu Gly Cys Leu Val  
 165 170 175  
 15 Glu Ser Tyr Gly Met Asn Val Cys Gln Pro Thr Pro Gly Lys Ala Leu  
 180 185 190  
 Lys Glu Ile Ala Val His Ile Gly Asp Arg Asp Asn Ala Val Arg Asn  
 195 200 205  
 Ala Ala Leu Asn Thr Ile Val Thr Val Tyr Asn Val His Gly Asp Gln  
 210 215 220  
 20 Val Phe Lys Leu Ile Gly Asn Leu Ser Glu Lys Asp Met Ser Met Leu  
 225 230 235 240  
 Glu Ser Thr Ser Arg Ala Ala Ala Gly Pro Ser Ile Phe His Pro Gly  
 245 250 255  
 25 Gly Tyr Gln Val Ser  
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<210> 1155  
 <211> 174  
 30 <212> PRT  
 <213> Homo sapiens

<400> 1155  
 Thr Glu Pro Cys Arg Thr Ala Glu Asn Cys Thr Ala Thr Met Ser Glu  
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 35 Asn Asn Lys Asn Ser Leu Glu Ser Ser Leu Arg Gln Leu Lys Cys His  
 20 25 30  
 Phe Thr Trp Asn Leu Met Glu Gly Glu Asn Ser Leu Asp Asp Phe Glu  
 35 40 45  
 40 Asp Lys Val Phe Tyr Arg Thr Glu Phe Gln Asn Arg Glu Phe Lys Ala  
 50 55 60  
 Thr Met Cys Asn Leu Leu Ala Tyr Leu Lys His Leu Lys Gly Gln Asn  
 65 70 75 80  
 Glu Ala Ala Leu Glu Cys Leu Arg Lys Ala Glu Glu Leu Ile Gln Gln  
 85 90 95  
 45 Glu His Ala Asp Gln Ala Glu Ile Arg Ser Leu Val Thr Trp Gly Asn  
 100 105 110  
 Tyr Ala Trp Val Tyr Tyr His Met Gly Arg Leu Ser Asp Val Gln Ile  
 115 120 125  
 50 Tyr Val Asp Lys Val Lys His Val Cys Glu Lys Phe Ser Ser Pro Tyr  
 130 135 140  
 Arg Ile Glu Ser Pro Glu Leu Asp Cys Glu Glu Gly Trp Thr Arg Leu  
 145 150 155 160  
 Lys Cys Gly Gly Asn Gln Asn Glu Arg Ala Lys Val Cys Phe  
 165 170  
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<210> 1156  
 <211> 211  
 <212> PRT  
 60 <213> Homo sapiens

<400> 1156  
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	1				5					10				15		
	Ala	Ala	Leu	Thr	Met	Lys	Gln	Ser	Ser	Asn	Val	Pro	Ala	Phe	Leu	Ser
				20					25					30		
5	Lys	Leu	Trp	Thr	Leu	Val	Glu	Glu	Thr	His	Thr	Asn	Glu	Phe	Ile	Thr
			35					40					45			
	Trp	Ser	Gln	Asn	Gly	Gln	Ser	Phe	Leu	Val	Leu	Asp	Glu	Gln	Arg	Phe
		50					55					60				
	Ala	Lys	Glu	Ile	Leu	Pro	Lys	Tyr	Phe	Lys	His	Asn	Asn	Met	Ala	Ser
	65					70					75					80
10	Phe	Val	Arg	Gln	Leu	Asn	Met	Tyr	Gly	Phe	Arg	Lys	Val	Val	His	Ile
				85						90					95	
	Asp	Ser	Gly	Ile	Val	Lys	Gln	Glu	Arg	Asp	Gly	Pro	Val	Glu	Phe	Gln
			100						105					110		
	His	Pro	Tyr	Phe	Lys	Gln	Gly	Gln	Asp	Asp	Leu	Leu	Glu	Asn	Ile	Lys
			115					120					125			
	Arg	Lys	Val	Ser	Ser	Ser	Lys	Pro	Glu	Glu	Asn	Lys	Ile	Arg	Gln	Glu
			130				135					140				
	Asp	Leu	Thr	Lys	Ile	Ile	Ser	Ser	Ala	Gln	Lys	Val	Gln	Ile	Lys	Gln
	145					150					155					160
20	Glu	Thr	Ile	Glu	Ser	Arg	Leu	Ser	Glu	Leu	Lys	Ser	Glu	Asn	Glu	Ser
					165					170					175	
	Leu	Trp	Xaa	Glu	Xaa	Ser	Glu	Phe	Gln	Gln	Lys	His	Xaa	Gln	Gln	Gln
				180					185					190		
	Gln	Val	Ile	Xaa	Lys	Asn	Val	Ser	Leu	Leu	Val	His	Trp	Phe	Lys	Ile
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25	Thr	Gln	Leu													
			210													
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30				<211>	231											
				<212>	PRT											
				<213>	Homo sapiens											
				<400>	1157											
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	1				5					10					15	
	His	Ala	Ile	Asp	Ser	Phe	Arg	Glu	Gly	Glu	Thr	Met	Ile	Leu	Thr	Leu
				20					25					30		
	Lys	Asp	Lys	Gly	Val	Leu	Gln	Glu	Glu	Glu	Asp	Val	Leu	Val	Asn	Val
			35					40					45			
40	Asn	Leu	Val	Asp	Lys	Glu	Arg	Ala	Glu	Lys	Asn	Val	Glu	Leu	Arg	Lys
		50					55					60				
	Lys	Lys	Pro	Asp	Tyr	Leu	Pro	Tyr	Ala	Glu	Asp	Glu	Ser	Val	Asp	Asp
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225

230

5 <210> 1158  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

10 <400> 1158  
 Ser Leu Arg Phe Tyr Leu Ser Leu Gly Gln Leu Tyr Leu Ser Met Asn  
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 Ile Asp Asp Lys Leu Glu Gly Leu Phe Leu Lys Cys Gly Gly Ile Xaa  
 20 25 30  
 Xaa Met Gln Ser Ser Arg Thr Met Val Xaa Met Gly Gly Val Ser Xaa  
 35 40 45  
 15 Xaa Leu Leu Cys Xaa Gly Lys Leu Pro Gly Phe Xaa Thr Xaa Lys Ile  
 50 55 60  
 Glu Xaa Xaa Pro Xaa Xaa Glu Asp Pro Cys Cys Xaa  
 65 70 75

20 <210> 1159  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

25 <400> 1159  
 Thr Ser Arg Xaa Met Xaa Pro Cys Pro Ser Ile Ala Phe Asp Pro Gly  
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 Met Asn Phe Xaa Leu Arg Thr Thr Pro Asp Lys Ser His Phe Gly Leu  
 20 25 30  
 30 Ile Val Gly Asp Ser Gln His Ser Phe Pro Phe Ser Gly Asp Glu Thr  
 35 40 45  
 Asn His Val Xaa Ala Thr Ser Thr Gln Asp Phe Xaa Asp Gln Val Thr  
 50 55 60  
 Ser Gln Lys Lys Ala Glu Ala Gln Pro Val His Gln Ala Tyr Gln Met  
 65 70 75 80  
 35 Ser Ser Phe Glu Gln Pro Phe Arg Ala Pro Tyr His Gly Ser Arg Ala  
 85 90 95  
 Gly Ile Ala Thr Gln Phe Ser Thr Ala Asn Gly Gln Val Asn Leu Arg  
 100 105 110  
 40 Gly Pro Gly Thr Ser Ala Glu Phe Ser Glu Phe Pro Leu Val Asn Val  
 115 120 125  
 Asn Asp Asn Arg Ala Gly Met Thr Ser Ser Pro Asp Ala Thr Thr Gly  
 130 135 140  
 Gln Thr Phe Gly  
 45 145

50 <210> 1160  
 <211> 217  
 <212> PRT  
 <213> Homo sapiens

<400> 1160  
 Ser Leu Pro Ala Ser Phe Ser Pro Leu Val Pro Ser Thr Ser Cys Glu  
 1 5 10 15  
 55 Gly Ile His Leu Cys Ala Glu Leu Leu Gly Thr Met Ala Ser Leu Ser  
 20 25 30  
 Leu Ala Pro Val Asn Ile Phe Lys Ala Gly Ala Asp Glu Glu Arg Ala  
 35 40 45  
 Glu Thr Ala Arg Leu Thr Ser Phe Ile Gly Ala Ile Ala Ile Gly Asp  
 50 55 60  
 60 Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met Asp Lys Ile Leu Leu  
 65 70 75 80  
 Ser Ser Gly Arg Asp Ala Ser Leu Met Val Thr Asn Asp Gly Ala Thr

85 90 95  
 Ile Leu Lys Asn Ile Gly Val Asp Asn Pro Ala Ala Lys Val Leu Val  
 100 105 110  
 5 Asp Met Ser Arg Val Gln Asp Asp Glu Val Gly Asp Gly Thr Thr Ser  
 115 120 125  
 Val Thr Val Leu Ala Ala Glu Leu Leu Arg Glu Ala Glu Ser Leu Ile  
 130 135 140  
 Ala Lys Lys Ile His Pro Gln Thr Ile Ile Ala Gly Trp Arg Glu Ala  
 145 150 155 160  
 10 Thr Lys Ala Ala Arg Xaa Ala Leu Leu Ser Ser Ala Val Asp His Gly  
 165 170 175  
 Ser His Glu Xaa Xaa Phe Arg Xaa Glu Leu Met Asn Ile Xaa Gly Pro  
 180 185 190  
 15 His Tyr Pro Gln Asn Phe Leu Leu Xaa Thr Lys Thr Thr Leu Gln Lys  
 195 200 205  
 Xaa Ala Val Xaa Xaa Val Leu Lys Leu  
 210 215

20 <210> 1161  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 1161  
 25 Pro Asp Gln Leu Asp Pro Xaa Val Ala Arg Lys Leu Leu Xaa Lys Lys  
 1 5 10 15  
 Asn Pro Ser Cys Phe Pro Arg Arg Arg Arg Ser Arg Leu Met Thr Leu  
 20 25 30  
 30 Thr Glu Val Ser Xaa Ser Met Lys Ala Phe Ile Ser Lys Val Ser Thr  
 35 40 45  
 Xaa Lys Gly Ala Glu Leu Pro Arg Glu Pro Phe Glu Ala Pro Ile Thr  
 50 55 60  
 Phe Asp Ala Asp Ser Phe Leu Asn Tyr Phe Asp Lys Ile Leu Gly Pro  
 65 70 75 80  
 35 Arg Pro Asn Glu Ser Asp Ser Asp Asp Leu Asp Asp Glu Asp Phe Glu  
 85 90 95  
 Cys Leu Asp Ser Asp Asp Asp Leu Asp Phe Glu Thr His Glu Pro Gly  
 100 105 110  
 40 Glu Glu Ala Ser Leu Lys Gly Thr Leu Asp Asn Leu Lys Ser Tyr Met  
 115 120 125  
 Ala Gln Met Asp Gln Glu Leu Ala His Thr Cys Ile Ser Lys Ser Phe  
 130 135 140  
 Thr Thr Arg Asn Gln Val Glu Pro Val Ser Gln Thr Thr Asp Asn Asn  
 145 150 155 160  
 45 Ser Asp Glu Glu Asp Xaa Gly Thr Gly Glu Ser Val Met Ala Pro Val  
 165 170 175  
 Asp Val Asp Leu Asn Leu Val Ser Asn Ile Leu Glu Ser Tyr Ser Ser  
 180 185 190  
 Gln Ala Gly Leu Ala Gly Pro Ala Ser Asn Leu Leu Gln Ser Met Gly  
 195 200 205  
 50 Val Gln Leu Pro Asp Asn Thr Asp His Arg Pro Thr Ser Lys Pro Thr  
 210 215 220  
 Lys Asn  
 225

55 <210> 1162  
 <211> 237  
 <212> PRT  
 <213> Homo sapiens

60 <400> 1162  
 Glu Val Thr Arg Ser Leu Leu Gln Arg Trp Gly Ala Ser Phe Arg Arg  
 1 5 10 15

Gly Ala Asp Phe Asp Ser Trp Gly Gln Leu Val Glu Ala Ile Asp Glu  
                           20                          25                          30  
 Tyr Gln Ile Leu Ala Arg His Leu Gln Lys Glu Ala Gln Ala Gln His  
                           35                          40                          45  
 5 Asn Asn Ser Glu Phe Thr Glu Glu Gln Lys Lys Thr Ile Gly Lys Ile  
       50                          55                          60  
 Ala Thr Cys Leu Glu Leu Arg Ser Ala Ala Leu Gln Ser Thr Gln Ser  
   65                          70                          75                          80  
 10 Gln Glu Glu Phe Lys Leu Glu Asp Leu Lys Lys Leu Glu Pro Ile Leu  
                           85                          90                          95  
 Lys Asn Ile Leu Thr Tyr Asn Lys Glu Phe Pro Phe Asp Val Gln Pro  
                           100                          105                          110  
 Val Pro Leu Arg Arg Ile Leu Ala Pro Gly Glu Glu Glu Asn Leu Glu  
                           115                          120                          125  
 15 Phe Glu Glu Asp Glu Glu Glu Gly Gly Ala Gly Ala Gly Ser Pro Asp  
       130                          135                          140  
 Ser Phe Pro Ala Arg Val Pro Gly Thr Leu Leu Pro Arg Leu Pro Ser  
   145                          150                          155                          160  
 20 Glu Pro Gly Met Thr Leu Leu Thr Ile Arg Ile Glu Lys Ile Gly Leu  
                           165                          170                          175  
 Lys Asp Ala Gly Gln Cys Ile Asp Pro Tyr Ile Thr Val Ser Val Lys  
       180                          185                          190  
 Asp Leu Asn Gly Ile Asn Leu Thr Pro Val Pro Arg Xaa Xaa Xaa Gly  
       195                          200                          205  
 25 Phe Lys Lys Lys Lys Ile His Met Phe Ile Leu Met Xaa Gly His Trp  
       210                          215                          220  
 Ser Phe Gln Lys Xaa Cys Trp Xaa Lys Leu Thr Gln Lys  
   225                          230                          235  
  
 30           <210> 1163  
               <211> 189  
               <212> PRT  
               <213> Homo sapiens  
  
 35           <400> 1163  
 Gly Ser Arg Phe Ser Ser Thr Leu Thr Gly Trp Leu Gly Gln Leu Arg  
   1                          5                          10                          15  
 Arg Gly Ser Gln Leu Thr Met Gly Asp Pro Ser Lys Gln Asp Ile Leu  
                           20                          25                          30  
 40 Thr Ile Phe Lys Arg Leu Arg Ser Val Pro Thr Asn Lys Val Cys Phe  
       35                          40                          45  
 Asp Cys Gly Ala Lys Asn Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val  
   50                          55                          60  
 Phe Leu Cys Ile Asp Cys Ser Gly Ser His Arg Ser Leu Gly Val His  
   65                          70                          75                          80  
 45 Leu Ser Phe Ile Arg Ser Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe  
                           85                          90                          95  
 Gln Leu Arg Cys Met Gln Val Gly Gly Asn Ala Ser Ala Ser Ser Phe  
                           100                          105                          110  
 50 Phe His Gln His Gly Cys Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn  
       115                          120                          125  
 Ser Arg Ala Ala Gln Leu Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser  
   130                          135                          140  
 Gln Ala Thr Arg Lys His Gly Thr Asp Leu Trp Leu Asp Ser Cys Val  
   145                          150                          155                          160  
 55 Val Pro Pro Leu Ser Pro Pro Pro Lys Glu Glu Asp Phe Phe Ala Ser  
                           165                          170                          175  
 His Val Ser Ser Glu Val Ser Asp Thr Xaa Val Gly Ile  
                           180                          185  
  
 60           <210> 1164  
               <211> 167  
               <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1164

5 Gly Glu Asp Val Arg Gly Val Leu Lys Arg Arg Val Glu Thr Arg Gln  
 1 5 10 15  
 His Thr Xaa Glu Ala Ile Arg Gln Gln Glu Val Glu Gln Leu Asp Phe  
 20 25 30  
 Arg Asp Leu Leu Gly Lys Lys Val Ser Thr Lys Thr Leu Ser Glu Asp  
 35 40 45  
 10 Asp Leu Lys Glu Ile Pro Ala Glu Gln Met Asp Phe Arg Ala Asn Leu  
 50 55 60  
 Gln Arg Gln Val Lys Pro Lys Thr Val Ser Glu Glu Glu Arg Lys Val  
 65 70 75 80  
 His Ser Pro Gln Gln Val Asp Phe Arg Ser Val Leu Ala Lys Lys Gly  
 85 90 95  
 15 Thr Ser Lys Thr Pro Val Pro Glu Lys Val Pro Pro Pro Lys Pro Ala  
 100 105 110  
 Thr Pro Asp Phe Arg Ser Val Leu Gly Gly Lys Lys Lys Leu Pro Ala  
 115 120 125  
 20 Glu Asn Gly Ser Ser Ser Ala Glu Thr Leu Asn Ala Lys Ala Val Glu  
 130 135 140  
 Ser Ser Lys Pro Leu Ser Asn Ala Gln Pro Ser Gly Pro Leu Lys Pro  
 145 150 155 160  
 Val Gly Asn Ala Gln Ala Cys  
 165  
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&lt;210&gt; 1165

&lt;211&gt; 242

&lt;212&gt; PRT

30 <213> Homo sapiens  
 <400> 1165

Tyr Leu Gln Pro Thr Trp Asp Phe Asp Xaa Arg Gly His Ser Met Arg  
 1 5 10 15  
 35 Phe Xaa Asp Asp Ala Lys Asp Phe Ile Ser Ile Leu Leu Lys Lys Asp  
 20 25 30  
 Met Lys Thr Xaa Leu Asp Cys Thr Gln Cys Xaa Gln His Pro Trp Xaa  
 35 40 45  
 Met Lys Asp Xaa Xaa Glu His Gly Gly Gln Glu Thr Phe Gln Gly Xaa  
 50 55 60  
 Met Lys Lys Tyr Met Ala Arg Xaa Lys Trp Gln Lys Thr Gly Asn Ala  
 65 70 75 80  
 Val Arg Ala Ile Gly Arg Leu Ser Ser Met Ala Met Ile Ser Gly Leu  
 85 90 95  
 45 Ser Gly Arg Lys Ser Ser Thr Gly Ser Pro Thr Ser Pro Leu Asn Ala  
 100 105 110  
 Glu Lys Leu Glu Ser Glu Asp Val Ser Gln Ala Phe Leu Glu Ala Val  
 115 120 125  
 Ala Glu Glu Lys Pro His Val Lys Pro Tyr Phe Ser Lys Thr Ile Arg  
 130 135 140  
 50 Asp Leu Glu Val Val Glu Gly Ser Ala Ala Arg Phe Asp Cys Lys Ile  
 145 150 155 160  
 Glu Gly Tyr Pro Asp Pro Glu Val Xaa Trp Phe Lys Asp Asp Gln Ser  
 165 170 175  
 55 Ile Arg Glu Ser Arg His Phe Gln Ile Asp Tyr Asp Glu Asp Gly Asn  
 180 185 190  
 Cys Ser Leu Ile Ile Ser Asp Val Cys Gly Asp Asp Asp Ala Lys Tyr  
 195 200 205  
 Thr Cys Lys Ala Val Asn Ser Leu Gly Glu Ala Thr Cys Thr Ala Glu  
 210 215 220  
 60 Leu Ile Val Glu Thr Met Glu Glu Gly Glu Gly Glu Glu Glu  
 225 230 235 240  
 Glu Glu

5 <210> 1166  
 <211> 221  
 <212> PRT  
 <213> Homo sapiens

<400> 1166  
 10 Ser Gly Lys Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu  
 1 5 10 15  
 Glu Met Arg Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn  
 20 25 30  
 Ser Glu Gln Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala  
 35 40 45  
 15 Ser Lys Leu Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile  
 50 55 60  
 Ala Ala Leu Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln  
 65 70 75 80  
 20 Glu Leu Arg Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr  
 85 90 95  
 Gly Met Arg Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu  
 100 105 110  
 Tyr Asp Arg Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys  
 115 120 125  
 25 Arg Lys Ile Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile  
 130 135 140  
 Arg Glu Leu Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala  
 145 150 155 160  
 30 Trp His Glu Leu Ala Glu Leu Tyr Ile Asn Glu His Asp Tyr Ala Lys  
 165 170 175  
 Ala Ala Phe Cys Leu Glu Glu Leu Met Met Thr Asn Pro His Asn His  
 180 185 190  
 Leu Tyr Cys Gln Gln Tyr Ala Glu Val Lys Tyr Thr Gln Xaa Gly Leu  
 195 200 205  
 35 Glu Asn Leu Asp Phe Gln Glu Ser Ile Leu His Arg His  
 210 215 220

40 <210> 1167  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens

<400> 1167  
 45 His Val Leu Ser Leu Ser Phe Pro Ile Arg Arg Asp Asp Gly Ser Trp  
 1 5 10 15  
 Glu Val Ile Glu Gly Tyr Arg Ala Gln His Ser Gln His Arg Thr Pro  
 20 25 30  
 Cys Lys Gly Gly Ile Arg Tyr Ser Thr Asp Val Ser Val Asp Glu Val  
 35 40 45  
 50 Lys Ala Leu Ala Ser Leu Met Thr Tyr Lys Cys Ala Val Val Asp Val  
 50 55 60  
 Pro Phe Gly Gly Ala Lys Ala Gly Val Lys Ile Asn Pro Lys Asn Tyr  
 65 70 75 80  
 55 Thr Asp Asn Glu Leu Glu Lys Ile Thr Arg Arg Phe Thr Met Glu Leu  
 85 90 95  
 Ala Lys Lys Gly Phe Ile Gly Pro Gly Ile Asp Val Pro Ala Pro Asp  
 100 105 110  
 Met Ser Thr Gly Glu Arg Glu Met Ser Trp Ile Ala Asp Thr Tyr Ala  
 115 120 125  
 60 Ser Thr Ile Gly His Tyr Asp Ile Asn Ala His Ala Cys Val Thr Gly  
 130 135 140  
 Lys Pro Ile Ser Gln Gly Gly Ile His Gly Arg Ile Ser Ala Thr Gly  
 145 150 155 160

Pro Trp Cys Leu Pro Trp Asp  
165

5 <210> 1168  
<211> 112  
<212> PRT  
<213> Homo sapiens

<400> 1168

10 Ile Phe Ile Ser Xaa Xaa Xaa Pro Tyr Phe Xaa Asn Lys Asp Leu Ser  
1 5 10 15  
Xaa Gln Xaa Tyr Xaa Ile Xaa Xaa Gly Asp Xaa Ser Ser Thr Ser Xaa  
20 25 30  
Xaa Leu Xaa Trp Xaa Ser Ala Xaa Asp Leu Thr Xaa Arg Xaa Xaa Xaa  
15 35 40 45  
Pro Ala Glu Xaa Ser His Gln Gly Xaa Gly Ile His Glu Glu Pro Glu  
50 55 60  
Ser Phe Phe Thr Trp Phe Thr Asp His Ser Asp Ala Gly Ala Asp Xaa  
65 70 75 80  
20 Leu Xaa Glu Val Xaa Lys Asp Asp Ile Trp Pro Asn Pro Leu Gln Xaa  
85 90 95  
Tyr Leu Val Pro Asp Met Asp Asp Glu Xaa Xaa Xaa Gly Glu Arg Arg  
100 105 110

25 <210> 1169  
<211> 67  
<212> PRT  
<213> Homo sapiens

<400> 1169

30 Thr His Ile Arg Tyr Asn Lys Ile Gly Val Val Lys Thr Met Ser Cys  
1 5 10 15  
Gly Asn Glu Phe Val Glu Thr Leu Lys Lys Ile Gly Tyr Pro Lys Ala  
20 25 30  
35 Asp Asn Leu Asn Gly Glu Asp Phe Asp Trp Leu Phe Glu Gly Val Glu  
35 40 45  
Xaa Glu Ser Phe Leu Lys Trp Phe Cys Gly Asn Val Asn Glu Gln Asn  
50 55 60  
Val Leu Ser  
40 65

<210> 1170  
<211> 208  
<212> PRT  
45 <213> Homo sapiens

<400> 1170

50 Glu Ser Ser Gly Thr Tyr Ile Val Asn Leu Glu Asn Leu Val Gln Glu  
1 5 10 15  
Leu Ser Gln Ser Asn Met Met Leu Xaa Lys Gln Leu Glu Met Leu Thr  
20 25 30  
Asp Pro Ser Val Ser Gln Gln Ile Asn Pro Arg Asn Thr Ile Asp Thr  
35 40 45  
Lys Asp Tyr Ser Thr His Arg Leu Tyr Gln Val Leu Glu Gly Glu Asn  
55 50 55 60  
Lys Lys Lys Glu Leu Phe Leu Thr His Gly Asn Leu Glu Glu Val Ala  
65 70 75 80  
Glu Lys Leu Lys Gln Asn Ile Ser Leu Val Gln Asp Gln Leu Ala Val  
85 90 95  
60 Ser Ala Gln Glu His Ser Phe Phe Leu Ser Lys Arg Asn Lys Asp Val  
100 105 110  
Asp Met Leu Cys Asp Thr Leu Tyr Gln Gly Gly Asn Gln Leu Leu Leu  
115 120 125

Ser Asp Gln Glu Leu Thr Glu Gln Phe His Lys Val Glu Ser Gln Leu  
 130 135 140  
 Asn Lys Leu Asn His Leu Leu Thr Asp Ile Leu Ala Asp Val Lys Thr  
 145 150 155 160  
 5 Lys Arg Lys Thr Leu Ala Asn Asn Lys Leu His Gln Met Glu Arg Glu  
 165 170 175  
 Phe Tyr Val Tyr Phe Leu Lys Asp Glu Asp Tyr Leu Lys Asp Ile Val  
 180 185 190  
 10 Glu Asn Leu Glu Thr Gln Ser Lys Ile Lys Ala Val Ser Leu Glu Asp  
 195 200 205

&lt;210&gt; 1171

&lt;211&gt; 227

&lt;212&gt; PRT

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 1171

Arg Leu Tyr Asn Ser Ala Val Val Thr Met Pro Val Val Arg Lys Ile  
 1 5 10 15  
 20 Phe Arg Arg Arg Arg Gly Asp Ser Glu Ser Glu Glu Asp Glu Gln Asp  
 20 25 30  
 Ser Glu Glu Val Arg Leu Lys Leu Glu Glu Thr Arg Glu Val Gln Asn  
 35 40 45  
 25 Leu Arg Lys Arg Pro Asn Gly Val Ser Ala Val Ala Leu Leu Val Gly  
 50 55 60  
 Glu Lys Val Gln Glu Glu Thr Thr Leu Val Asp Asp Pro Phe Gln Met  
 65 70 75 80  
 Lys Thr Gly Gly Met Val Asp Met Lys Lys Leu Lys Glu Arg Gly Lys  
 85 90 95  
 30 Asp Lys Ile Ser Glu Glu Glu Asp Leu His Leu Gly Thr Ser Phe Ser  
 100 105 110  
 Ala Glu Thr Asn Arg Arg Asp Glu Asp Ala Asp Met Met Lys Tyr Ile  
 115 120 125  
 35 Glu Thr Glu Leu Lys Lys Arg Lys Gly Ile Val Glu His Glu Glu Gln  
 130 135 140  
 Lys Val Lys Pro Lys Asn Ala Glu Asp Cys Leu Tyr Glu Leu Pro Glu  
 145 150 155 160  
 Asn Ile Arg Val Ser Ser Ala Lys Lys Thr Glu Glu Met Leu Ser Asn  
 165 170 175  
 40 Gln Met Leu Ser Gly Ile Pro Glu Val Asp Leu Gly Ile Asp Ala Lys  
 180 185 190  
 Ile Lys Asn Ile Ile Xaa Thr Glu Asp Ala Lys Ala Arg Leu Leu Ala  
 195 200 205  
 45 Glu Xaa Arg Thr Arg Lys Lys Asp Arg Glu Thr Ser Leu Cys Leu Pro  
 210 215 220  
 Thr Trp Leu  
 225

&lt;210&gt; 1172

50 &lt;211&gt; 209

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1172

Glu Arg Leu Arg Asp Ile Tyr Arg Pro Pro Xaa Lys Phe Gly Ser Lys  
 1 5 10 15  
 Asn Leu Ser Gln Ser Asn Met Met Leu Xaa Lys Gln Leu Glu Met Leu  
 20 25 30  
 Thr Asp Pro Ser Val Ser Xaa Gln Ile Asn Pro Arg Asn Thr Ile Asp  
 35 40 45  
 60 Thr Lys Asp Tyr Ser Thr His Arg Leu Tyr Gln Val Leu Glu Gly Glu  
 50 55 60  
 Asn Lys Lys Lys Glu Leu Phe Leu Thr His Gly Asn Leu Glu Glu Val



[illegible]

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<210> 1173
<211> 178
<212> PRT -
<213> Homo sapiens
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25

[illegible]

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<210> 1174
<211> 166
<212> PRT
<213> Homo sapiens
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55

	<u>&lt;400&gt; 1174</u>															
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	1				5					10					15	
60	Gly	Glu	Asn	Val	Pro	Ala	Phe	Leu	Pro	Trp	Val	Gln	Gly	Leu	His	Ile
				20					25					30		
	Leu	Gln	Gly	Thr	Val	Gly	Cys	Gly	Ser	Lys	Val	Gly	Ile	Thr	Ser	Gly
			35					40					45			

Glu Gln Val Glu Asp Thr Gly Leu Glu Ile Asp Val Leu His Trp His  
 50 55 60  
 Leu Leu Met Ala Leu Ser Val Gly Ser Leu Gln Cys Val Ala Arg Pro  
 65 70 75 80  
 5 Gly Leu His Gln Gly Gly Ala Arg Gln Ala Val Ser Gln Asp Gly Arg  
 85 90 95  
 His Leu Ala Leu Pro Val Ile Asp Ala Phe Thr Gln Gly Ala Ala Val  
 100 105 110  
 His Ala Gln Leu Gln Val Leu Ala Leu Leu Val Gly His Gly Gln Val  
 115 120 125  
 10 Phe Arg His Thr Asp Gly Lys Gly Gln Val Ala Thr His Leu Pro His  
 130 135 140  
 Lys His Cys Gly Pro Tyr Ile Ala Gly Val His Leu His Ile Val Ala  
 145 150 155 160  
 15 Thr Leu Pro Phe His Asp  
 165

<210> 1175  
 <211> 118  
 20 <212> PRT  
 <213> Homo sapiens

<400> 1175  
 Ala Gly Arg Arg His Arg Thr Gly Asn Arg Cys Pro Ser Leu Ala Ser  
 1 5 10 15  
 Ser His Gly Ile Glu Cys Trp Gln Ser Pro Val Cys Ser Gln Ala Arg  
 20 25 30  
 Pro Ala Pro Arg Arg Cys Glu Ala Gly Cys Val Pro Gly Trp Gln Thr  
 35 40 45  
 30 Pro Gly Pro Ala Arg His Arg Cys Val His Ser Gly Gly Ser Arg Ser  
 50 55 60  
 Arg Thr Ala Ala Gly Pro Gly Ser Pro Arg Arg Thr Trp Pro Gly Leu  
 65 70 75 80  
 Gln Ala Tyr Gly Trp Gln Gly Ser Gly Ser Asp Pro Pro Ala Ala Gln  
 85 90 95  
 35 Thr Leu Trp Ser Leu Tyr Ser Gly Arg Ala Ser Pro His Ser Gly His  
 100 105 110  
 Ser Pro Phe Pro Arg Tyr  
 115

<210> 1176  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 1176  
 Lys Lys Cys Cys Leu His Met Leu Val Xaa Glu Thr Leu Ala Arg Arg  
 1 5 10 15  
 Ile Ser Gly His Thr Asn Met Trp Ile Gly Xaa Ser Cys Ser Glu Xaa  
 20 25 30  
 Ser Trp Gly Ser Leu Lys Arg Gly Lys Xaa Trp Phe Ser Xaa Met Leu  
 35 40 45  
 His Met Ala Xaa Phe Lys Arg Leu Lys Thr Phe Phe Cys Pro Leu Cys  
 50 55 60  
 55 Xaa Ala Trp Lys Leu Pro Xaa Gln Cys Val Glu Xaa Leu Gln Arg  
 65 70 75 80  
 Asn Leu

<210> 1177  
 <211> 44  
 <212> PRT  
 <213> Homo sapiens

<400> 1177  
 Thr Gln Thr Tyr Xaa Asn Ser Ser Ile Xaa Phe Thr Ser Leu Ser Ser  
 1 5 10 15  
 5 Ile Cys Gln Lys Xaa Gly Val Ser Pro Asp Phe Phe Xaa Leu Gly Pro  
 20 25 30  
 Pro Xaa Xaa Lys Gln Ile Phe Thr Met Leu Leu Asn  
 35 40

10 <210> 1178  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

15 <400> 1178  
 Leu Ser Glu Lys Phe Phe Lys Ala Ala Ser Asn Cys Gly Ile Val Glu  
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 Ser Ile Leu Asn Trp Val Lys Phe Lys Ala Gln Thr Gln Leu Asn Lys  
 20 20 25 30  
 Lys Cys Ser Ser Val Lys Tyr Ser Lys Ile Lys Gly Ile Pro Lys Leu  
 35 40 45  
 Asp Asp Ala Asn Asp Ala Gly Gly Lys His Ser Leu Glu Cys Thr Leu  
 50 55 60  
 Ile Leu Thr Glu Gly Asp Ser Ala Lys Ser Leu Ala Val Ser Gly Leu  
 25 65 70 75 80  
 Gly Val Ile Gly Arg Asp Arg Tyr Gly Val Phe Pro Leu Arg Gly Lys  
 85 90 95  
 Ile Leu Asn Val Arg Glu Ala Ser His Lys Gln Ile Met Glu Asn Ala  
 100 105 110  
 30 Glu Ile Asn Asn Ile Ile Lys Ile Val Gly Leu Gln Tyr Lys Lys Ser  
 115 120 125  
 Tyr Asp Asp Ala Glu Ser Leu Lys Thr Leu Arg Tyr Gly Lys Ile Met  
 130 135 140  
 Ile Met Thr Asp Gln Asp Gln Asp Gly Ser His Ile Lys Gly Leu Leu  
 35 145 150 155 160  
 Ile Asn Phe Ile His His Asn Trp Pro Ser Leu Leu Lys His Gly Phe  
 165 170 175  
 Leu Glu Glu Phe Ile Thr Pro Ile Xaa Lys Ala Ser Lys Asn Lys Gln  
 180 185 190  
 40 Glu Leu Ser Phe Tyr Ser Ile Pro Glu Phe Ala Asn Gly Lys Asn Ile  
 195 200 205  
 Xaa Lys Thr Arg Lys Pro Gly Lys  
 210 215

45 <210> 1179  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

50 <400> 1179  
 Lys Pro Phe Ser Xaa Pro Val Leu Lys Pro Xaa Xaa Thr Xaa Lys Thr  
 1 5 10 15  
 Lys Xaa Arg Xaa Lys Gly Cys Xaa Leu Xaa Leu Gly Ile Gln Asn Leu  
 20 25 30  
 55 Ala Phe Gln Xaa Lys Pro Xaa Pro Lys Gly Lys Gly Xaa Gly Ala  
 35 40 45  
 Xaa Lys Arg Lys Ala Xaa Gly Phe Glu Asn Glu Gly Asp Tyr Asn Pro  
 50 55 60  
 Gly Arg Xaa Xaa Ser Lys Xaa Xaa Ser Lys Lys Pro Lys Lys Thr Xaa  
 60 65 70 75 80  
 Phe Asp Gln Asp Ser Asp Val Asp Ile Phe Pro Ser Xaa Phe Pro Asn  
 85 90 95  
 Glu Xaa Pro Phe Leu Pro Arg Thr Gly Xaa Val Xaa Xaa Lys

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	<211> 176		
5	<212> PRT		
	<213> Homo sapiens		
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10	Val Gly Arg Tyr Leu Thr Leu Ala Ile Arg Met Pro Glu Asp Leu Ala		
	1 5 10 15		
	Met Ser Tyr Glu Ser Gln Asp Leu Gln Leu Cys Val Asn Gly Cys		
	20 25 30		
	Pro Leu Ser Glu Arg Ile Asp Asp Gly Gln Gly Gln Val Ser Ala Ile		
	35 40 45		
15	Leu Gly His Ser Leu Pro Arg Thr Ser Leu Val Gln Ala Trp Pro Gly		
	50 55 60		
	Tyr Thr Leu Glu Thr Ala Asn Thr Gln Cys His Glu Lys Met Pro Val		
	65 70 75 80		
20	Lys Asp Ile Tyr Phe Gln Ser Cys Val Phe Asp Leu Leu Thr Thr Gly		
	85 90 95		
	Asp Ala Asn Phe Thr Ala Ala Ala His Ser Ala Leu Glu Asp Val Glu		
	100 105 110		
	Ala Leu His Pro Arg Lys Glu Arg Trp His Ile Phe Pro Ser Ser Gly		
	115 120 125		
25	Asn Gly Thr Pro Arg Gly Gly Ser Asp Leu Ser Val Lys Ser Arg Thr		
	130 135 140		
	His Leu Leu Asp Pro Tyr Arg Val Phe Val Gly Val Xaa Phe Xaa Phe		
	145 150 155 160		
30	Gly Phe Leu Phe Phe Xaa Tyr Asn Lys Ile Leu Lys Tyr Ile Leu Xaa		
	165 170 175		
	<210> 1181		
	<211> 87		
	<212> PRT		
35	<213> Homo sapiens		
	<400> 1181		
	Lys Lys Cys Cys Leu His Met Leu Val Xaa Glu Thr Leu Ala Arg Arg		
	1 5 10 15		
40	Ile Ser Gly His Thr Asn Met Trp Ile Gly Tyr Ser Cys Ser Glu Xaa		
	20 25 30		
	Ser Trp Gly Ser Leu Lys Arg Gly Lys His Trp Phe Ser Gln Met Leu		
	35 40 45		
	His Met Ala Xaa Phe Lys Arg Leu Lys Thr Phe Phe Cys Pro Leu Cys		
45	50 55 60		
	Xaa Ala Trp Lys Leu Pro Pro Pro His Ser Val Ser Ser Leu Cys Lys		
	65 70 75 80		
	Glu Thr Phe Arg Cys Gly Ser		
	85		
50	<210> 1182		
	<211> 85		
	<212> PRT		
	<213> Homo sapiens		
55	<400> 1182		
	Phe Arg Ser Xaa Val Lys Ile Cys Phe Xaa Ile Trp Xaa Ala Gln Xaa		
	1 5 10 15		
60	Arg Lys Lys Ser Gly Xaa Tyr Pro Pro Phe Phe Val Gln Lys Tyr Glu		
	20 25 30		
	Ser Glu Val Lys Xaa Ile Glu Glu Phe Xaa Lys Asp Leu Gly Xaa Glu		
	35 40 45		
	Cys Val Ser Leu Ile Xaa Asn Leu Cys Ser Phe Gln Xaa Lys Tyr His		

50 55 60  
 Xaa Xaa Leu Leu Asp Ser Gly Lys Arg Arg Leu Gly Tyr Phe Ala Ile  
 65 70 75 80  
 Ser Phe Ser Trp Lys  
 85  
 5  
 <210> 1183  
 <211> 83  
 <212> PRT  
 10 <213> Homo sapiens  
 <400> 1183  
 Asn Gly Gly Asn Thr Gly Phe His Arg Cys Ser Thr Trp Leu Xaa Leu  
 1 5 10 15  
 15 Lys Asp Ser Lys Leu Phe Phe Val Leu Phe Val Xaa Leu Gly Ser Ser  
 20 25 30  
 Pro Pro Pro Thr Val Cys Arg Val Phe Ala Lys Lys Pro Leu Asp Val  
 35 40 45  
 Val His Arg Tyr Met Asn Thr Tyr Leu Cys Lys Thr Val Ser Val Gln  
 50 55 60  
 20 Cys Val Asn Thr Leu Asn Tyr Tyr Ala Arg Lys Ile Lys Leu His Thr  
 65 70 75 80  
 Leu Leu Trp  
 25  
 <210> 1184  
 <211> 229  
 <212> PRT  
 30 <213> Homo sapiens  
 <400> 1184  
 Glu Ile Thr Glu Leu Lys Val Lys Glu Phe Glu Asn Ile Lys Leu Gln  
 1 5 10 15  
 35 Leu Gln Glu Asn His Glu Asp Glu Val Lys Lys Val Lys Ala Glu Val  
 20 25 30  
 Glu Asp Leu Lys Tyr Xaa Leu Asp Gln Ser Gln Lys Glu Ser Gln Cys  
 35 40 45  
 Leu Lys Ser Glu Leu Gln Ala Gln Lys Glu Ala Asn Ser Arg Ala Pro  
 50 55 60  
 40 Thr Thr Thr Met Arg Asn Leu Val Glu Arg Leu Lys Ser Gln Leu Ala  
 65 70 75 80  
 Leu Lys Glu Lys Gln Gln Lys Ala Leu Ser Arg Ala Leu Leu Glu Leu  
 85 90 95  
 Arg Ala Glu Met Thr Ala Ala Ala Glu Glu Arg Ile Ile Ser Ala Thr  
 100 105 110  
 45 Ser Gln Lys Glu Ala His Leu Asn Val Gln Gln Ile Val Asp Arg His  
 115 120 125  
 Thr Arg Glu Leu Lys Thr Gln Val Glu Asp Leu Asn Glu Asn Leu Leu  
 130 135 140  
 50 Lys Leu Lys Glu Ala Leu Lys Thr Ser Lys Asn Arg Glu Asn Ser Leu  
 145 150 155 160  
 Thr Asp Asn Leu Asn Asp Leu Asn Asn Glu Leu Gln Lys Lys Gln Lys  
 165 170 175  
 Ala Tyr Asn Lys Ile Leu Arg Glu Lys Glu Glu Ile Asp Gln Glu Asn  
 180 185 190  
 55 Asp Glu Leu Lys Arg Gln Ile Lys Arg Leu Thr Xaa Gly Leu Gln Gly  
 195 200 205  
 Lys Pro Leu Thr Asp Asn Lys Pro Arg Ser Asn Trp Arg Asn Ser Xaa  
 210 215 220  
 60 Gly Arg Leu Lys Thr  
 225  
 <210> 1185

<211> 182  
 <212> PRT  
 <213> Homo sapiens

5 <400> 1185  
 Cys Lys Xaa Gly Pro Gln Xaa Gly Xaa Gln Lys Gly Phe Pro Asn Pro  
 1 5 10 15  
 Met Lys Pro Leu Xaa Thr Arg Leu Arg Xaa Leu Asn His Val Xaa Xaa  
 20 25 30  
 10 Gly Val Glu Thr Glu Gln Ala Phe Lys Gly Ser Phe Gln Val Phe Arg  
 35 40 45  
 Xaa Ala Asn His Pro Ala Asp Lys Glu Lys Ala Glu Leu Ile His Gln  
 50 55 60  
 Ile Glu Ala Thr Lys Asp Gln Ser Gly Ala Glu Ser Xaa Ile Pro Asp  
 15 65 70 75 80  
 Ala Asp Gln Leu Lys Glu Lys Ile Lys Asp Leu Glu Xaa Gln Leu Lys  
 85 90 95  
 Met Ser Asp Xaa Glu Lys Gln His Leu Lys Glu Glu Ile Lys Lys Leu  
 100 105 110  
 20 Lys Lys Glu Leu Glu Asn Phe Asp Pro Ser Phe Phe Glu Glu Ile Glu  
 115 120 125  
 Asp Xaa Lys Tyr Asn Tyr Lys Glu Glu Val Lys Lys Asn Ile Xaa Leu  
 130 135 140  
 Glu Glu Lys Val Lys Lys Leu Ser Glu Gln Leu Gly Val Glu Leu Thr  
 25 145 150 155 160  
 Ser Pro Val Ala Ala Xaa Glu Glu Phe Glu Asp Glu Glu Glu Ser Pro  
 165 170 175  
 Val Asn Phe Pro Ile Tyr  
 180

30  
 <210> 1186  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens

35 <400> 1186  
 Arg Glu Leu Glu Pro Ala Glu Phe Glu Thr Met Leu Leu Phe Cys Pro  
 1 5 10 15  
 Gly Cys Gly Asn Gly Leu Ile Val Glu Gly Gln Arg Cys His Arg  
 40 20 25 30  
 Phe Ala Cys Asn Thr Cys Pro Tyr Val His Asn Ile Thr Arg Lys Val  
 35 40 45  
 Thr Asn Arg Lys Tyr Pro Lys Leu Lys Glu Val Asp Asp Val Leu Gly  
 50 55 60  
 45 Gly Ala Ala Ala Trp Glu Asn Val Asp Ser Thr Ala Glu Ser Cys Pro  
 65 70 75 80  
 Lys Cys Glu His Pro Arg Ala Tyr Phe Met Gln Leu Gln Thr Arg Ser  
 85 90 95  
 Ala Asp Glu Pro Met Thr Thr Phe Tyr Lys Cys Cys Asn Ala Gln Cys  
 50 100 105 110  
 Gly His Arg Trp Arg Asp  
 115

55 <210> 1187  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

60 <400> 1187  
 Cys Asn Thr Cys Pro Leu Arg Ala Gln His His Xaa Gln Gly Asn Lys  
 1 5 10 15  
 Ser Xaa Asp Pro Lys Leu Lys Glu Val Asp Xaa Val Leu Gly Gly Ala  
 20 25 30

Ala Ala Trp Glu Asn Val Asp Ser Thr Ala Glu Ser Cys Pro Lys Cys  
 35 40 45  
 Glu His Pro Arg Ala Tyr Phe Met Gln Leu Gln Thr Arg Ser Ala Asp  
 50 55 60  
 5 Glu Pro Met Thr Xaa Phe Tyr Lys Cys Cys Asn Ala Gln Cys Gly His  
 65 70 75 80  
 Arg Trp Arg Asp

10 <210> 1188  
 <211> 190  
 <212> PRT  
 <213> Homo sapiens

15 <400> 1188  
 Leu Gln Asp Ile Lys Glu Lys Ile Ser Lys Gly Glu Tyr Gly Asn Ala  
 1 5 10 15  
 Gly Ile Met Ala Glu Val Glu Glu Leu Arg Lys Arg Val Leu Asp Met  
 20 20 25 30  
 Glu Gly Lys Asp Glu Glu Leu Ile Lys Met Glu Glu Gln Cys Arg Asp  
 35 40 45  
 Leu Asn Lys Arg Leu Glu Arg Glu Thr Leu Gln Ser Lys Asp Phe Lys  
 50 55 60  
 Leu Glu Val Glu Lys Leu Ser Lys Arg Ile Met Ala Leu Glu Lys Leu  
 25 65 70 75 80  
 Glu Asp Ala Phe Asn Lys Ser Lys Gln Glu Cys Tyr Ser Leu Lys Cys  
 85 90 95  
 Asn Leu Glu Lys Glu Arg Met Thr Thr Lys Gln Leu Ser Gln Glu Leu  
 100 105 110  
 30 Glu Ser Leu Lys Val Arg Ile Lys Glu Leu Glu Ala Ile Glu Ser Arg  
 115 120 125  
 Leu Glu Lys Thr Glu Phe Thr Leu Lys Glu Asp Leu Thr Lys Leu Lys  
 130 135 140  
 Thr Leu Thr Val Met Phe Val Asp Glu Arg Lys Thr Met Ser Glu Lys  
 35 145 150 155 160  
 Leu Lys Lys Thr Glu Asp Lys Leu Gln Ala Ala Ser Ser Gln Leu Gln  
 165 170 175  
 Val Glu Gln Asn Lys Val Thr Thr Val Thr Glu Lys Val Asn  
 180 185 190

40 <210> 1189  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

45 <400> 1189  
 Val Arg Val Asp Ser Thr Ala Lys Val Ala Glu Ile Glu His Ala Glu  
 1 5 10 15  
 Lys Glu Lys Met Lys Glu Lys Val Glu Arg Ile Leu Lys His Gly Ile  
 50 20 25 30  
 Asn Cys Phe Ile Asn Arg Gln Leu Ile Tyr Asn Tyr Pro Glu Gln Leu  
 35 40 45  
 Phe Gly Ala Ala Gly Val Met Ala Ile Glu His Ala Asp Phe Ala Gly  
 50 55 60  
 55 Val Glu Arg Leu Ala Leu Val Thr Gly Gly Glu Ile Ala Ser Thr Phe  
 65 70 75 80  
 Asp His Pro Glu Leu Val Lys Leu Gly Ser Cys Lys Leu Ile Glu Glu  
 85 90 95  
 Val Met Ile Gly Glu Asp Lys Leu Ile His Phe Ser Gly Val Ala Leu  
 100 105 110  
 60 Gly Glu Ala Cys Thr Ile Val Leu Arg Gly Ala Thr Gln Gln Ile Leu  
 115 120 125  
 Asp Glu Ala Glu Arg Ser Leu His Asp Ala Leu Cys Val Leu Ala Gln

130 135 140  
 Thr Val Lys Asp Ser Arg Thr Val Tyr Gly Gly Cys Ser Glu Met  
 145 150 155 160  
 Leu Met Ala His Ala Val Thr Gln Leu Ala Asn Arg Thr Pro Gly Lys  
 5 165 170 175  
 Glu Ala Val Ala Met Glu Ser Tyr Ala Lys Ala Leu Arg Met Leu Pro  
 180 185 190  
 Thr Ile Ile Ala Asp Asn Ala Ala Met Thr Val Gln Thr Trp Trp His  
 195 200 205  
 10 Ser Ser Arg Leu Leu Gln  
 210  
 <210> 1190  
 <211> 245  
 15 <212> PRT  
 <213> Homo sapiens  
 <400> 1190  
 Ser Arg Thr Arg Thr Ser Asp Arg Leu Asn Arg Ile Ala Asn Gln Val  
 20 1 5 10 15  
 Ala Ile Gln Arg Lys Lys Gln Phe Val Glu Arg Ala His Ser Tyr Trp  
 20 25 30  
 Leu Leu Lys Arg Leu Ser Arg Asn Gly Ala Pro Leu Leu Arg Arg Leu  
 35 40 45  
 25 Gln Ser Ser Leu Gln Ser Gln Arg Ser Ser Gln Gln Arg Glu Asn Asp  
 50 55 60  
 Glu Glu Met Lys Ala Ala Lys Glu Lys Leu Lys Tyr Trp Gln Arg Leu  
 65 70 75 80  
 Arg His Asp Leu Glu Arg Ala Arg Leu Leu Ile Glu Leu Leu Arg Lys  
 30 85 90 95  
 Arg Glu Lys Leu Lys Arg Glu Gln Val Lys Val Glu Gln Val Ala Met  
 100 105 110  
 Glu Leu Arg Leu Thr Pro Leu Thr Val Leu Leu Arg Ser Val Leu Asp  
 115 120 125  
 35 Gln Leu Gln Asp Lys Asp Pro Ala Arg Ile Phe Ala Gln Pro Val Ser  
 130 135 140  
 Leu Lys Glu Val Pro Asp Tyr Leu Asp His Ile Lys His Pro Met Asp  
 145 150 155 160  
 Phe Ala Thr Met Arg Lys Arg Leu Glu Ala Gln Gly Tyr Lys Asn Leu  
 40 165 170 175  
 His Glu Phe Glu Glu Asp Phe Asp Leu Ile Ile Asp Asn Cys Met Lys  
 180 185 190  
 Tyr Asn Ala Arg Asp Thr Val Phe Tyr Lys Xaa Arg Gly Glu Ala Cys  
 195 200 205  
 45 Ala Ile Lys Glu Val Leu Phe Leu Xaa Gln Ala Pro Xaa Arg Xaa Gly  
 210 215 220  
 Thr Ser Ile Arg Leu Gly Lys Arg Xaa Ser Gly Ile Ala Pro Cys Leu  
 225 230 235 240  
 Lys Pro Gly Leu Leu  
 50 245  
 <210> 1191  
 <211> 190  
 <212> PRT  
 55 <213> Homo sapiens  
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 Pro Glu Ala Glu Thr Thr Gly Cys Gly Ala Ala Gly Arg Asp Thr Cys  
 1 5 10 15  
 60 Ser Pro Phe Asp Pro Ile Met Ser Arg Gly Ser Ile Glu Ile Pro Leu  
 20 25 30  
 Arg Asp Thr Asp Glu Val Ile Glu Leu Asp Phe Asp Gln Leu Pro Glu  
 35 40 45



Gly Asp Glu Val Ile Ser Ile Leu Lys Gln Glu His Thr Gln Leu His  
     50                    55                    60  
 Ile Trp Ile Ala Leu Ala Leu Glu Tyr Tyr Lys Gln Gly Lys Thr Glu  
     65                    70                    75                    80  
 5 Glu Phe Val Lys Leu Leu Glu Ala Ala Arg Ile Asp Gly Asn Leu Asp  
                     85                    90                    95  
 Tyr Arg Asp His Glu Lys Asp Gln Met Thr Cys Leu Asp Thr Leu Ala  
                     100                    105                    110  
 10 Ala Tyr Tyr Val Gln Gln Ala Arg Lys Glu Lys Asn Lys Asp Asn Lys  
                     115                    120                    125  
 Lys Asp Leu Ile Thr Gln Ala Thr Leu Leu Tyr Thr Met Ala Asp Lys  
     130                    135                    140  
 Ile Ile Met Tyr Asp Gln Asn His Leu Leu Gly Arg Ala Cys Phe Cys  
     145                    150                    155                    160  
 15 Leu Leu Glu Gly Asp Lys Met Asp Gln Ala Asp Ala Gln Phe His Phe  
                     165                    170                    175  
 Val Leu Asn Gln Ser Xaa Asn Asn Ile Xaa Ser Pro Ser Trp  
                     180                    185                    190  
  
 20 <210> 1192  
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     <212> PRT  
     <213> Homo sapiens  
  
 25 <400> 1192  
 Ala Glu Ala Gly Ser Ser Gln Gln Met Val Leu Ile Ile His Asn Asn  
     1                    5                    10                    15  
 Phe Ile Gly His Cys Ile Gln Gln Gly Gly Leu Cys Asn Lys Ile Leu  
                     20                    25                    30  
 30 Phe Ile Val Leu Ile Leu Phe Phe Pro Ser Leu Leu Tyr Ile Ile Arg  
                     35                    40                    45  
 Cys Gln Cys Ile Gln Ala Ser His Leu Val Phe Phe Met Val Ser Ile  
     50                    55                    60  
 Val Gln Ile Ala Ile Tyr Thr Cys Cys Phe Gln Gln Phe Tyr Lys Leu  
     65                    70                    75                    80  
 35 Phe Cys Phe Ser Leu Leu Val Val Phe Gln Arg Gln Ser Asn Pro Tyr  
                     85                    90                    95  
 Val Gln Leu Cys Val Phe Leu Phe Gln Asn Thr Asp Asn Phe Ile Ser  
                     100                    105                    110  
 40 Leu Arg  
  
     <210> 1193  
     <211> 40  
 45 <212> PRT  
     <213> Homo sapiens  
  
     <400> 1193  
 Lys Arg Phe Leu Thr Asn Glu Gly Ser Gly Xaa Lys Xaa Leu Glu Met  
     1                    5                    10                    15  
 Asn Xaa Asn Gln Arg Asp Pro Pro Pro Lys Xaa Ser Asp Lys Gly Ser  
                     20                    25                    30  
 Glu His Gly Ser Asp Asp Ser Asp  
                     35                    40  
 55  
     <210> 1194  
     <211> 196  
     <212> PRT  
     <213> Homo sapiens  
  
 60 <400> 1194  
 Glu Arg Xaa Leu Glu Arg Ala Arg Glu Arg Asp Lys Glu Arg Glu Arg  
     1                    5                    10                    15

Gln Arg Asp Trp Glu Asp Lys Asp Lys Gly Arg Asp Asp Arg Arg Glu  
 20 25 30  
 Lys Arg Glu Glu Ile Arg Glu Asp Arg Asn Pro Arg Asp Gly His Asp  
 35 40 45  
 5 Glu Arg Lys Ser Lys Lys Arg Tyr Arg Asn Glu Gly Ser Pro Ser Pro  
 50 55 60  
 Arg Gln Ser Pro Lys Arg Arg Arg Glu His Ser Pro Asp Ser Asp Ala  
 65 70 75 80  
 10 Tyr Asn Ser Gly Asp Asp Lys Asn Glu Lys His Arg Leu Leu Ser Gln  
 85 90 95  
 Val Val Arg Pro Gln Glu Ser Arg Ser Leu Ser Pro Ser His Leu Thr  
 100 105 110  
 Glu Asp Arg Gln Gly Arg Trp Lys Glu Glu Asp Arg Lys Pro Glu Arg  
 115 120 125  
 15 Lys Glu Ser Ser Arg Arg Tyr Glu Glu Gln Glu Leu Lys Glu Lys Val  
 130 135 140  
 Ser Ser Val Asp Lys Gln Arg Glu Gln Thr Glu Ile Leu Glu Ser Ser  
 145 150 155 160  
 20 Arg Met Arg Ala Gln Asp Ile Ile Gly His His Gln Ser Glu Asp Arg  
 165 170 175  
 Glu Thr Ser Asp Arg Ala Leu Met Lys Thr Arg Arg Lys Pro Lys Phe  
 180 185 190  
 Lys Glu Xaa Ile  
 195  
 25  
 <210> 1195  
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 <212> PRT  
 <213> Homo sapiens  
 30  
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 Glu Lys Ser Glu Lys Lys Xaa Ile Lys Xaa Glu Xaa Pro Lys Gly Leu  
 1 5 10 15  
 Gly Xaa Xaa Xaa Xaa Lys Ala Glu Met Xaa Xaa Xaa Lys Ser Xaa Lys  
 20 25 30  
 35 Arg Ser Glu Lys Ile Gly Ile Gln Glu Met Xaa Met Met Lys Glu Asn  
 35 40 45  
 Gln Arg Ser Gly Tyr Arg Asn Glu Gly Xaa Pro Ser Pro Arg Gln Ser  
 50 55 60  
 40 Pro Lys Arg Arg Gly Glu His Xaa Pro Asp Ser Asp Ala Xaa Xaa Xaa  
 65 70 75 80  
 Gly Asp Asp Lys Asn Glu Lys Pro Arg Xaa Leu Ser Gln Val Val Xaa  
 85 90 95  
 Xaa Gln Xaa Phe Xaa Phe Phe Ser Pro Ser Pro Leu Xaa Xaa Asp Arg  
 100 105 110  
 45 Gln Gly Arg Trp Lys Xaa Glu Xaa Cys Xaa Pro Glu Arg Lys Xaa Ser  
 115 120 125  
 Ser Arg Xaa Tyr Glu Glu Gln Glu Leu Lys Xaa Lys Val Phe Phe Val  
 130 135 140  
 50 Asp Lys Gln Arg Glu Gln Thr Glu Ile Leu Glu Ser Ser Arg Met Xaa  
 145 150 155 160  
 Xaa Gln Xaa Ile Ile Xaa Pro Pro Gln Phe Glu Asp Arg Xaa Thr Xaa  
 165 170 175  
 Asp Xaa Ala His Asp Glu Asn Lys Lys Lys Ala Lys Ile Gln Lys Xaa  
 180 185 190  
 55 Xaa Xaa  
 60  
 <210> 1196  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 1196

	Gln	Asp	Leu	Tyr	Ser	Ala	Arg	Asp	Leu	Gln	Gly	Leu	Thr	Val	Glu	His
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5	Ala	Ile	Asp	Ser	Phe	Arg	Glu	Gly	Glu	Thr	Met	Ile	Leu	Thr	Leu	Lys
				20					25					30		
	Asp	Lys	Gly	Val	Leu	Gln	Glu	Glu	Glu	Asp	Val	Leu	Val	Asn	Val	Asn
			35					40					45			
	Leu	Val	Asp	Lys	Glu	Arg	Ala	Glu	Lys	Asn	Val	Glu	Leu	Arg	Lys	Lys
		50					55					60				
10	Lys	Pro	Asp	Tyr	Leu	Pro	Tyr	Ala	Glu	Asp	Glu	Ser	Val	Asp	Asp	Leu
	65				70					75					80	
	Ala	Gln	Gln	Lys	Pro	Arg	Ser	Ile	Leu	Ser	Lys	Tyr	Asp	Glu	Glu	Leu
				85					90						95	
15	Glu	Gly	Glu	Arg	Pro	His	Ser	Phe	Arg	Leu	Glu	Gln	Gly	Gly	Thr	Ala
				100					105					110		
	Asp	Gly	Leu	Arg	Glu	Arg	Glu	Leu	Glu	Glu	Ile	Arg	Ala	Lys	Leu	Arg
		115					120						125			
	Leu	Gln	Ala	Gln	Ser	Leu	Ser	Thr	Val	Gly	Pro	Arg	Leu	Ala	Ser	Glu
		130				135						140				
20	Tyr	Leu	Thr	Pro	Glu	Glu	Met	Val	Thr	Phe	Lys	Lys	Thr	Lys	Arg	Arg
	145					150					155				160	
	Val	Lys	Lys	Ile	Arg	Lys	Lys	Glu	Lys	Glu	Val	Val	Val	Arg	Ala	Asp
				165					170						175	
25	Asp	Leu	Leu	Pro	Leu	Gly	Asp	Gln	Thr	Gln	Asp	Gly	Asp	Phe	Gly	Ser
				180				185						190		
	Xaa	Thr	Ala	Gly	Asp	Xaa	Val	Pro	Gln	Cys	Xaa	Glu	Trp	Arg	Lys	
		195				200						205				
	Lys	Xaa	Glu	Pro	Cys	Ala	Leu	Thr	Pro	Gly	Val	Gly	Arg	His	Pro	Asn
		210				215						220				
30	Xaa	Arg	Thr	Leu	Asp	Ile	Ile	Asp								
	225					230										

<210> 1197  
 <211> 165  
 35 <212> PRT  
 <213> Homo sapiens

<400> 1197

	Ile	Gly	Gly	Trp	Gln	Leu	Pro	Cys	Ser	Cys	Val	Arg	Thr	Lys	Gly	Cys
	1				5					10					15	
40	Trp	Arg	Pro	Gln	Ser	Glu	Gly	Gly	Pro	Gly	Lys	Ala	Pro	Asn	Lys	Ser
				20				25						30		
	Leu	Pro	Ser	Ala	Val	Xaa	Cys	Ile	Glu	Asp	Lys	Met	Ala	Ile	Asp	Asp
			35				40						45			
45	Lys	Tyr	Ser	Arg	Arg	Glu	Glu	Tyr	Arg	Gly	Phe	Thr	Gln	Asp	Phe	Lys
		50				55					60					
	Glu	Lys	Asp	Gly	Tyr	Lys	Pro	Asp	Val	Lys	Ile	Glu	Tyr	Val	Asp	Glu
	65				70					75					80	
	Thr	Gly	Arg	Lys	Leu	Thr	Pro	Lys	Glu	Ala	Phe	Arg	Gln	Leu	Ser	His
				85					90					95		
50	Arg	Phe	His	Gly	Lys	Gly	Ser	Gly	Lys	Met	Lys	Thr	Glu	Arg	Arg	Met
				100				105						110		
	Lys	Lys	Leu	Asp	Glu	Glu	Ala	Leu	Leu	Lys	Lys	Met	Ser	Ser	Ser	Asp
			115				120						125			
55	Thr	Pro	Leu	Gly	Thr	Val	Ala	Leu	Leu	Gln	Glu	Lys	Gln	Lys	Ala	Gln
		130				135						140				
	Lys	Thr	Pro	Tyr	Ile	Val	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Met	Asn	Ala
	145				150						155				160	
60	Asn	Thr	Ile	Thr	Lys											
				165												

<210> 1198  
 <211> 206

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1198

5 Lys Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu Glu Met  
 1 5 10 15  
 Arg Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn Ser Glu  
 20 25 30  
 10 Gln Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala Ser Lys  
 35 40 45  
 Leu Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile Ala Ala  
 50 55 60  
 Leu Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln Glu Leu  
 65 70 75 80  
 15 Arg Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr Gly Met  
 85 90 95  
 Arg Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu Tyr Asp  
 100 105 110  
 Arg Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys Arg Lys  
 115 120 125  
 20 Ile Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile Arg Glu  
 130 135 140  
 Leu Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala Trp His  
 145 150 155 160  
 25 Glu Leu Ala Glu Leu Tyr Ile Asn Glu His Asp Tyr Ala Lys Ala Ala  
 165 170 175  
 Phe Cys Leu Glu Glu Leu Met Met Thr Asn Pro His Asn His Leu Tyr  
 180 185 190  
 30 Cys Gln Gln Tyr Ala Glu Val Lys Tyr Thr Gln Xaa Trp Thr  
 195 200 205

&lt;210&gt; 1199

&lt;211&gt; 62

&lt;212&gt; PRT

35 <213> Homo sapiens  
 <400> 1199

Cys Gln Gln Tyr Ala Glu Val Lys Tyr Thr Gln Gly Xaa Leu Glu Thr  
 1 5 10 15  
 40 Leu Glu Leu Ser Arg Lys Tyr Phe Ala Gln Ala Leu Lys Leu Asn Asn  
 20 25 30  
 Arg Asn Met Arg Ala Leu Phe Gly Leu Tyr Met Ser Ala Ser His Ile  
 35 40 45  
 45 Ala Xaa Asn Pro Lys Ala Ser Ala Lys Thr Lys Lys Ala Thr  
 50 55 60

&lt;210&gt; 1200

&lt;211&gt; 147

&lt;212&gt; PRT

50 <213> Homo sapiens  
 <400> 1200

Ser Pro Cys Arg Ser Pro His Arg Trp Val Asn Ser Thr Cys Arg Ser  
 1 5 10 15  
 55 Thr Leu Lys Thr Arg Arg Leu Trp Tyr Asn Thr Pro His Thr His Ser  
 20 25 30  
 Gln Pro Pro Asp Lys Thr His Ser Leu Pro Leu Pro Cys Thr Ile Pro  
 35 40 45  
 60 Met Arg His Asn Tyr Asn Lys Leu His Leu Pro Thr Thr Asn Arg Pro  
 50 55 60  
 Lys Ile Ala His Cys Ile Leu Phe Asn Gln Pro His Ser Pro Arg Ser  
 65 70 75 80  
 Asn Ser His Ser His Pro Asn Pro Leu Lys Leu His Arg Arg Ser His

85 90 95  
 Ser His Asn Arg Pro Arg Thr Tyr Ile Leu Ile Thr Ile Leu Pro Ser  
 100 105 110  
 5 Lys Leu Lys Leu Arg Thr His Ser Gln Ser His His Asn Pro Leu Ser  
 115 120 125  
 Arg Thr Ser Asn Ser Thr Pro Thr Asn Ser Phe Leu Met Thr Ser Ser  
 130 135 140  
 Lys Pro Arg  
 145  
 10  
 <210> 1201  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 1201  
 Ser Asn Ile Thr Leu Leu Thr Gly Leu Asn Ile Leu Val Thr Ala  
 1 5 10 15  
 20 Leu Tyr Ser Leu Tyr Ile Phe Thr Thr Thr Gln Trp Gly Ser Leu Thr  
 20 25 30  
 His His Ile Asn Asn Ile Lys Pro Ser Phe Thr Arg Glu Asn Thr Leu  
 35 40 45  
 Met Phe Ile His Leu Ser Pro Ile Leu Leu Leu Ser Leu Asn Pro Asp  
 50 55 60  
 25 Ile Ile Thr Gly Phe Ser Ser  
 65 70  
 <210> 1202  
 <211> 93  
 30 <212> PRT  
 <213> Homo sapiens  
 <400> 1202  
 35 Ala His His Ser Leu Ile Glu Asn Asn Arg Asn Gln Ile Ile Gln Ala  
 1 5 10 15  
 Leu Leu Ile Thr Ile Leu Leu Gly Leu Tyr Phe Thr Leu Leu Gln Ala  
 20 25 30  
 Ser Glu Tyr Phe Glu Ser Pro Phe Thr Ile Ser Asp Gly Ile Tyr Gly  
 35 40 45  
 40 Ser Thr Phe Phe Val Ala Thr Gly Phe His Gly Leu His Val Ile Ile  
 50 55 60  
 Gly Ser Thr Phe Leu Thr Ile Cys Phe Ile Arg Gln Leu Ile Phe His  
 65 70 75 80  
 Phe Thr Ser Lys His His Phe Gly Phe Glu Ala Ala Ala  
 45 85 90  
 <210> 1203  
 <211> 159  
 <212> PRT  
 50 <213> Homo sapiens  
 <400> 1203  
 Val Ser Ser Arg Tyr Xaa Pro Asn Glu Gly Ser His His Xaa Phe Leu  
 1 5 10 15  
 55 Lys Xaa Gln Arg Lys Ser Lys Ser Xaa Lys Ile Ile Phe Asn Tyr Xaa  
 20 25 30  
 Xaa Asp Ala Xaa Arg Glu Xaa Thr Leu Val Ser Glu Xaa Ala Gln Arg  
 35 40 45  
 Ala Gln Arg Glu Xaa Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr  
 50 55 60  
 60 Gln Asn Glu Gln Asp Asn Val Asn Lys Xaa Xaa Gln Xaa Xaa Ser  
 65 70 75 80  
 Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Xaa

85 90 95  
 Gln Gln Leu Val Xaa Xaa His Lys Lys Xaa Ala Xaa Lys Ser Lys Ile  
 100 105 110  
 5 Xaa Ile Asp Ile His Phe Leu Glu Arg Lys Xaa Xaa His His Xaa Leu  
 115 120 125  
 Lys Glu Lys Asn Glu Glu Ile Phe Asn Ser Asn Xaa His Leu Lys Xaa  
 130 135 140  
 Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Xaa Glu Asn Ser  
 145 150 155  
 10  
 <210> 1204  
 <211> 53  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 1204  
 Ser Gln Pro Tyr Thr Pro Ser Thr Tyr Leu Pro Gln His Asn Gly Ala  
 1 5 10 15  
 His Ser Pro His Ile Asn Asn Ile Lys Pro Ser Phe Thr Arg Glu Asn  
 20 20 25 30  
 Thr Leu Met Ser Tyr Thr Tyr Pro His Ser Leu Tyr Ser Ser Thr Arg  
 35 40 45  
 Ile Leu Pro Gly Phe  
 50  
 25  
 <210> 1205  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens  
 30  
 <400> 1205  
 Ser Asn Ile Thr Leu Leu Leu Thr Gly Leu Asn Ile Leu Val Thr Ala  
 1 5 10 15  
 Leu Tyr Ser Leu Tyr Ile Phe Thr Thr Gln Trp Gly Ser Leu Thr  
 35 20 25 30  
 His His Ile Asn Asn Ile Lys Pro Ser Phe Thr Arg Glu Asn Thr Leu  
 35 40 45  
 Met Phe Ile His Leu Ser Pro Ile Leu Leu Leu Ser Leu Asn Pro Asp  
 50 55 60  
 40 Ile Ile Thr Gly Phe Ser Ser  
 65 70  
 <210> 1206  
 <211> 279  
 <212> PRT  
 <213> Homo sapiens  
 45  
 <400> 1206  
 Glu Ile His Arg Lys Leu Ser Glu Ala Thr Arg Glu Leu Gln Asn Ala  
 50 1 5 10 15  
 Pro Asp Ala Ile Pro Glu Ser Gly Val Glu Pro Pro Ala Leu Asp Thr  
 20 25 30  
 Ala Trp Val Glu Ala Thr Arg Lys Lys Ala Leu Leu Lys Leu Glu Lys  
 35 40 45  
 55 Leu Asp Thr Asp Leu Lys Asn Tyr Lys Gly Asn Ser Ile Lys Glu Ser  
 50 55 60  
 Ile Arg Arg Gly His Asp Asp Leu Gly Asp His Tyr Leu Asp Cys Gly  
 65 70 75 80  
 Asp Leu Ser Asn Ala Leu Lys Cys Tyr Ser Arg Ala Arg Asp Tyr Cys  
 85 90 95  
 60 Thr Ser Ala Lys His Val Ile Asn Met Cys Leu Asn Val Ile Lys Val  
 100 105 110  
 Ser Val Tyr Leu Gln Asn Trp Ser His Val Leu Ser Tyr Val Ser Lys

115 120 125  
 Ala Glu Ser Thr Pro Glu Ile Ala Glu Gln Arg Gly Glu Arg Asp Ser  
 130 135 140  
 Gln Thr Gln Ala Ile Leu Thr Lys Leu Lys Cys Ala Ala Gly Leu Ala  
 145 150 155 160  
 5 Glu Leu Ala Ala Arg Lys Tyr Lys Gln Ala Ala Lys Cys Leu Leu Leu  
 165 170 175  
 Ala Ser Phe Asp His Cys Asp Phe Pro Glu Leu Leu Ser Pro Ser Asn  
 180 185 190  
 10 Val Ala Ile Tyr Gly Gly Leu Cys Ala Leu Ala Thr Phe Asp Arg Gln  
 195 200 205  
 Glu Leu Gln Arg Asn Val Ile Phe Ser Ser Ser Phe Lys Leu Phe Leu  
 210 215 220  
 Glu Leu Glu Pro Xaa Val Arg Asp Ile Ile Phe Lys Phe Tyr Glu Xaa  
 15 225 230 235 240  
 Lys Tyr Ala Ser Cys Leu Lys Asn Ala Gly Pro Arg Met Lys Gly Gln  
 245 250 255  
 Pro Cys Ser Leu Asp Ile Val Xaa Trp Ala Pro Ile Val Lys Asp Pro  
 260 265 270  
 20 Cys Thr Pro Gln Ile Ser Lys  
 275

<210> 1207  
 <211> 178  
 25 <212> PRT  
 <213> Homo sapiens

<400> 1207  
 Glu Ile His Arg Lys Leu Ser Glu Ala Thr Arg Glu Leu Gln Asn Ala  
 1 5 10 15  
 Pro Asp Ala Ile Pro Glu Ser Gly Val Glu Pro Pro Ala Leu Asp Thr  
 20 25 30  
 Ala Trp Val Glu Ala Thr Arg Lys Ala Leu Leu Lys Leu Glu Lys  
 35 35 40 45  
 Leu Asp Thr Asp Leu Lys Asn Tyr Lys Gly Asn Ser Ile Lys Glu Ser  
 50 55 60  
 Ile Arg Arg Gly His Asp Asp Leu Gly Asp His Tyr Leu Asp Cys Gly  
 65 70 75 80  
 Asp Leu Ser Asn Ala Leu Lys Cys Tyr Ser Arg Ala Arg Asp Tyr Cys  
 40 85 90 95  
 Thr Ser Ala Lys His Val Ile Asn Met Cys Leu Asn Val Ile Lys Val  
 100 105 110  
 Ser Val Tyr Leu Gln Asn Trp Ser His Val Leu Ser Tyr Val Ser Lys  
 115 120 125  
 45 Ala Glu Ser Thr Pro Glu Ile Ala Glu Gln Arg Gly Glu Arg Asp Ser  
 130 135 140  
 Gln Thr Gln Ala Ile Leu Thr Lys Leu Lys Cys Ala Ala Ser Leu Ala  
 145 150 155 160  
 Lys Leu Xaa Ala Arg Xaa Tyr Lys Gln Ala Cys Gln Val Leu Cys Trp  
 50 165 170 175  
 Leu Leu

<210> 1208  
 55 <211> 120  
 <212> PRT  
 <213> Homo sapiens

<400> 1208  
 60 Ser Phe Gln Tyr Phe Lys Pro Leu Arg Phe Lys Pro Thr Met His Xaa  
 1 5 10 15  
 Met Gly Gln Pro Phe Lys Tyr His Gly Ala Xaa Leu Xaa Gly Arg Val  
 20 25 30

Asp Ala Val Asn Leu Glu Gly Val Asp Gln Cys Xaa Cys Gly Leu Thr  
           35                          40                          45  
 Gln Ala Arg Ser Tyr Thr Ala Xaa Xaa Val Asp Gln Arg Ser Thr Thr  
           50                          55                          60  
 5 Phe Glu Lys Xaa Leu Leu Met Gly Lys Glu Phe Gln Arg Arg Ala Lys  
    65                          70                          75                          80  
 Ala Met Met Leu Arg Ala Ala Val Leu Arg Asn Gln Ile His Val Lys  
                           85                          90                          95  
 10 Ser Pro Pro Arg Glu Gly Ser Gln Gly Glu Leu Thr Pro Ala Asn Ser  
                           100                          105                          110  
 Gln Ser Arg Met Ser Thr Asn Met  
           115                          120  
  
 <210> 1209  
 15 <211> 182  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 1209  
 20 Gly Val Glu Pro Pro Ala Leu Asp Thr Ala Trp Val Glu Ala Thr Arg  
    1                          5                          10                          15  
 Lys Lys Ala Leu Leu Lys Leu Glu Lys Leu Asp Thr Asp Leu Lys Asn  
           20                          25                          30  
 25 Tyr Lys Gly Asn Ser Ile Lys Glu Ser Ile Arg Arg Gly His Asp Asp  
    35                          40                          45  
 Leu Gly Asp His Tyr Leu Asp Cys Gly Asp Leu Ser Asn Ala Leu Lys  
    50                          55                          60  
 Cys Tyr Ser Arg Ala Arg Asp Tyr Cys Thr Ser Ala Lys His Val Ile  
    65                          70                          75                          80  
 30 Asn Met Cys Leu Asn Val Ile Lys Val Ser Val Tyr Leu Gln Asn Trp  
                           85                          90                          95  
 Ser His Val Leu Ser Tyr Val Ser Lys Ala Glu Ser Thr Pro Glu Ile  
                           100                          105                          110  
 35 Ala Glu Gln Arg Gly Glu Arg Asp Ser Gln Thr Gln Ala Ile Leu Thr  
    115                          120                          125  
 Lys Leu Lys Cys Ala Ala Gly Leu Ala Glu Leu Ala Ala Arg Lys Tyr  
    130                          135                          140  
 Lys Gln Ala Ala Lys Cys Leu Leu Leu Ala Ser Phe Asp His Xaa Asp  
    145                          150                          155                          160  
 40 Phe Pro Glu Leu Leu Ser Pro Asn Asn Val Ala Ile Tyr Gly Gly Leu  
                           165                          170                          175  
 Cys Ala Leu Ala Thr Phe  
           180  
  
 45 <210> 1210  
       <211> 239  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 1210  
 50 Lys Lys Ala Leu Leu Lys Leu Glu Lys Leu Asp Thr Asp Leu Lys Asn  
    1                          5                          10                          15  
 Tyr Lys Gly Asn Ser Ile Lys Glu Ser Ile Arg Arg Gly His Asp Asp  
           20                          25                          30  
 55 Leu Gly Asp His Tyr Leu Asp Cys Gly Asp Leu Ser Asn Ala Leu Lys  
    35                          40                          45  
 Cys Tyr Ser Arg Ala Arg Asp Tyr Cys Thr Ser Ala Lys His Val Ile  
    50                          55                          60  
 Asn Met Cys Leu Asn Val Ile Lys Val Ser Val Tyr Leu Gln Asn Trp  
    65                          70                          75                          80  
 60 Ser His Val Leu Ser Tyr Val Ser Lys Ala Glu Ser Thr Pro Glu Ile  
                           85                          90                          95  
 Ala Glu Arg Gly Glu Arg Asp Ser Gln Thr Gln Ala Ile Leu Thr Lys



100 105 110  
 Leu Lys Cys Ala Ala Gly Leu Ala Glu Leu Ala Ala Arg Lys Tyr Lys  
 115 120 125  
 Gln Ala Ala Lys Cys Leu Leu Leu Ala Ser Phe Asp His Cys Asp Phe  
 130 135 140  
 5 Pro Glu Leu Leu Ser Pro Ser Asn Val Ala Ile Tyr Gly Gly Leu Cys  
 145 150 155 160  
 Ala Leu Ala Thr Phe Asp Arg Gln Glu Leu Gln Arg Asn Val Ile Phe  
 165 170 175  
 10 Ser Ser Ser Phe Lys Leu Phe Leu Glu Leu Glu Pro Xaa Val Arg Asp  
 180 185 190  
 Ile Ile Phe Lys Phe Tyr Glu Xaa Lys Tyr Ala Ser Cys Leu Lys Asn  
 195 200 205  
 Ala Gly Pro Arg Met Lys Gly Gln Pro Cys Ser Leu Asp Ile Val Xaa  
 210 215 220  
 15 Trp Ala Pro Ile Val Lys Asp Pro Cys Thr Pro Gln Ile Ser Lys  
 225 230 235

20 <210> 1211  
 <211> 245  
 <212> PRT  
 <213> Homo sapiens

<400> 1211  
 25 Lys Lys Ala Leu Leu Lys Leu Glu Lys Leu Asp Thr Asp Leu Lys Asn  
 1 5 10 15  
 Tyr Lys Gly Asn Ser Ile Lys Glu Ser Ile Arg Arg Gly His Asp Asp  
 20 25 30  
 30 Leu Gly Asp His Tyr Leu Asp Cys Gly Asp Leu Ser Asn Ala Leu Lys  
 35 40 45  
 Cys Tyr Ser Arg Ala Arg Asp Tyr Cys Thr Ser Ala Lys His Val Ile  
 50 55 60  
 Asn Met Cys Leu Asn Val Ile Lys Val Ser Val Tyr Leu Gln Asn Trp  
 65 70 75 80  
 35 Ser His Val Leu Ser Tyr Val Ser Lys Ala Glu Ser Thr Pro Glu Ile  
 85 90 95  
 Ala Glu Arg Gly Glu Arg Asp Ser Gln Thr Gln Ala Ile Leu Thr Lys  
 100 105 110  
 40 Leu Lys Cys Ala Ala Gly Leu Ala Glu Leu Ala Ala Arg Lys Tyr Lys  
 115 120 125  
 Gln Ala Ala Lys Cys Leu Leu Leu Ala Ser Phe Asp His Cys Asp Phe  
 130 135 140  
 Pro Glu Leu Leu Ser Pro Ser Asn Val Ala Ile Tyr Gly Gly Leu Cys  
 145 150 155 160  
 45 Ala Leu Ala Thr Phe Asp Arg Gln Glu Leu Gln Arg Asn Val Ile Phe  
 165 170 175  
 Ser Ser Phe Phe Lys Leu Phe Leu Glu Leu Glu Pro Gln Xaa Arg Asp  
 180 185 190  
 Ile Ile Phe Lys Phe Tyr Glu Xaa Gln Val Pro Leu Met Phe Xaa Arg  
 195 200 205  
 50 Cys Leu Asp Glu Asn Glu Arg Thr Thr Leu Xaa Leu Asp Asn Val Xaa  
 210 215 220  
 Trp Pro Pro Leu Leu Xaa Thr Leu Tyr Asn Pro Lys Phe Arg Asn Arg  
 225 230 235 240  
 55 Xaa Pro Ser Phe Ser  
 245

60 <210> 1212  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 1212

Ser Glu Met Ile Phe Ser Asp Met Asn Thr Val Ser Gly Ser Pro Lys  
 1 5 10 15  
 Val His Pro Pro Asn Gly Thr Arg Phe Tyr Thr Phe Gln Glu Phe Ala  
 20 25 30  
 5 Ala Leu Thr Lys Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys  
 35 40 45  
 Glu Glu Glu Ile Ser Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu  
 50 55 60  
 Leu Leu Glu His Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu  
 65 70 75 80  
 10 Arg Met Thr Val Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser  
 85 90 95  
 Ser Glu Val Glu Val Leu Lys Ala Leu Lys Ser Leu Phe Glu His His  
 100 105 110  
 15 Lys Ala Leu Asp Glu Lys Val Arg Glu Arg Leu Arg Val Ser Leu Glu  
 115 120 125  
 Arg Val Ser Ala Leu Glu Glu Glu Leu Ala Ala Ala Asn Gln Glu Ile  
 130 135 140  
 Val Ala Leu Arg Glu Gln Asn Val His Ile Gln Arg Lys Met Ala Ser  
 145 150 155 160  
 20 Ser Glu Gly Ser Thr Glu Ser Glu His Leu Glu Gly Met Glu Pro Gly  
 165 170 175  
 Gln Lys Val His Glu Lys Arg Leu Ser Asn Gly Ser Ile Asp Ser Thr  
 180 185 190  
 25 Asp Glu Thr Ser Gln Ile Val Glu Leu Gln Glu Leu Leu Glu Lys Gln  
 195 200 205  
 Asn Gln  
 210  
 30 <210> 1213  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens  
 35 <400> 1213  
 Ser Glu Met Ile Phe Ser Asp Met Asn Thr Val Ser Gly Ser Pro Lys  
 1 5 10 15  
 Val His Pro Pro Asn Gly Thr Arg Phe Tyr Thr Phe Gln Glu Phe Ala  
 20 25 30  
 40 Ala Leu Thr Lys Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys  
 35 40 45  
 Glu Glu Glu Ile Ser Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu  
 50 55 60  
 Leu Leu Glu His Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu  
 65 70 75 80  
 45 Arg Met Thr Val Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser  
 85 90 95  
 Lys  
 50 <210> 1214  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens  
 55 <400> 1214  
 Glu Met Ile Phe Ser Asp Met Asn Thr Val Ser Gly Ser Pro Lys Val  
 1 5 10 15  
 His Pro Pro Asn Gly Thr Arg Phe Tyr Thr Phe Gln Glu Phe Ala Ala  
 20 25 30  
 60 Leu Thr Lys Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys Glu  
 35 40 45  
 Glu Glu Ile Ser Glu Leu Lys Ala Glu Arg Asn Asn Thr Arg Leu Leu

50 55 60  
 Leu Glu His Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu Arg  
 65 70 75 80  
 Met Thr Val Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser Ser  
 85 90 95  
 5 Glu Val Glu Val Leu Lys Ala Leu Lys Ser Leu Phe Glu His His Lys  
 100 105 110  
 Ala Leu Asp Glu Lys Val Arg Glu Arg Leu Arg Val Ser Leu Glu Arg  
 115 120 125  
 10 Val Ser Ala Leu Glu Glu Glu Leu Ala Ala Ala Asn Gln Glu Ile Val  
 130 135 140  
 Ala Leu Arg Glu Gln Asn Val His Ile Gln Arg Lys Met Ala Ser Ser  
 145 150 155 160  
 Glu Gly Ser Thr Glu Ser Glu His Leu Glu Gly Met Glu Pro Gly Gln  
 15 165 170 175  
 Lys Val His Glu Lys Arg Leu Ser Asn Gly Ser Ile Asp Ser Thr Asp  
 180 185 190  
 Glu Thr Ser Gln Ile Val Glu Leu Gln Glu Leu Leu Glu Lys Gln Asn  
 195 200 205  
 20 Gln

<210> 1215  
 <211> 98  
 25 <212> PRT  
 <213> Homo sapiens

<400> 1215  
 Gly Gly Met Asn Asp Leu Phe Phe Gln Glu Phe Ala Ala Leu Thr Lys  
 1 5 10 15  
 Glu Leu Asn Ala Cys Arg Glu Gln Leu Leu Glu Lys Glu Glu Ile  
 20 25 30  
 Ser Glu Leu Lys Ala Glu Arg Asn Thr Arg Leu Leu Glu His  
 35 35 40 45  
 Leu Glu Cys Leu Val Ser Arg His Glu Arg Ser Leu Arg Met Thr Val  
 50 55 60  
 Val Lys Arg Gln Ala Gln Ser Pro Ser Gly Val Ser Ser Glu Val Glu  
 65 70 75 80  
 Val Leu Lys Ala Leu Lys Ser Leu Phe Glu Pro Thr Arg Pro Trp Met  
 40 85 90 95  
 Lys Xaa

<210> 1216  
 45 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 1216  
 50 Xaa Gln Arg Thr Asn Phe Xaa Leu Lys Xaa Ile Phe Ser Leu Pro Ser  
 1 5 10 15  
 Gly His Ser Asp Ala Gln Thr Leu Ala Met Met Leu Gln Glu Gln Leu  
 20 25 30  
 Asp Ala Ile Asn Lys Glu Ile Arg Leu Ile Gln Glu Glu Lys Glu Ser  
 55 35 40 45  
 Thr Glu Leu Arg Ala Glu Glu Ile Glu Asn Arg Val Ala Ser Val Ser  
 50 55 60  
 Leu Glu Gly Leu Asn Leu Ala Arg Val His Pro Gly Thr Ser Ile Thr  
 65 70 75 80  
 60 Ala Ser Val Thr Ala Ser Ser Leu Ala Ser Ser Ser Pro Pro Ser Gly  
 85 90 95  
 His Ser Thr Pro Lys Leu Thr Pro Arg Ser Pro Ala Arg Glu Met Asp  
 100 105 110

Arg Met Gly Val Met Thr Leu Pro Ser Asp Xaa Arg Lys His Arg Arg  
                   115                  120                  125  
 Lys Ile Ala Val Val Glu Glu Asp Gly Arg Glu Asp Lys Ala Thr Ile  
                   130                  135                  140  
 5 Lys Cys Glu Thr Ser Pro Pro Pro Thr Pro Arg Ala Leu Arg Met Thr  
    145                  150                  155                  160  
 His Thr Leu Pro Ser Ser Tyr His Asn Asp Ala Arg Ser Ser Leu Ser  
                   165                  170                  175  
 Val Ser Leu Glu Pro Glu Ser Leu Gly Leu Gly Ser Ala Asn Ser Ser  
 10                  180                  185                  190  
 Gln Asp Ser Xaa His Lys Ala Pro Lys Lys Lys Gly Ile Lys Ser Ser  
                   195                  200                  205  
 Ile Gly Arg Leu Phe Gly  
                   210  
 15  
       <210> 1217  
       <211> 63  
       <212> PRT  
       <213> Homo sapiens  
 20  
       <400> 1217  
 Leu Leu Leu Ile Arg Arg Trp Trp Pro Cys Val Asn Gln Asn Val His  
    1                  5                  10                  15  
 Xaa Gln Arg Lys Met Ala Ser Ser Arg Gly Ile Xaa Gln Ser Gln Asn  
 25                  20                  25                  30  
 Xaa Phe Glu Gly Met Glu Pro Gly Thr Glu Ser Pro Xaa Lys Ser Val  
                   35                  40                  45  
 Xaa Pro Met Gly Phe Leu Asp Leu Thr Arg Xaa Lys Leu Val Gln  
                   50                  55                  60  
 30  
       <210> 1218  
       <211> 169  
       <212> PRT  
       <213> Homo sapiens  
 35  
       <400> 1218  
 Arg Cys Glu Pro Phe Thr Met Lys Met Leu Lys Asp Ile Lys Glu Gly  
    1                  5                  10                  15  
 Val Lys Gln Tyr Gly Ser Asn Ser Pro Tyr Ile Arg Thr Leu Leu Asp  
 40                  20                  25                  30  
 Ser Ile Ala His Gly Asn Arg Leu Thr Pro Tyr Asp Trp Glu Ile Leu  
                   35                  40                  45  
 Ala Lys Ser Ser Leu Ser Ser Ser Gln Tyr Leu Gln Phe Lys Thr Trp  
                   50                  55                  60  
 45 Trp Ile Asp Gly Val Gln Glu Gln Val Arg Lys Asn Gln Ala Thr Lys  
    65                  70                  75                  80  
 Pro Thr Val Asn Ile Asp Ala Asp Gln Leu Gly Thr Gly Pro Asn  
                   85                  90                  95  
 Trp Ser Thr Ile Asn Gln Gln Ser Val Met Gln Asn Glu Ala Ile Glu  
 50                  100                  105                  110  
 Gln Val Arg Ala Ile Cys Leu Arg Ala Trp Gly Lys Ile Gln Asp Pro  
                   115                  120                  125  
 Gly Thr Ala Phe Pro Ile Asn Ser Ile Arg Gln Gly Ser Lys Glu Pro  
                   130                  135                  140  
 55 Tyr Pro Ala Leu Trp Gln Asp Tyr Lys Met Leu Leu Lys Ser Leu Leu  
    145                  150                  155                  160  
 Gln Met Thr Met Pro Glu Lys Leu Leu  
                   165  
 60  
       <210> 1219  
       <211> 224  
       <212> PRT  
       <213> Homo sapiens

<400> 1219

	Trp	Met	Ile	Arg	Leu	Asn	Xaa	Ala	Xaa	Leu	Ile	Trp	Phe	Xaa	Gln	Asn
	1				5					10					15	
5	Val	Arg	Lys	Xaa	Asn	Phe	Pro	Ile	Leu	Tyr	Xaa	Ser	Xaa	Xaa	Glu	Pro
				20					25					30		
	His	Leu	Ile	Tyr	Gln	Gly	Pro	Leu	Xaa	Lys	Ala	Asn	Asp	Gln	Ala	Asp
				35				40					45			
10	Leu	Leu	Val	Ser	Ser	Ala	Phe	Met	Xaa	Ala	Gln	Glu	Leu	His	Ala	Leu
		50					55					60				
	Thr	His	Val	Asn	Ala	Ile	Gly	Leu	Lys	Asn	Lys	Phe	Asp	Ile	Thr	Trp
	65					70					75				80	
	Lys	Gln	Pro	Lys	Asn	Ile	Val	Gln	His	Cys	Thr	Gln	Cys	Gln	Ile	Leu
					85					90					95	
15	His	Leu	Ala	Thr	Gln	Glu	Ala	Arg	Val	Asn	Pro	Arg	Gly	Leu	Cys	Pro
				100					105					110		
	Asn	Val	Leu	Trp	Gln	Met	Asp	Val	Met	His	Val	Pro	Ser	Phe	Gly	Lys
			115					120					125			
20	Leu	Ser	Phe	Val	His	Val	Thr	Val	Asp	Thr	Tyr	Ser	His	Phe	Ile	Trp
		130					135					140				
	Ala	Thr	Cys	Gln	Thr	Gly	Glu	Ser	Thr	Ser	His	Val	Lys	Arg	His	Leu
	145					150					155				160	
	Leu	Ser	Cys	Phe	Pro	Val	Met	Gly	Val	Pro	Glu	Lys	Val	Lys	Thr	Asp
					165					170					175	
25	Asn	Gly	Pro	Gly	Tyr	Cys	Ser	Lys	Ala	Phe	Gln	Lys	Xaa	Leu	Asn	Gln
					180				185					190		
	Trp	Lys	Ile	Thr	His	Thr	Ile	Gly	Ile	Leu	Tyr	Asn	Ser	Gln	Gly	Gln
			195					200					205			
30	Ala	Ile	Ile	Glu	Arg	Thr	Asn	Arg	Thr	Leu	Lys	Ala	Gln	Leu	Val	Lys
		210					215					220				

&lt;210&gt; 1220

&lt;211&gt; 178

&lt;212&gt; PRT

35 &lt;213&gt; Homo sapiens

<400> 1220

	Gln	Pro	Thr	Ala	Met	Ala	Ser	Asn	Ser	Pro	Ala	Thr	Gln	Asp	Ala	Ala
	1				5					10					15	
40	Leu	Tyr	Pro	Gln	Pro	Pro	Thr	Val	Arg	Leu	Asn	Pro	Thr	Ala	Ser	Arg
				20					25					30		
	Ser	Gly	Gln	Gly	Gly	Ala	Leu	His	Ala	Val	Ile	Asp	Glu	Ala	Arg	Lys
				35				40					45			
45	Gln	Gly	Asp	Leu	Glu	Ala	Trp	Arg	Phe	Leu	Val	Ile	Leu	Gln	Leu	Val
		50					55					60				
	Gln	Ala	Gly	Glu	Glu	Thr	Gln	Val	Gly	Ala	Pro	Ala	Arg	Ala	Glu	Thr
	65					70					75				80	
	Arg	Cys	Glu	Pro	Phe	Thr	Met	Lys	Met	Leu	Lys	Asp	Ile	Lys	Glu	Gly
					85					90					95	
50	Val	Lys	Gln	Tyr	Gly	Ser	Asn	Ser	Pro	Tyr	Ile	Arg	Thr	Leu	Leu	Asp
					100				105					110		
	Ser	Ile	Ala	His	Gly	Asn	Arg	Leu	Thr	Pro	Tyr	Asp	Trp	Glu	Ile	Leu
			115					120					125			
55	Ala	Lys	Ser	Ser	Phe	His	Pro	Leu	Ser	Ile	Tyr	Ser	Leu	Lys	Pro	Gly
		130					135					140				
	Gly	Leu	Met	Glu	Tyr	Lys	Glu	Gln	Val	Arg	Lys	Asn	Gln	Ala	Thr	Asn
	145					150					155				160	
	Pro	Cys	Tyr	Ile	Asp	Ala	Asp	Gln	Leu	Leu	Gly	Thr	Gly	Gln	Ile	Gly
					165					170					175	
60	Ala	His														

&lt;210&gt; 1221

<211> 152  
 <212> PRT  
 <213> Homo sapiens

5           <400> 1221  
 Lys Ile Asn Leu Ile Ser His Gly Asn Arg Gln Lys Ile Leu Tyr Asn  
   1                  5                  10                  15  
 Ile Ala Pro Ser Val Arg Phe Tyr Thr Trp Pro Leu Arg Arg Gln Glu  
           20                  25                  30  
 10 Leu Ile Pro Glu Val Tyr Val Leu Met Cys Tyr Gly Lys Trp Met Ser  
           35                  40                  45  
 Cys Thr Val Pro Ser Phe Gly Lys Leu Ser Phe Val His Val Thr Val  
   50                  55                  60  
 Asp Thr Tyr Ser His Phe Ile Trp Ala Thr Cys Gln Thr Gly Glu Ser  
 15 65                  70                  75                  80  
 Thr Ser His Val Lys Arg His Leu Leu Ser Cys Phe Pro Val Met Gly  
           85                  90                  95  
 Val Pro Glu Lys Val Lys Thr Asp Asn Gly Pro Gly Tyr Cys Ser Lys  
           100                  105                  110  
 20 Ala Phe Gln Lys Phe Leu Asn Gln Trp Lys Ile Thr His Thr Ile Gly  
           115                  120                  125  
 Ile Leu Tyr Asn Ser Gln Gly Gln Ala Ile Ile Glu Arg Thr Asn Arg  
   130                  135                  140  
 Thr Leu Lys Ala Gln Leu Val Lys  
 25 145                  150

<210> 1222  
 <211> 231  
 <212> PRT  
 30 <213> Homo sapiens

          <400> 1222  
 Arg Glu Ser Pro Lys Tyr Val His Gly Gln Pro Cys Gly Lys Leu Val  
   1                  5                  10                  15  
 35 Cys Leu Glu Glu Pro Arg Val Thr Met Gly Gln Thr Glu Ser Lys Tyr  
           20                  25                  30  
 Ala Ser Tyr Leu Ser Phe Ile Lys Ile Leu Leu Arg Arg Gly Gly Val  
   35                  40                  45  
 Arg Ala Ser Thr Glu Asn Leu Ile Thr Leu Phe Gln Thr Ile Glu Gln  
 40 50                  55                  60  
 Phe Cys Pro Trp Phe Pro Glu Gln Gly Thr Leu Asp Leu Lys Asp Trp  
   65                  70                  75                  80  
 Glu Lys Ile Gly Lys Glu Leu Lys Gln Ala Asn Arg Glu Gly Lys Ile  
           85                  90                  95  
 45 Ile Pro Leu Thr Val Trp Asn Asp Trp Ala Ile Ile Lys Ala Thr Leu  
           100                  105                  110  
 Glu Pro Phe Gln Thr Gly Glu Asp Ile Val Ser Val Ser Asp Ala Pro  
   115                  120                  125  
 Lys Ser Cys Val Thr Asp Cys Glu Glu Glu Ala Gly Thr Glu Ser Gln  
 50 130                  135                  140  
 Gln Gly Thr Glu Ser Ser His Cys Lys Tyr Val Ala Glu Ser Val Met  
   145                  150                  155                  160  
 Ala Gln Ser Thr Gln Asn Val Asp Tyr Ser Gln Leu Gln Glu Ile Ile  
           165                  170                  175  
 55 Tyr Pro Glu Ser Ser Lys Leu Gly Glu Gly Gly Pro Glu Ser Leu Gly  
           180                  185                  190  
 Pro Ser Glu Pro Lys Pro Arg Ser Pro Ser Thr Pro Pro Ser Ala Val  
   195                  200                  205  
 Gln Met Pro Val His Ser Thr Ser Asn Arg Arg Leu Asp Lys Pro Lys  
 60 210                  215                  220  
 Pro Pro Arg Glu Asn Gln Val  
 225                  230

<210> 1223  
 <211> 299  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1223

Glu Glu Gly Ser Arg Gly Gly Arg Glu Gly Ala Gly Lys Met Val Val  
 1 5 10 15  
 Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala Ser Ala Glu  
 20 25 30  
 Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln Ala His Pro  
 35 40 45  
 Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Ala Glu Ser Gln Thr  
 50 55 60  
 Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala Arg Lys Arg  
 65 70 75 80  
 Lys Ser Arg Thr Thr Gly Ser Leu Pro Lys Gly Thr Glu Pro Ser Thr  
 85 90 95  
 Asp Gly Glu Thr Ser Glu Ala Glu Ser Asn Tyr Ser Val Ser Glu His  
 100 105 110  
 His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile Ala  
 115 120 125  
 Cys Ser Pro Val Ser Ser Val Arg Lys Lys Pro Lys Val Thr Pro Thr  
 130 135 140  
 Lys Glu Ser Tyr Thr Glu Glu Ile Val Ser Glu Ala Glu Ser His Val  
 145 150 155 160  
 Ser Gly Ile Ser Arg Ile Val Leu Pro Thr Glu Lys Thr Thr Gly Ala  
 165 170 175  
 Arg Arg Ser Lys Ala Lys Ser Leu Thr Asp Pro Ser Gln Glu Ser His  
 180 185 190  
 Thr Glu Ala Ile Ser Asp Ala Glu Thr Ser Ser Ser Asp Ile Ser Phe  
 195 200 205  
 Ser Gly Ile Ala Thr Arg Arg Thr Arg Ser Met Gln Arg Lys Leu Lys  
 210 215 220  
 Ala Gln Thr Glu Lys Lys Asp Ser Lys Ile Val Pro Gly Asn Glu Lys  
 225 230 235 240  
 Gln Ile Val Gly Thr Pro Val Asn Ser Glu Asp Ser Asp Thr Arg Gln  
 245 250 255  
 Thr Ser His Leu Gln Ala Arg Ser Leu Ser Glu Ile Asn Lys Pro Asn  
 260 265 270  
 Phe Tyr Asn Asn Asp Phe Asp Asp Asp Phe Ser His Arg Ser Ser Glu  
 275 280 285  
 Asn Ile Leu Thr Val His Arg Thr Gly Gln Cys  
 290 295

45

<210> 1224  
 <211> 182  
 <212> PRT  
 <213> Homo sapiens

50

<400> 1224

Val Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala Ser Ala  
 1 5 10 15  
 Glu Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln Ala His  
 20 25 30  
 Pro Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Ala Glu Ser Gln  
 35 40 45  
 Thr Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala Arg Lys  
 50 55 60  
 Arg Lys Ser Arg Thr Thr Gly Ser Leu Pro Lys Gly Thr Glu Pro Ser  
 65 70 75 80  
 Thr Asp Gly Glu Thr Ser Glu Ala Glu Ser Asn Tyr Ser Val Ser Glu  
 85 90 95

His His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile  
                   100                  105                  110  
 Ala Cys Ser Pro Val Ser Ser Val Arg Lys Lys Pro Lys Val Thr Pro  
                   115                  120                  125  
 5 Thr Lys Glu Ser Tyr Thr Glu Glu Ile Val Ser Glu Ala Glu Ser His  
                   130                  135                  140  
 Val Ser Gly Ile Ser Arg Ile Xaa Leu Pro Thr Glu Lys Thr Thr Gly  
                   145                  150                  155                  160  
 10 Ala Arg Arg Ser Lys Xaa Lys Ser Leu Asp Arg Ser Asn Gln Glu Ser  
                   165                  170                  175  
 His Thr Arg Asn Tyr Ile  
                   180  
  
 <210> 1225  
 15 <211> 194  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 1225  
 20 Ser Ile Ala Leu Gly Leu Arg Ile Xaa Gln Leu Gly Gly Leu Tyr Ile  
       1                  5                  10                  15  
 Asn Phe Xaa Ala Asp Lys Xaa Gln Phe Asn Lys Arg Thr Xaa Xaa Gln  
                   20                  25                  30  
 25 Xaa Lys Xaa Lys Lys Lys Asn Glu Phe Xaa Gln Lys Ala Val Ile Thr  
                   35                  40                  45  
 Pro Asp Phe Glu Lys Asn His Cys Val Xaa Pro Tyr Ser Glu Ser Lys  
                   50                  55                  60  
 Xaa Gln Leu Gln Lys Lys Arg Arg Lys Xaa Arg Gln Lys Pro Xaa Gly  
                   65                  70                  75                  80  
 30 Asp Gly Trp Phe Gly Met Lys Ala Pro Glu Met Thr Asn Glu Leu Lys  
                   85                  90                  95  
 Asn Asp Xaa Lys Ala Xaa Lys Met Arg Ala Ser Met Asp Pro Lys Arg  
                   100                  105                  110  
 35 Phe Xaa Lys Lys Asn Asp Arg Asp Gly Phe Pro Lys Tyr Phe Gln Ile  
                   115                  120                  125  
 Gly Thr Ile Val Asp Asn Pro Ala Asp Xaa Tyr His Ser Xaa Ile Pro  
                   130                  135                  140  
 Lys Lys Gln Arg Lys Arg Thr Ile Val Glu Glu Leu Leu Ala Asp Xaa  
                   145                  150                  155                  160  
 40 Glu Phe Arg Arg Tyr Asn Arg Arg Lys Xaa Ser Glu Ile Met Ala Glu  
                   165                  170                  175  
 Lys Ala Ala Asn Ala Ala Gly Lys Lys Phe Arg Lys Lys Lys Lys Phe  
                   180                  185                  190  
 Arg Asn  
  
 <210> 1226  
 45 <211> 188  
       <212> PRT  
       <213> Homo sapiens  
  
       <400> 1226  
 55 Ser His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile  
       1                  5                  10                  15  
 Ala Cys Ser Pro Val Ser Ser Val Arg Lys Lys Pro Lys Val Thr Pro  
                   20                  25                  30  
 Thr Lys Glu Ser Tyr Thr Glu Glu Ile Val Ser Glu Ala Glu Ser His  
                   35                  40                  45  
 60 Val Ser Gly Ile Ser Arg Ile Val Leu Pro Thr Glu Lys Thr Thr Gly  
                   50                  55                  60  
 Ala Arg Arg Ser Lys Ala Lys Ser Leu Thr Asp Pro Ser Gln Glu Ser  
                   65                  70                  75                  80  
 His Thr Glu Ala Ile Ser Asp Ala Glu Thr Ser Ser Ser Asp Ile Ser



85 90 95  
 Phe Ser Gly Ile Ala Thr Arg Arg Thr Arg Ser Met Gln Arg Lys Leu  
 100 105 110  
 5 Lys Ala Gln Thr Glu Lys Lys Asp Ser Lys Ile Val Pro Gly Asn Glu  
 115 120 125  
 Lys Gln Ile Val Gly Thr Pro Val Asn Ser Glu Asp Ser Asp Thr Arg  
 130 135 140  
 Gln Thr Ser His Leu Gln Ala Arg Ser Leu Ser Glu Ile Asn Lys Pro  
 145 150 155 160  
 10 Asn Phe Tyr Asn Asn Asp Phe Asp Asp Asp Phe Ser His Arg Ser Ser  
 165 170 175  
 Glu Asn Ile Leu Thr Val His Arg Thr Gly Gln Cys  
 180 185  
 15 <210> 1227  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens  
 20 <400> 1227  
 Glu Glu Gly Ser Arg Gly Gly Arg Glu Gly Ala Gly Lys Met Val Val  
 1 5 10 15  
 Thr Arg Ser Ala Arg Ala Lys Ala Ser Ile Gln Ala Ala Ser Ala Glu  
 20 25 30  
 25 Ser Ser Gly Gln Lys Ser Phe Ala Ala Asn Gly Ile Gln Ala His Pro  
 35 40 45  
 Glu Ser Ser Thr Gly Ser Asp Ala Arg Thr Thr Ala Glu Ser Gln Thr  
 50 55 60  
 Thr Gly Lys Gln Ser Leu Ile Pro Arg Thr Pro Lys Ala Arg Lys Arg  
 65 70 75 80  
 30 Lys Ser Arg Thr Thr Gly Ser Leu Pro Lys Gly Thr Glu Pro Ser Thr  
 85 90 95  
 Asp Gly Glu Thr Ser Glu Ala Glu Ser Asn Tyr Ser Val Ser Glu His  
 100 105 110  
 35 His Asp Thr Ile Leu Arg Val Thr Arg Arg Arg Gln Ile Leu Ile Ala  
 115 120 125  
 Cys Ser Pro Val Ser Xaa Val Arg Lys Lys Pro Lys Val Thr Pro Thr  
 130 135 140  
 Lys Glu Ser Tyr Thr Glu Glu Ile Xaa Ser Glu Ala Lys Xaa His Val  
 145 150 155 160  
 40 Ser Xaa Ile Ser Arg Ile Xaa Leu Pro Thr Xaa Lys Thr Thr Gly Ala  
 165 170 175  
 Arg Xaa Ser Lys Ala Lys Ser Leu Thr Xaa Pro Ser Gln Glu Ser His  
 180 185 190  
 45 Thr Glu Ala Ile Ser Asp Ala  
 195  
 <210> 1228  
 <211> 132  
 50 <212> PRT  
 <213> Homo sapiens  
 <400> 1228  
 Ile Lys Asp Gln Leu Gln Lys Lys Arg Arg Lys Glu Arg Gln Lys Thr  
 1 5 10 15  
 Ala Gly Asp Gly Trp Phe Gly Met Lys Ala Pro Glu Met Thr Asn Glu  
 20 25 30  
 Leu Lys Asn Asp Leu Lys Ala Leu Lys Met Arg Ala Ser Met Asp Pro  
 35 40 45  
 60 Lys Arg Phe Xaa Lys Lys Asn Asp Arg Asp Gly Phe Pro Lys Tyr Phe  
 50 55 60  
 Gln Ile Gly Thr Ile Val Xaa Asn Pro Ala Asp Phe Tyr His Ser Arg  
 65 70 75 80

Ile Pro Lys Lys Gln Arg Lys Arg Thr Ile Val Glu Glu Leu Leu Ala  
                     85                    90                    95  
 Asp Ser Glu Phe Arg Arg Tyr Asn Arg Arg Lys Tyr Ser Glu Ile Met  
                     100                    105                    110  
 5 Ala Glu Lys Ala Ala Asn Ala Ala Gly Lys Lys Phe Arg Lys Lys Lys  
                     115                    120                    125  
 Lys Phe Arg Asn  
                     130  
  
 10 <210> 1229  
       <211> 117  
       <212> PRT  
       <213> Homo sapiens  
  
 15 <400> 1229  
 Ser Pro Ser Ile Leu Ser Asp Ser Ser Ser Cys Glu Ile Ala Tyr Gln  
   1                    5                    10                    15  
 Asp Ala Val Asn Leu Gln Asn Tyr Val Glu Glu Lys Leu Ile Pro Thr  
                     20                    25                    30  
 20 Trp Asn Trp Met Val Ser Ile Met Asp Ser Thr Glu Ala Gln Leu Arg  
                     35                    40                    45  
 Tyr Gly Ser Ala Leu Ala Ser Ala Gly Asp Pro Gly His Pro Asn His  
                     50                    55                    60  
 Pro Leu His Ala Ser Gln Asn Ser Ala Arg Arg Glu Arg Met Thr Ala  
 25 65                    70                    75                    80  
 Arg Glu Glu Ala Ser Leu Arg Thr Leu Glu Gly Arg Arg Arg Ala Thr  
                     85                    90                    95  
 Leu Leu Ser Ala Arg Gln Gly Met Met Ser Ala Arg Gly Asp Phe Leu  
                     100                    105                    110  
 30 Asn Tyr Ala Leu Leu  
                     115  
  
       <210> 1230  
       <211> 143  
 35 <212> PRT  
       <213> Homo sapiens  
  
       <400> 1230  
 Asp Asp Ile Glu Gln Glu Thr Phe Met Leu Asp Glu Pro Leu Glu Arg  
 40 1                    5                    10                    15  
 Thr Thr Asn Ser Ser His Ala Asn Gly Ala Ala Gln Ala Pro Arg Ser  
                     20                    25                    30  
 Met Gln Trp Ala Val Arg Asn Thr Gln His Gln Arg Ala Ala Ser Thr  
                     35                    40                    45  
 45 Ala Pro Ser Ser Thr Ser Thr Pro Ala Ala Ser Ser Ala Gly Leu Ile  
                     50                    55                    60  
 Tyr Ile Asp Pro Ser Asn Leu Arg Arg Ser Gly Thr Ile Ser Thr Ser  
 65                    70                    75                    80  
 Ala Ala Ala Ala Ala Ala Ala Leu Glu Ala Ser Asn Ala Ser Ser Tyr  
 50                    85                    90                    95  
 Leu Thr Ser Ala Ser Ser Leu Ala Arg Ala Tyr Ser Ile Val Ile Arg  
                     100                    105                    110  
 Gln Ile Ser Asp Leu Met Gly Leu Ile Pro Lys Tyr Asn His Leu Val  
                     115                    120                    125  
 55 Tyr Ser Gln Ile Pro Ala Ala Val Lys Leu Leu Thr Lys Met Gln  
                     130                    135                    140  
  
       <210> 1231  
       <211> 140  
 60 <212> PRT  
       <213> Homo sapiens  
  
       <400> 1231

Leu Ala Arg Ala Tyr Ser Ile Val Ile Arg Gln Ile Ser Asp Leu Met  
 1 5 10 15  
 Gly Leu Ile Pro Lys Tyr Asn His Leu Val Tyr Ser Gln Ile Pro Ala  
 20 25 30  
 5 Ala Val Lys Leu Thr Tyr Gln Asp Ala Val Asn Leu Gln Asn Tyr Val  
 35 40 45  
 Glu Glu Lys Leu Ile Pro Thr Trp Asn Trp Met Val Ser Ile Met Asp  
 50 55 60  
 Ser Thr Glu Ala Gln Leu Arg Tyr Gly Ser Ala Leu Ala Ser Ala Gly  
 65 70 75 80  
 10 Asp Pro Gly His Pro Asn His Pro Leu His Ala Ser Gln Asn Ser Ala  
 85 90 95  
 Arg Arg Glu Arg Met Thr Ala Arg Glu Glu Ala Ser Leu Arg Thr Leu  
 100 105 110  
 15 Glu Gly Arg Arg Arg Ala Thr Leu Leu Ser Ala Arg Gln Gly Met Met  
 115 120 125  
 Ser Ala Arg Gly Asp Phe Leu Asn Tyr Ala Leu Leu  
 130 135 140  
  
 20 <210> 1232  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens  
  
 25 <400> 1232  
 Asp Asp Ile Glu Gln Glu Thr Phe Met Leu Asp Glu Pro Leu Glu Arg  
 1 5 10 15  
 Thr Thr Asn Ser Ser His Ala Asn Gly Ala Ala Gln Ala Pro Arg Ser  
 20 25 30  
 30 Met Gln Trp Ala Val Arg Asn Thr Gln His Gln Arg Ala Ala Ser Thr  
 35 40 45  
 Ala Pro Ser Ser Thr Ser Thr Pro Ala Ala Ser Ser Ala Gly Leu Ile  
 50 55 60  
 Tyr Ile Asp Pro Ser Asn Leu Arg Arg Ser Gly Thr Ile Ser Thr Ser  
 65 70 75 80  
 35 Ala Ala Ala Ala Ala Ala Ala Leu Glu Ala Ser Asn Ala Ser Ser Tyr  
 85 90 95  
 Leu Thr Ser Ala Ser Ser Leu Ala Arg Ala Tyr Ser Ile Val Ile Arg  
 100 105 110  
 40 Gln Ile Ser Asp Leu Met Gly Leu Ile Pro Lys Tyr Asn His Leu Val  
 115 120 125  
 Tyr Ser Gln Ile Pro Ala Ala Val Lys Leu Leu Thr Lys Met Gln  
 130 135 140  
  
 45 <210> 1233  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens  
  
 50 <400> 1233  
 Phe Phe Gln Phe Lys Arg Trp Xaa Trp Ser Ile Val Glu Lys Met Ser  
 1 5 10 15  
 Met Xaa Asp Xaa Gln Asp Leu Val Tyr Phe Trp Thr Ser Ser Pro Ser  
 20 25 30  
 55 Leu Pro Ala Ser Glu Glu Gly Phe Gln Pro Met Pro Ser Ile Thr Ile  
 35 40 45  
 Arg Pro Pro Asp Asp Gln His Leu Pro Thr Ala Asn Thr Cys Ile Ser  
 50 55 60  
 Arg Leu Tyr Val Pro Leu Tyr Ser Ser Lys Gln Ile Leu Lys Gln Lys  
 65 70 75 80  
 60 Leu Leu Leu Ala Ile Lys Thr Lys Asn Phe Gly Phe Val  
 85 90

<210> 1234  
 <211> 196  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1234  
 Arg Val Pro Val Val Ile Ala Gly Val Val Tyr Cys Gln Glu Ala Leu  
 1 5 10 15  
 Arg Asp Trp Gly Arg Val Thr Ala Ser Ser Thr Gly Ala Met Ala Phe  
 10 20 25 30  
 Leu Arg Ser Met Trp Gly Val Leu Ser Ala Leu Gly Arg Ser Gly Ala  
 35 40 45  
 Glu Leu Cys Thr Gly Cys Gly Ser Arg Leu Arg Ser Pro Phe Ser Phe  
 50 55 60  
 Val Tyr Leu Pro Arg Trp Phe Ser Ser Val Leu Ala Ser Cys Pro Lys  
 15 65 70 75 80  
 Lys Pro Val Ser Ser Tyr Leu Arg Phe Ser Lys Glu Gln Leu Pro Ile  
 85 90 95  
 Phe Lys Ala Gln Asn Pro Asp Ala Lys Thr Thr Glu Leu Ile Arg Arg  
 100 105 110  
 Ile Ala Gln Arg Trp Arg Glu Leu Pro Asp Ser Lys Lys Lys Ile Tyr  
 115 120 125  
 Gln Asp Ala Tyr Arg Ala Glu Trp Gln Val Tyr Lys Glu Glu Ile Ser  
 130 135 140  
 Arg Phe Lys Glu Gln Leu Thr Pro Ser Gln Ile Met Ser Leu Glu Lys  
 145 150 155 160  
 Glu Ile Met Asp Lys His Leu Lys Arg Lys Ala Met Thr Lys Lys Lys  
 165 170 175  
 Glu Leu Thr Leu Leu Gly Lys Pro Lys Arg Pro Arg Ser Ala Tyr Asn  
 180 185 190  
 Arg Leu Cys Ser  
 195

20

25

30

35

<210> 1235  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 1235  
 Trp Lys Asn Leu Ser Asp Ser Glu Lys Glu Leu Tyr Ile Gln His Ala  
 1 5 10 15  
 Lys Glu Asp Glu Thr Arg Tyr His Asn Glu Met Lys Ser Trp Glu Glu  
 20 25 30  
 Gln Met Ile Glu Val Gly Arg Lys Asp Leu Leu Arg Arg Thr Ile Lys  
 35 40 45  
 Lys Gln Arg Lys Tyr Gly Ala Glu Glu Cys  
 50 55

40

45

50

<210> 1236  
 <211> 196  
 <212> PRT  
 <213> Homo sapiens

<400> 1236  
 Arg Val Pro Val Val Ile Ala Gly Val Val Tyr Cys Gln Glu Ala Leu  
 1 5 10 15  
 Arg Asp Trp Gly Arg Val Thr Ala Ser Ser Thr Gly Ala Met Ala Phe  
 20 25 30  
 Leu Arg Ser Met Trp Gly Val Leu Ser Ala Leu Gly Arg Ser Gly Ala  
 35 40 45  
 Glu Leu Cys Thr Gly Cys Gly Ser Arg Leu Arg Ser Pro Phe Ser Phe  
 50 55 60  
 Val Tyr Leu Pro Arg Trp Phe Ser Ser Val Leu Ala Ser Cys Pro Lys

55

60

[illegible]

20           <210> 1237  
              <211> 225  
              <212> PRT  
              <213> Homo sapiens

[illegible]

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<210> 1238
<211> 95
<212> PRT
<213> Homo sapiens

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<400> 1238

Gly	Gly	Arg	Gln	Ser	Leu	Pro	Leu	Thr	Leu	Tyr	Phe	Gln	Gly	Asp	Thr
1				5					10					15	

Asp Tyr Lys Lys Arg Asn Ser Ala Leu Gly Lys Lys Ala Leu Pro Gly  
                   20                  25                  30  
 Leu Thr Val Gln His Ser Leu Ala Ser Gly Ile Leu Ser Leu Leu Thr  
                   35                  40                  45  
 5 Val Tyr Ile Thr Thr Leu Val His Ser Gly His Phe Ser Phe Leu Glu  
                   50                  55                  60  
 Ser Pro Val Asp Leu Thr Pro Met Pro Met Ile Phe Phe Ser Trp Leu  
   65                  70                  75                  80  
 10 Ile Lys Asn Ser Leu Phe Leu Leu Arg His Pro Cys His Tyr Lys  
                   85                  90                  95

&lt;210&gt; 1239

&lt;211&gt; 113

&lt;212&gt; PRT

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 1239

Thr Glu Val Arg Ala Ser Gln Val Val Phe Xaa Thr Ser Val Ser Pro  
   1                  5                  10                  15  
 20 Lys Xaa Ser Ser Leu Gln Xaa Asp Met Arg Xaa Xaa Arg Gly Lys Lys  
                   20                  25                  30  
 Val Phe Xaa Val Leu His Leu Gln Lys Xaa Val Xaa Ser Gln Asp Pro  
                   35                  40                  45  
 25 Leu Gly Ala Thr Arg Gly Pro Ala Gln Cys Gln Gln Trp Thr Pro Pro  
                   50                  55                  60  
 Ala Gly Thr Pro Pro Gly Ala Arg Ala Gly Pro Gly Val Val Ala  
   65                  70                  75                  80  
 Cys Thr Glu Gly Thr Thr Tyr Val Cys Ser Val Cys Pro Ala Lys Phe  
                   85                  90                  95  
 30 Asp Gln Ile Glu Gln Phe Asn Asp His Met Arg Met His Val Ser Asp  
                   100                  105                  110  
 Gly

35 &lt;210&gt; 1240

&lt;211&gt; 177

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

40 &lt;400&gt; 1240

Ala Ala Cys Cys Gly Thr Ala Ala Ala Phe Leu Leu Gly Arg Arg Gly  
   1                  5                  10                  15  
 Gln Val Ala Gly Pro Arg Gln Gln Ser Pro Pro Gly Pro Gly Gly Ala  
                   20                  25                  30  
 45 Ala Glu Arg Ala Ala Gly His Ala Arg Pro His Leu Arg Tyr Glu Val  
                   35                  40                  45  
 Gln Arg Leu Pro Glu Gln Ala Gly Lys Ala Ala Gln Lys Gly Asn Cys  
   50                  55                  60  
 Pro Ser Pro Lys Gln Ala Glu Pro Ala Ala Gln Pro Ala Pro Ala His  
   65                  70                  75                  80  
 50 Gly Ala Arg Leu Gly Arg Leu Arg Arg Gly Arg Ser Cys Ala Gly Ala  
                   85                  90                  95  
 Arg Arg Arg Ala Lys Lys Ser Phe Arg Gly Trp Arg Leu Phe Cys Ser  
                   100                  105                  110  
 55 Gln Gly Lys Gly Arg Gly Ala His Ala Glu Thr Xaa Xaa Val Glu Glu  
                   115                  120                  125  
 Glu Xaa Pro Xaa Lys Ala Pro Gly Arg Arg Ser Ser Pro Xaa Ala Phe  
   130                  135                  140  
 Gly Val Xaa Arg Ala Asn Xaa Glu Pro Gly Arg Gly Pro Trp Gly Arg  
   145                  150                  155                  160  
 60 Lys Ala Thr Pro Arg Arg Pro Trp Ala Phe Glu Phe Lys Ile Phe Phe  
                   165                  170                  175  
 Gln

5           <210> 1241  
           <211> 270  
           <212> PRT  
           <213> Homo sapiens

10           <400> 1241  
 Leu Lys Glu Val Pro Asp Tyr Leu Asp His Ile Lys His Pro Met Asp  
 1           5           10           15  
 Phe Ala Thr Met Arg Lys Arg Leu Glu Ala Gln Gly Tyr Lys Asn Leu  
           20           25           30  
 His Glu Phe Glu Glu Asp Phe Asp Leu Ile Ile Asp Asn Cys Met Lys  
           35           40           45  
 15 Tyr Asn Ala Arg Asp Thr Val Phe Tyr Arg Ala Ala Val Arg Leu Arg  
           50           55           60  
 Asp Gln Gly Gly Val Val Leu Arg Gln Ala Arg Arg Glu Val Asp Ser  
 65           70           75           80  
 Ile Gly Leu Glu Glu Ala Ser Gly Met His Leu Pro Glu Arg Pro Ala  
 20           85           90           95  
 Ala Ala Pro Arg Arg Pro Phe Ser Trp Glu Asp Val Asp Arg Leu Leu  
           100           105           110  
 Asp Pro Ala Asn Arg Ala His Leu Gly Leu Glu Glu Gln Leu Arg Glu  
           115           120           125  
 25 Leu Leu Asp Met Leu Asp Leu Thr Cys Ala Met Lys Ser Ser Gly Ser  
           130           135           140  
 Arg Ser Lys Arg Ala Lys Leu Leu Lys Lys Glu Ile Ala Leu Leu Arg  
 145           150           155           160  
 Asn Lys Leu Ser Gln Gln His Ser Gln Pro Leu Pro Thr Gly Pro Gly  
 30           165           170           175  
 Leu Glu Gly Phe Glu Glu Asp Gly Ala Ala Leu Gly Pro Gly Gly Gly  
           180           185           190  
 Arg Arg Ser Pro Ser Glu Val Gly Asp Ser Ser Ala Ala Lys Glu Lys  
           195           200           205  
 35 Val Ala Glu His Met Arg Arg Leu Xaa Xaa Trp Arg Arg Ser Xaa Xaa  
           210           215           220  
 Glu Lys Arg Leu Asp Ala Gly Leu His Gln Xaa Leu Leu Gly Cys Xaa  
 225           230           235           240  
 Glu Pro Thr Xaa Asn Pro Ala Gly Gly Leu Gly Gly Gly Arg Pro His  
 40           245           250           255  
 Pro Asp Asp Leu Gly Pro Ser Ser Ser Arg Phe Ser Phe Lys  
           260           265           270

45           <210> 1242  
           <211> 66  
           <212> PRT  
           <213> Homo sapiens

50           <400> 1242  
 Met Phe Asn Asn Phe Val Asn His Ala Leu Tyr Xaa Glu Tyr His Leu  
 1           5           10           15  
 Phe Asn Lys Thr Gly Cys Lys Phe Thr Met Thr Asn Val Tyr Phe Lys  
           20           25           30  
 Lys Glu Asn Xaa Ile Ile Leu Asn Gly Thr Leu Trp Lys Glu Gly Arg  
 55           35           40           45  
 Ile Lys Leu Cys Cys Asp Ile Thr Cys Arg Ser Pro Lys Thr Leu Arg  
           50           55           60  
 Cys Pro  
 65

60           <210> 1243  
           <211> 85  
           <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1243

5 Ser Tyr Ala Val Thr Ser Leu Ala Asp His Gln Lys His Ser Ala Ala  
 1 5 10 15  
 Arg Asp Arg Arg Trp Val Cys Pro Arg Ser Arg Arg Pro Ala His Leu  
 20 25 30  
 Lys Pro Arg Arg Cys Ala Ser Gln Arg Ile Ile Tyr Cys Arg Lys Cys  
 35 40 45  
 10 Ile His Leu Leu Tyr Asn Glu Lys Tyr Ile Cys Lys Gly Ile Leu Ile  
 50 55 60  
 Cys Ile Phe Ile Gln Ala His Lys Asn Ser Thr Trp Leu Gly Ser Arg  
 65 70 75 80  
 15 Met His Cys Ile Val  
 85

&lt;210&gt; 1244

&lt;211&gt; 56

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 1244

25 Val Val Leu Xaa Val Lys Ser Met Ile Tyr Lys Ile Ile Lys His Ser  
 1 5 10 15  
 Lys Val Phe Lys Lys Lys Leu His Ile Lys Xaa Ser Asp Ala Xaa Thr  
 20 25 30  
 Pro Xaa Leu Gly Asp Val Arg Xaa Xaa Xaa Leu Gly Leu Pro Gly Arg  
 35 40 45  
 30 Ala Pro Pro Leu Tyr Arg Ala Lys  
 50 55

&lt;210&gt; 1245

&lt;211&gt; 227

&lt;212&gt; PRT

35 &lt;213&gt; Homo sapiens

&lt;400&gt; 1245

40 Gly Asp Pro Val Gly Arg Glu Glu Gly Gly Lys Met Val Leu Glu Ser  
 1 5 10 15  
 Thr Met Val Cys Val Asp Asn Ser Glu Tyr Met Arg Asn Gly Asp Phe  
 20 25 30  
 Leu Pro Thr Arg Leu Gln Ala Gln Asp Ala Val Asn Ile Val Cys  
 35 40 45  
 45 His Ser Lys Thr Arg Ser Asn Pro Glu Asn Asn Val Gly Leu Ile Thr  
 50 55 60  
 Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu Thr Pro Asp Thr Gly  
 65 70 75 80  
 Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro Lys Gly Lys Ile Thr  
 85 90 95  
 50 Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala Leu Lys His Arg Gln  
 100 105 110  
 Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe Val Gly Ser Pro Val  
 115 120 125  
 55 Glu Asp Asn Glu Lys Asp Leu Val Lys Leu Ala Lys Arg Leu Lys Lys  
 130 135 140  
 Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly Glu Glu Glu Val Asn  
 145 150 155 160  
 Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu Asn Gly Lys Asp Gly  
 165 170 175  
 60 Thr Gly Ser Tyr Leu Val Thr Val Pro Ser Gly Pro Ser Leu Ala Asp  
 180 185 190  
 Ala Leu Ile Ser Ser Xaa Ile Leu Ala Gly Glu Xaa Gly Ala Leu Ala  
 195 200 205



Gly Ser Trp Val Pro Val Thr Phe Glu Phe Trp Ser Xaa Ile Pro Xaa  
 210 215 220  
 Leu Asp Pro  
 225

5  
 <210> 1246  
 <211> 141  
 <212> PRT  
 <213> Homo sapiens

10  
 <400> 1246  
 Gln Asn Thr Ala Lys Val Asn Cys Val Gly Glu Pro His Leu His Arg  
 1 5 10 15  
 Asn Gln Ile Asn Glu Phe Arg Gly Tyr Asp Tyr Ser Asn Leu Arg Ala  
 20 25 30  
 His Gln Lys Gln Ala Ser Arg Ser Gln Phe Ala Ser Val Cys Leu Ser  
 35 40 45  
 Gly Asp Lys Trp Glu Asn Met Val Pro Pro Val Arg Asp Pro Leu Ser  
 50 55 60  
 20 Cys Ala Ala His Ser Thr Thr Ser Leu Cys Cys Phe His Gln Ala Glu  
 65 70 75 80  
 Thr Leu Pro Tyr Gly Val Tyr Gly Leu Leu Pro Val His Gln Cys Asp  
 85 90 95  
 Arg Lys Asp Ser Cys His Tyr Cys Pro Trp Leu Gln Phe Lys Gly Ile  
 100 105 110  
 25 Gln Cys Arg Cys Lys Phe Tyr Gly Thr Ile Phe Ile Gly Gly Phe Gly  
 115 120 125  
 Gln Asn Ala Val Val Val Gln Leu Ile Asn Thr Asn Cys  
 130 135 140

30  
 <210> 1247  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

35  
 <400> 1247  
 Gly Pro Thr Arg Ser Arg Pro Arg Gly Val Asn Leu Pro Leu Cys Ala  
 1 5 10 15  
 Ser Val Glu Thr Ser Gly Lys Thr Trp Ser His Leu Cys Glu Thr Pro  
 20 25 30  
 Cys Pro Val Leu Leu Thr Gln Gln His Leu Cys Val Ala Phe Thr Arg  
 35 40 45  
 Leu Arg Pro Tyr Pro Met Gly Tyr Met Gly Phe Tyr Leu Cys Thr Ser  
 50 55 60  
 45 Val Thr Gly Lys Ile His Val Thr Thr Val Arg Gly Tyr Asn Ser Lys  
 65 70 75 80  
 Val Ser Asn Val Ala Val Asn Phe Met Ala Leu Phe Leu Leu Glu Asp  
 85 90 95  
 Leu Val Arg Met Gln Leu Leu Tyr Asn Ser  
 100 105

50  
 <210> 1248  
 <211> 194  
 <212> PRT  
 <213> Homo sapiens

55  
 <400> 1248  
 Pro Lys Glu Glu Asp Met Glu Val Asp Ile Pro Ala Val Lys Val Lys  
 1 5 10 15  
 Glu Glu Pro Arg Asp Glu Glu Glu Glu Ala Lys Met Lys Ala Pro Pro  
 20 25 30  
 Lys Ala Ala Arg Lys Thr Pro Gly Leu Pro Lys Asp Val Ser Val Ala  
 35 40 45

Glu Leu Leu Arg Glu Leu Ser Leu Thr Lys Glu Glu Glu Leu Leu Phe  
 50 55 60  
 Leu Gln Leu Pro Asp Thr Leu Pro Gly Gln Pro Pro Thr Gln Asp Ile  
 65 70 75 80  
 5 Lys Pro Ile Lys Thr Glu Val Gln Gly Glu Asp Gly Gln Val Val Leu  
 85 90 95  
 Ile Lys Gln Glu Lys Asp Arg Glu Ala Lys Leu Ala Glu Asn Ala Cys  
 100 105 110  
 10 Thr Leu Ala Asp Leu Thr Glu Gly Gln Val Gly Lys Leu Leu Ile Arg  
 115 120 125  
 Lys Ser Gly Arg Val Gln Leu Leu Gly Lys Val Thr Leu Asp Val  
 130 135 140  
 Thr Met Gly Thr Ala Cys Ser Phe Leu Gln Glu Leu Val Ser Val Gly  
 145 150 155 160  
 15 Leu Gly Asp Ser Arg Thr Gly Glu Met Thr Val Leu Gly His Val Lys  
 165 170 175  
 His Lys Leu Val Cys Ser Pro Asp Phe Glu Ser Leu Leu Asp His Lys  
 180 185 190  
 His Arg

20

&lt;210&gt; 1249

&lt;211&gt; 106

&lt;212&gt; PRT

25

&lt;213&gt; Homo sapiens

&lt;400&gt; 1249

Gln Gly Gln Val Pro Ser Ser Lys Asp Val Pro Ser Pro Arg Cys Arg  
 1 5 10 15  
 30 Lys Val Thr Val Pro Phe Thr Ala Ala Val Gly Gly Asn Pro Gly Gly  
 20 25 30  
 Pro Gly Thr Met Val Ala Lys Gly Trp Asn Glu Trp Ala Gln Met Gly  
 35 40 45  
 35 Pro Leu Leu Gly Xaa Gln Asn Ser Arg Thr Lys Cys Xaa Gly Gln Gly  
 50 55 60  
 Xaa Asn Pro Gly Ala Gln Gly Ala Xaa Leu Pro Ser Pro Xaa Tyr Phe  
 65 70 75 80  
 Tyr Arg Xaa Phe Gly Ile Pro Xaa Gly Ile Xaa Lys Ser Arg Gly Xaa  
 85 90 95  
 40 Tyr Xaa Phe Val Ala Tyr Val Phe Pro Arg  
 100 105

&lt;210&gt; 1250

&lt;211&gt; 113

&lt;212&gt; PRT

45

&lt;213&gt; Homo sapiens

&lt;400&gt; 1250

Asp Ile Asn Thr Lys Ile Asn Ser Arg Ala Lys Ser Pro Ala Ala Arg  
 1 5 10 15  
 50 Met Cys His Leu His Ala Ala Gly Arg Ser Leu Cys His Ser Gln Leu  
 20 25 30  
 Leu Trp Glu Glu Thr Leu Gly Asp Leu Glu Gln Trp Leu Pro Lys Ala  
 35 40 45  
 55 Gly Met Ser Gly Leu Lys Trp Gly Pro Phe Trp Gly Xaa Lys Ile Gln  
 50 55 60  
 Glu Gln Asn Xaa Leu Asp Lys Ala Xaa Thr Arg Gly Pro Lys Ala Pro  
 65 70 75 80  
 Xaa Phe Leu His Leu Xaa Ile Phe Thr Xaa Gly Leu Gly Ser Gln Xaa  
 85 90 95  
 60 Gly Xaa Lys Asn Gln Gly Glu Xaa Thr Xaa Leu Trp Leu Thr Phe Ser  
 100 105 110  
 Gln

5           <210> 1251  
           <211> 114  
           <212> PRT  
           <213> Homo sapiens  
  
           <400> 1251  
 10   Ala His Ser Phe Gln Pro Leu Ala Thr Ile Val Pro Gly Pro Pro Gly  
       1                   5                   10                   15  
       Phe Pro Pro Thr Ala Ala Val Asn Gly Thr Val Thr Phe Leu Gln Arg  
           20                   25                   30  
       Gly Asp Gly Thr Ser Leu Leu Leu Gly Thr Trp Pro Cys Tyr Leu Phe  
           35                   40                   45  
 15   Leu Tyr Leu Cys Leu Asn Leu Phe His Leu Met His Pro Pro Arg Val  
       50                   55                   60  
       Asp Gly Glu Gly Leu Cys Glu Gly Ala Gly Phe Ser Trp Cys Leu Leu  
       65                   70                   75                   80  
       Gly Cys Arg Gly Arg Lys Arg Val Asp Cys Ser Phe Cys Trp Cys Ser  
           85                   90                   95  
 20   Pro Arg Pro Pro Gly Gly Ser Ile Gly Glu Arg Ala Arg Ile Glu Ser  
           100                   105                   110  
       Glu Thr  
  
 25  
           <210> 1252  
           <211> 126  
           <212> PRT  
           <213> Homo sapiens  
  
 30           <400> 1252  
       Ser Glu Arg Ser Ser Met Ser Val Gly Leu Gly Arg Ser Gln Leu Asp  
       1                   5                   10                   15  
       Ser Lys Gly Gly Val Val Gly Gly Thr Ile Asp Val Asn Ala Leu Glu  
           20                   25                   30  
       Met Xaa Ala His Ile Ser Glu His Pro Asn Gln Gln Pro Xaa His Lys  
           35                   40                   45  
       Ile Gln Ile Thr Met Gly Ser Thr Glu Ala Arg Val Asp Tyr Met Gly  
           50                   55                   60  
 40   Ser Ser Ile Leu Met Gly Ile Phe Ser Asn Ala Asp Leu Lys Leu Gln  
       65                   70                   75                   80  
       Asp Glu Trp Lys Val Asn Leu Tyr Asn Thr Leu Asp Ser Ser Ile Thr  
           85                   90                   95  
       Asp Lys Ser Glu Ile Phe Val Xaa Trp Arg Phe Glu Xaa Gly Ile Phe  
           100                   105                   110  
 45   Phe Gln Xaa Asn Xaa Xaa Xaa Xaa Gln Pro His Xaa Ile Trp  
           115                   120                   125  
  
           <210> 1253  
 50           <211> 87  
           <212> PRT  
           <213> Homo sapiens  
  
           <400> 1253  
 55   Lys Ser Leu Phe Phe Gly Gly Arg Leu Arg Asn Trp Ser Pro Arg Lys  
       1                   5                   10                   15  
       Thr Glu Xaa Val Cys Trp Ile Lys Leu Leu Cys Glu Lys Ile Xaa Xaa  
           20                   25                   30  
       Ala Ser Phe Leu Phe Phe Thr Arg Xaa Gly Val Val Xaa Leu Xaa Xaa  
           35                   40                   45  
 60   Xaa Xaa Xaa Gly Lys Ile Ser His Xaa Gln Ile Ser Xaa Gly Arg Lys  
       50                   55                   60  
       Ser His Phe Tyr Gln Leu Cys Leu Asn Pro Met Tyr Tyr Thr Ser Leu

494

20 25 30  
 Ala Thr Leu Asn Cys Ser Val Arg Gly Asn Pro Lys Pro Lys Ile Thr  
 35 40 45  
 Trp Met Lys Asn Lys Val Ala Ile Val Asp Asp Pro Arg Tyr Arg Met  
 5 50 55 60  
 Phe Ser Asn Gln Gly Val Cys Thr Leu Glu Ile Arg Lys Pro Ser Pro  
 65 70 75 80  
 Tyr Asp Gly Gly Thr Tyr Cys Cys Lys Ala Val Asn Asp Leu Gly Thr  
 85 90 95  
 10 Val Glu Ile Glu Cys Lys Leu Glu Val Lys Gly Gly Leu Ser Xaa Cys  
 100 105 110  
 Arg Leu Leu Leu Gln Xaa Val Pro Pro Asn Ile Ile Asp Ser Tyr Xaa  
 115 120 125  
 Arg Asp Leu His Ser Ser Asn Pro Glu Glu Tyr  
 15 130 135

&lt;210&gt; 1257

&lt;211&gt; 210

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 1257

Cys Leu Ser Leu Pro Ser Ser Trp Asp His Arg Gln Leu Tyr Leu Ser  
 1 5 10 15  
 25 Met Asn Ile Asp Asp Lys Leu Glu Gly Leu Phe Leu Lys Cys Gly Gly  
 20 25 30  
 Ile Asp Glu Met Gln Ser Ser Arg Thr Met Val Val Met Gly Gly Val  
 35 40 45  
 Ser Gly Gln Ser Thr Val Ser Gly Glu Leu Gln Asp Ser Val Leu Gln  
 30 50 55 60  
 Asp Arg Ser Met Pro His Gln Glu Ile Leu Ala Ala Asp Glu Val Leu  
 65 70 75 80  
 Gln Glu Ser Glu Met Arg Gln Gln Asp Met Ile Ser His Asp Glu Leu  
 85 90 95  
 35 Met Val His Glu Glu Thr Val Lys Asn Asp Glu Glu Gln Met Glu Thr  
 100 105 110  
 His Glu Arg Leu Pro Gln Gly Leu Gln Tyr Ala Leu Asn Val Pro Ile  
 115 120 125  
 Ser Val Lys Gln Glu Ile Thr Phe Thr Asp Val Ser Glu Gln Leu Met  
 40 130 135 140  
 Arg Asp Lys Lys Gln Ile Arg Glu Pro Val Asp Leu Gln Lys Lys Lys  
 145 150 155 160  
 Lys Arg Lys Gln Arg Ser Pro Ala Lys Ile Leu Thr Ile Asn Glu Asp  
 165 170 175  
 45 Gly Ser Leu Gly Leu Lys Thr Pro Lys Ser His Val Cys Glu His Cys  
 180 185 190  
 Asn Ala Ala Phe Arg Thr Asn Tyr Pro Tyr Arg Asp Met Ser Ser Ser  
 195 200 205  
 Tyr Arg  
 50 210

&lt;210&gt; 1258

&lt;211&gt; 198

&lt;212&gt; PRT

55 &lt;213&gt; Homo sapiens

&lt;400&gt; 1258

Ser Phe Ser Asp Ser Asp Asp Asp Ser Cys Leu Trp Lys Arg Lys Arg  
 1 5 10 15  
 60 Gln Lys Cys Phe Asn Pro Pro Pro Lys Pro Glu Pro Phe Gln Phe Gly  
 20 25 30  
 Gln Ser Ser Gln Lys Pro Pro Val Ala Gly Gly Lys Lys Ile Asn Asn  
 35 40 45

Ile Trp Gly Ala Val Leu Gln Glu Gln Asn Gln Asp Ala Val Ala Thr  
 50 55 60  
 Glu Leu Gly Ile Leu Gly Met Glu Gly Thr Ile Asp Arg Ser Arg Gln  
 65 70 75 80  
 5 Ser Glu Thr Tyr Asn Tyr Leu Leu Ala Lys Lys Leu Arg Lys Glu Ser  
 85 90 95  
 Gln Glu His Thr Lys Asp Leu Asp Lys Glu Leu Asp Glu Tyr Met His  
 100 105 110  
 10 Gly Gly Lys Lys Met Gly Ser Lys Glu Glu Glu Asn Gly Gln Gly His  
 115 120 125  
 Leu Lys Arg Lys Arg Pro Val Lys Asp Arg Leu Gly Asn Arg Pro Glu  
 130 135 140  
 Met Asn Tyr Lys Gly Arg Tyr Gln Ile Thr Ala Glu Asp Ser Gln Glu  
 145 150 155 160  
 15 Lys Val Ala Asp Glu Ile Ser Phe Arg Leu Gln Glu Pro Lys Lys Asp  
 165 170 175  
 Leu Ile Ala Pro Ser Ser Glu Asp Tyr Trp Tyr Lys Lys Ala Ile Glu  
 180 185 190  
 Leu Leu Met Glu Thr Arg  
 195  
 20  
 <210> 1259  
 <211> 103  
 <212> PRT  
 25 <213> Homo sapiens  
 <400> 1259  
 Arg Gln Ser Leu Ala Leu Ser Pro Arg Leu Glu Tyr Ser Gly Thr Ile  
 1 5 10 15  
 30 Ser Ala His Cys Asn Leu Cys Leu Pro Gly Ser Gly Asp Ser Pro Ala  
 20 25 30  
 Ser Ala Ser Arg Val Ala Gly Ile Ile Gly Met Glu Asn His Thr Trp  
 35 35 40 45  
 Leu Xaa Phe Val Phe Leu Val Xaa Met Lys Phe His His Val Gly Leu  
 50 55 60  
 35 Ala Gly Leu Lys Leu Leu Thr Ser Ser Asp Leu Pro Ala Leu Val Ser  
 65 70 75 80  
 Gln Ser Val Gly Ile Thr Gly Val Ser His Arg Ala Trp Pro Met Leu  
 85 90 95  
 40 Val Phe Ile Leu Lys Ile Ala  
 100  
 <210> 1260  
 <211> 98  
 45 <212> PRT  
 <213> Homo sapiens  
 <400> 1260  
 Phe Thr Ala Lys Ile Asn Leu Lys Lys Gln Thr Asn Leu Gln Met Val  
 1 5 10 15  
 50 Cys Tyr Asp Leu Asp Lys Thr Asp Tyr Gln Leu Val Ile Leu Ile Ile  
 20 25 30  
 Ser Thr Cys Asn Lys Ile Glu Lys Leu Asn Pro Val Leu Tyr Thr Leu  
 35 40 45  
 55 Lys Val Phe Leu Xaa Lys Tyr Ile Phe Lys Met Phe Tyr Gln Leu His  
 50 55 60  
 Phe Phe Pro His Ile Phe Leu Asn Gln Glu Lys Gln Xaa Gly Leu Phe  
 65 70 75 80  
 Leu Gln Glu Phe Ser Trp Phe Ile Gln Val Ala Lys Thr Leu Ala Ile  
 85 90 95  
 60 Ser Ser

<210> 1261  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1261  
 Glu Leu Ala Arg Leu Gln Val Asp Thr Ser Gly Ser Lys Ala Ala Phe  
 1 5 10 15  
 Glu Pro Ala Ile Asp Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu  
 10 20 25 30  
 Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu  
 35 40 45  
 Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu  
 50 55 60  
 Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His  
 15 65 70 75 80  
 Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val  
 85 90 95  
 Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro  
 100 105 110  
 Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro  
 115 120 125  
 Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser  
 130 135 140  
 Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala  
 145 150 155 160  
 Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser  
 165 170 175  
 Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val  
 180 185 190  
 Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly  
 195 200 205  
 Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys  
 210 215 220  
 Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met  
 225 230 235 240  
 Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro  
 245 250 255  
 Ala Ile Glu Met Gln Lys Val Cys Ser Lys  
 260 265

<210> 1262  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

45

<400> 1262  
 Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln  
 1 5 10 15  
 Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His  
 20 25 30  
 Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys  
 35 40 45  
 Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln  
 50 55 60  
 Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys  
 65 70 75 80  
 Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser  
 85 90 95  
 Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile  
 100 105 110  
 Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys  
 115 120 125

Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser  
 130 135 140  
 Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu  
 145 150 155 160  
 5 Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn  
 165 170 175  
 Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro  
 180 185 190  
 10 Leu Phe Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Xaa Asn  
 195 200 205  
 Tyr Ala Gly Asp Ala Xaa Arg Glu Asn Thr Leu Val Ser Glu His Ala  
 210 215 220  
 Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His  
 225 230 235 240  
 15 Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln  
 245 250 255  
 Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp  
 260 265 270  
 20 Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser  
 275 280 285  
 Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His  
 290 295 300  
 Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu  
 305 310 315 320  
 25 Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Arg Lys Gln Lys Gln Lys  
 325 330 335

<210> 1263  
 <211> 225  
 30 <212> PRT  
 <213> Homo sapiens

<400> 1263  
 35 Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met  
 1 5 10 15  
 Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr  
 20 25 30  
 Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr  
 35 40 45  
 40 Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln  
 50 55 60  
 Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys  
 65 70 75 80  
 45 Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys  
 85 90 95  
 Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu  
 100 105 110  
 Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ile Cys  
 115 120 125  
 50 Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu  
 130 135 140  
 Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser  
 145 150 155 160  
 Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser  
 165 170 175  
 55 Leu Cys Glu Thr Val Ser Xaa Arg Met Cys Val Ser Gln Gly Cys Ala  
 180 185 190  
 Ser Lys Arg Asn Arg Leu Asn Asn Gly Lys Leu Glu Xaa Leu Leu Leu  
 195 200 205  
 60 Arg Xaa Leu Leu Lys Leu Thr Ala Asp Glu Ser Ser Xaa Pro Leu Lys  
 210 215 220  
 Pro  
 225



<210> 1264  
 <211> 153  
 <212> PRT  
 5 <213> Homo sapiens

<400> 1264  
 Arg Gln Ser Leu Thr Leu Ser Leu Arg Leu Glu Cys Ser Ser Gly Ile  
 1 5 10 15  
 10 Ser Ala His Leu Pro Leu Gly Phe Lys Pro Phe Ser Cys Leu Ser Leu  
 20 25 30  
 Pro Ser Ser Trp Asp Tyr Arg Gly Val His His His Asp His Leu Ile  
 35 40 45  
 15 Phe Ser Cys Leu Phe Cys Phe Phe Gly Phe Cys Phe Phe Leu Xaa Trp  
 50 55 60  
 Ser Leu Ser Leu Ser Pro Arg Leu Glu Cys Ser Ser Gly Ile Ser Ala  
 65 70 75 80  
 His Leu Pro Pro Gly Phe Lys Pro Phe Ser Cys Leu Ser Leu Pro Ser  
 85 90 95  
 20 Ser Trp Asp Tyr Arg Gly Val His His His Ala His Leu Ile Phe Ser  
 100 105 110  
 Cys Phe Xaa Phe Leu Val Leu Phe Xaa Thr Xaa Ser Cys Ser Val Ala  
 115 120 125  
 25 Gln Ala Gly Val Xaa Trp Arg Asp Leu Ser Ser Leu Gln Ala Pro Pro  
 130 135 140  
 Pro Arg Phe Thr Pro Phe Cys Tyr Glu  
 145 150

<210> 1265  
 30 <211> 223  
 <212> PRT  
 <213> Homo sapiens

<400> 1265  
 35 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp  
 1 5 10 15  
 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu  
 20 25 30  
 40 Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu  
 35 40 45  
 Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met  
 50 55 60  
 Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr  
 65 70 75 80  
 45 Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile  
 85 90 95  
 Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu  
 100 105 110  
 Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys  
 115 120 125  
 50 Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val  
 130 135 140  
 Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile  
 145 150 155 160  
 55 Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu  
 165 170 175  
 Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu  
 180 185 190  
 Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro  
 195 200 205  
 60 Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Val Cys Xaa Lys  
 210 215 220

<210> 1266  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1266  
 Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val  
 1 5 10 15  
 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile  
 20 25 30  
 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu  
 35 40 45  
 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr  
 50 55 60  
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Pro  
 65 70 75 80  
 Ser Asn Phe Pro Phe Ile Leu Ser Ile Ser Phe  
 85 90

20

<210> 1267  
 <211> 171  
 <212> PRT  
 <213> Homo sapiens

25

<400> 1267  
 Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys  
 1 5 10 15  
 Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu  
 20 25 30  
 Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys  
 35 40 45  
 Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp  
 50 55 60  
 Gly Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys  
 65 70 75 80  
 Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu  
 85 90 95  
 Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro  
 100 105 110  
 Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln  
 115 120 125  
 Met Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp  
 130 135 140  
 Asp Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val  
 145 150 155 160  
 Pro Arg Leu His Ile Lys Lys Lys Trp Ile Lys  
 165 170

40

<210> 1268  
 <211> 169  
 <212> PRT  
 <213> Homo sapiens

50

<400> 1268  
 Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu  
 1 5 10 15  
 Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys  
 20 25 30  
 Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp  
 35 40 45  
 Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys  
 50 55 60  
 Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu  
 65 70 75 80

60

500

65 70 75 80  
 Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro  
 85 90 95  
 Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu  
 100 105 110  
 5 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp  
 115 120 125  
 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu  
 130 135 140  
 10 Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu  
 145 150 155 160  
 Glu Gly Ser Pro Val Lys Asp Gly Phe  
 165  
 15 <210> 1269  
 <211> 196  
 <212> PRT  
 <213> Homo sapiens  
 20 <400> 1269  
 Arg Gln Lys Leu Asn His Xaa His Pro Arg Leu Ala Ser Ala Gly Gln  
 1 5 10 15  
 Ala His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe  
 20 25 30  
 25 His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val  
 35 40 45  
 Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Xaa Glu  
 50 55 60  
 30 Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly  
 65 70 75 80  
 Asp Ala Xaa Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp  
 85 90 95  
 Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln  
 100 105 110  
 35 Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Xaa Xaa  
 115 120 125  
 Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln  
 130 135 140  
 40 Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr  
 145 150 155 160  
 Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys  
 165 170 175  
 Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg  
 180 185 190  
 45 Ile Tyr Gln Tyr  
 195  
 <210> 1270  
 <211> 106  
 50 <212> PRT  
 <213> Homo sapiens  
 <400> 1270  
 Ile Ser Pro His Phe Ser Leu Leu Gly Asp Asp Val Ala Phe Ser Ser  
 1 5 10 15  
 Gln Glu Asn Glu Tyr Gln Leu Leu Ser Cys Phe Cys Cys Gln Leu Ser  
 20 25 30  
 Tyr Val His Glu Leu Ile Ala Val Glu Ala Thr Tyr Phe Cys Phe Val  
 35 40 45  
 60 Val Glu Ile Ile Ser Asp Leu Xaa Thr Pro Ala Val Gln Cys Val Cys  
 50 55 60  
 Ser His Tyr Leu Val Arg Phe Asp Thr Cys Val Gln Leu Pro Ser Phe  
 65 70 75 80

Asp Thr Val Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met  
                     85                    90                    95  
 Tyr Phe Leu Leu Xaa His Leu Arg His Asn  
                     100                    105

5

<210> 1271  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

10

<400> 1271  
 Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys  
   1                    5                    10                    15  
 Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu  
                     20                    25                    30  
 Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys  
                     35                    40                    45  
 Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys Asp  
                     50                    55                    60  
 Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys  
   65                    70                    75                    80  
 Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu  
                     85                    90                    95  
 Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro  
                     100                    105                    110  
 Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu  
                     115                    120                    125  
 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp  
                     130                    135                    140  
 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Xaa Lys Asp Val Cys Phe  
   145                    150                    155                    160  
 Pro Arg Leu Arg Ile Lys Lys Lys  
                     165

20

<210> 1272  
 <211> 91  
 <212> PRT  
 <213> Homo sapiens

35

<400> 1272  
 Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val  
   1                    5                    10                    15  
 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile  
                     20                    25                    30  
 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu  
                     35                    40                    45  
 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr  
                     50                    55                    60  
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Pro  
   65                    70                    75                    80  
 Ser Asn Phe Pro Phe Ile Leu Ser Ile Ser Phe  
                     85                    90

40

<210> 1273  
 <211> 177  
 <212> PRT  
 <213> Homo sapiens

55

<400> 1273  
 Ser Asn Trp Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Xaa Ala  
   1                    5                    10                    15  
 Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr  
                     20                    25                    30

60

Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Xaa Xaa Ala Gln Arg  
 35 40 45  
 Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Xaa  
 50 55 60  
 5 Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln Arg Glu  
 65 70 75 80  
 Xaa Gln Cys Gln Met Lys Glu Ala Glu Xaa Met Tyr Gln Asn Glu Gln  
 85 90 95  
 10 Asp Asn Val Asn Lys His Thr Glu Gln Glu Ser Xaa Asp Gln Lys  
 100 105 110  
 Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln Gln Leu Val  
 115 120 125  
 His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile  
 130 135 140  
 15 His Phe Leu Glu Arg Lys Met Gln His His Xaa Leu Lys Glu Lys Asn  
 145 150 155 160  
 Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile Tyr Gln  
 165 170 175  
 Tyr

20

&lt;210&gt; 1274

&lt;211&gt; 106

&lt;212&gt; PRT

25

&lt;213&gt; Homo sapiens

&lt;400&gt; 1274

Ile Ser Pro His Phe Ser Leu Leu Gly Xaa Asp Val Ala Phe Ser Ser  
 1 5 10 15  
 30 Gln Glu Asn Glu Tyr Gln Leu Leu Ser Cys Phe Cys Cys Gln Leu Ser  
 20 25 30  
 Tyr Val His Glu Leu Ile Ala Val Glu Ala Thr Tyr Phe Cys Phe Val  
 35 40 45  
 Val Glu Ile Ile Ser Asp Leu Xaa Thr Pro Ala Val Gln Cys Val Cys  
 50 55 60  
 35 Ser His Tyr Leu Val Arg Phe Asp Thr Xaa Val Gln Leu Pro Ser Phe  
 65 70 75 80  
 Asp Thr Xaa Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met  
 85 90 95  
 40 Tyr Phe Leu Leu Xaa His Leu Arg His Asn  
 100 105

&lt;210&gt; 1275

&lt;211&gt; 181

&lt;212&gt; PRT

45

&lt;213&gt; Homo sapiens

&lt;400&gt; 1275

Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser  
 1 5 10 15  
 Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu  
 20 25 30  
 Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn  
 35 40 45  
 55 Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro  
 50 55 60  
 Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn  
 65 70 75 80  
 Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala  
 85 90 95  
 60 Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His  
 100 105 110  
 Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln

115 120 125  
 Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp  
 130 135 140  
 Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser  
 5 145 150 155 160  
 Lys Ile Gln Leu Ile Phe Ile Phe Leu Arg Gly Lys Cys Asn Ile Ser  
 165 170 175  
 Pro Lys Arg Glu Lys  
 180  
 10  
 <210> 1276  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 1276  
 Ser Phe Cys Xaa Pro Gln Ala Val Xaa Pro Phe Ser Val Phe Val His  
 1 5 10 15  
 Leu Ser Xaa Ile His Ser Asp Leu Val Xaa Thr Phe Ser Ile Phe Ile  
 20 20 25 30  
 Lys Leu Ser Leu Thr Val Leu Thr Leu Ile Ala Leu Met Leu Gln Asp  
 35 40 45  
 Val Phe Ser Ser Trp Cys Arg Thr Ile  
 50 55  
 25  
 <210> 1277  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens  
 30  
 <400> 1277  
 Phe Phe Glu Ala Gln Lys Xaa Ile Pro Lys Ser Leu Lys Ile Ile Phe  
 1 5 10 15  
 Asn Tyr Ala Gly Asp Gly Phe Lys Arg Lys Xaa Met Gly Phe Arg Thr  
 35 20 25 30  
 Cys Thr Lys Ser Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Xaa Glu  
 35 40 45  
 His Met Phe Gln Asn Glu Gln Asp Asn Val Asn Lys His Ile Glu Gln  
 50 55 60  
 40 Gln Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met  
 65 70 75 80  
 Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Xaa Asn Lys  
 85 90 95  
 Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His  
 45 100 105 110  
 His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His  
 115 120 125  
 Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu  
 130 135 140  
 50 Asn Ser  
 145  
 <210> 1278  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens  
 55  
 <400> 1278  
 Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln  
 60 1 5 10 15  
 Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His  
 20 25 30  
 Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys

35 40 45  
 Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln  
 50 55 60  
 Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys  
 5 65 70 75 80  
 Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser  
 85 90 95  
 Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile  
 100 105 110  
 10 Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys  
 115 120 125  
 Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser  
 130 135 140  
 Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu  
 15 145 150 155 160  
 Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn  
 165 170 175  
 Val Asp Val Ser Ser Thr Asp Ile  
 180  
 20  
 <210> 1279  
 <211> 220  
 <212> PRT  
 <213> Homo sapiens  
 25  
 <400> 1279  
 Ala Phe Glu Pro Ala Ile Asp Met Gln Lys Ser Val Pro Asn Lys Ala  
 1 5 10 15  
 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro  
 20 25 30  
 Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu  
 35 40 45  
 Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala  
 50 55 60  
 35 Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser  
 65 70 75 80  
 Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser  
 85 90 95  
 Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala  
 100 105 110  
 40 Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln  
 115 120 125  
 Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu  
 130 135 140  
 45 Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu  
 145 150 155 160  
 Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Arg Arg  
 165 170 175  
 Met Cys Val Tyr Pro Xaa Leu Ala Xaa Gln Lys Glu Ile Asp Lys Ile  
 180 185 190  
 50 Asn Gly Lys Leu Glu Xaa Arg Tyr Ala Ala Glu Phe Lys Thr Phe Phe  
 195 200 205  
 Ala Met Ile Arg Ala Ser Val Lys Glu Gly Leu Leu  
 210 215 220  
 55  
 <210> 1280  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens  
 60  
 <400> 1280  
 Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala  
 1 5 10 15

His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro  
                   20                  25                  30  
 Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile  
                   35                  40                  45  
 5 Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu  
       50                  55                  60  
 Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys  
   65                  70                  75                  80  
 Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg  
                   85                  90                  95  
 10 Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu  
                   100                  105                  110  
 Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp  
                   115                  120                  125  
 15 Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Xaa Ile Xaa  
                   130                  135                  140  
 Gly Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn  
   145                  150                  155                  160  
 20 Cys Gly Met Lys Val Ser Ile Ser Thr Lys Ala Leu Arg Ile Asp Gly  
                   165                  170                  175  
 His Ala Asn Phe Gln Ser Arg Ala Xaa Arg Glu Ala Ile Cys Leu Arg  
                   180                  185                  190  
 Ala Cys His  
                   195  
 25  
       <210> 1281  
       <211> 209  
       <212> PRT  
       <213> Homo sapiens  
 30  
       <400> 1281  
 Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu  
   1                  5                  10                  15  
 35 His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu  
                   20                  25                  30  
 Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe  
                   35                  40                  45  
 Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr  
   50                  55                  60  
 40 Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser  
   65                  70                  75                  80  
 Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys  
                   85                  90                  95  
 Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser  
                   100                  105                  110  
 45 His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val  
                   115                  120                  125  
 Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala  
   130                  135                  140  
 50 Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn  
   145                  150                  155                  160  
 Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys  
                   165                  170                  175  
 Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn  
                   180                  185                  190  
 55 His Trp Phe Gln Asn Met Xaa Lys Glu Thr Asn Val Lys His Ser Val  
                   195                  200                  205  
 Lys

60  
       <210> 1282  
       <211> 120  
       <212> PRT



&lt;213&gt; Homo sapiens

&lt;400&gt; 1282

5 Ser Tyr Asn Phe Ala Ala Lys Asn Ser Ala Val Val Pro Gln Gly Phe  
 1 5 10 15  
 Met Ile Lys Ser Lys Leu Leu Gly Val Val Tyr Arg Val Leu Arg Ile  
 20 25 30  
 Trp Thr Phe Leu Leu Leu His Val Phe Thr Gly Leu Phe Gly Leu  
 35 40 45  
 10 Glu His Phe Ser Gln Val Leu Gly Leu Leu Pro Gln Phe Leu Ser Leu  
 50 55 60  
 Ser Pro Phe Cys Pro Thr Pro Trp Leu Gly Leu Ser Leu Pro Leu Thr  
 65 70 75 80  
 Pro Pro Cys Arg Tyr Leu Ser Gln Ser Leu Ser His Arg Ile Ile Cys  
 85 90 95  
 15 Phe Phe Thr Cys Leu Phe Leu Pro Leu Asn His Glu Val Phe Glu Gly  
 100 105 110  
 Arg Val Arg Gly Leu Val Ile Phe  
 115 120

20

&lt;210&gt; 1283

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

25

&lt;400&gt; 1283

Lys Ile Thr Lys Pro Leu Thr Arg Pro Ser Lys Thr Ser Trp Phe Lys  
 1 5 10 15  
 Gly Arg Asn Arg Gln Val Lys Lys Gln Ile Ile Leu Cys Asp Arg Asp  
 20 25 30  
 Cys Asp Lys Tyr Leu Gln Gly Gly Val Ser Gly Arg Leu Asn Pro Ser  
 35 40 45  
 Gln Gly Val Gly Gln Lys Gly Glu Arg Glu Arg Asn Trp Gly Arg Ser  
 50 55 60  
 35 Pro Asn Thr Trp Glu Lys Cys Ser Lys Pro Lys Asn Ser Pro Val Asn  
 65 70 75 80  
 Thr

40

&lt;210&gt; 1284

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

45

&lt;400&gt; 1284

Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala  
 1 5 10 15  
 Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp  
 20 25 30  
 50 Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Phe  
 35 40 45  
 Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Xaa Asn Tyr Ala  
 50 55 60  
 Gly Asp Ala Xaa Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg  
 65 70 75 80  
 55 Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr  
 85 90 95  
 Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser  
 100 105 110  
 60 Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln  
 115 120 125  
 Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile  
 130 135 140

Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu  
 145 150 155 160  
 Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn  
 165 170 175  
 5 Arg Ile Tyr Gln Tyr  
 180  
 <210> 1285  
 <211> 106  
 10 <212> PRT  
 <213> Homo sapiens  
 <400> 1285  
 Ile Ser Pro His Phe Ser Leu Leu Gly Asp Asp Val Ala Phe Ser Ser  
 15 1 5 10 15  
 Gln Glu Asn Glu Tyr Gln Leu Leu Ser Cys Phe Cys Cys Gln Leu Ser  
 20 20 25 30  
 Tyr Val His Glu Leu Ile Ala Val Glu Ala Thr Tyr Phe Cys Phe Val  
 35 40 45  
 20 Val Glu Ile Ile Ser Asp Leu Xaa Thr Pro Ala Val Gln Cys Val Cys  
 50 55 60  
 Ser His Tyr Leu Val Arg Phe Asp Thr Cys Val Gln Leu Pro Ser Phe  
 65 70 75 80  
 Asp Thr Val Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met  
 25 85 90 95  
 Tyr Phe Leu Leu Xaa His Leu Arg His Asn  
 100 105  
 <210> 1286  
 30 <211> 105  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1286  
 35 Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val  
 1 5 10 15  
 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile  
 20 25 30  
 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu  
 40 35 40 45  
 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr  
 50 55 60  
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Leu  
 65 70 75 80  
 45 Ile Ile Ala Glu Asn Val Leu Asn Ser Ala Ala Tyr Leu Pro Ser Asn  
 85 90 95  
 Phe Pro Phe Ile Leu Ser Ile Ser Phe  
 100 105  
 <210> 1287  
 50 <211> 229  
 <212> PRT  
 <213> Homo sapiens  
 <400> 1287  
 55 Cys Val Ser Leu Lys Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala  
 1 5 10 15  
 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn  
 20 25 30  
 60 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln  
 35 40 45  
 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr  
 50 55 60

Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu  
 65 70 75 80  
 Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Arg Tyr Ala Ala Glu Phe  
 85 90 95  
 5 Arg Thr Phe Ser Ala Met Ile Arg Ser Pro Val Lys Asp Gly Leu Leu  
 100 105 110  
 Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu  
 115 120 125  
 10 Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser  
 130 135 140  
 Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala  
 145 150 155 160  
 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro  
 165 170 175  
 15 Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu  
 180 185 190  
 Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala  
 195 200 205  
 20 Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Ala Ile  
 210 215 220  
 Arg Asp Gly Ser Thr  
 225

<210> 1288  
 <211> 174  
 <212> PRT  
 <213> Homo sapiens

<400> 1288  
 30 Cys Val Ser Leu Lys Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala  
 1 5 10 15  
 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn  
 20 25 30  
 35 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln  
 35 40 45  
 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr  
 50 55 60  
 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu  
 65 70 75 80  
 40 Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Arg Tyr Ala Ala Glu Phe  
 85 90 95  
 Arg Thr Phe Ser Ala Met Ile Arg Ser Pro Val Lys Asp Gly Leu Leu  
 100 105 110  
 45 Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu  
 115 120 125  
 Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser  
 130 135 140  
 Ala Phe Glu Pro Xaa Ile Gly Lys Pro Lys Val Cys Xaa Gln Ile Lys  
 145 150 155 160  
 50 Ala Phe Gly Ile Gly Arg Met Asp Gln Xaa Leu Gly Ala Arg  
 165 170

<210> 1289  
 <211> 108  
 <212> PRT  
 <213> Homo sapiens

<400> 1289  
 60 Pro Phe Gly Trp Xaa Ser Glu Gly Xaa Tyr Ser His Arg Ala Pro Xaa  
 1 5 10 15  
 Gly Trp Ser Ile Leu Pro Ile Pro Lys Ala Phe Ile Trp Xaa Gln Thr  
 20 25 30  
 Phe Gly Phe Pro Met Xaa Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly

35 40 45  
 Ser Ala Leu Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly  
 50 55 60  
 Ile Glu Thr Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr  
 65 70 75 80  
 Gly Asp Leu Ile Ile Ala Glu Asn Val Leu Asn Ser Ala Ala Tyr Leu  
 85 90 95  
 Pro Ser Asn Phe Pro Phe Ile Leu Ser Ile Ser Phe  
 100 105  
 10  
 <210> 1290  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens  
 15  
 <400> 1290  
 Ile Gln Gln His Ile Tyr Leu Leu Ile Phe His Leu Phe Tyr Leu Phe  
 1 5 10 15  
 Leu Phe Asp Ala Gln Pro Trp Val Asn Thr His Pro Ser Val Lys Gln  
 20 20 25 30  
 Ser His Arg Asp Ser Gln Asn Pro Lys Asn Phe Leu His Ser Pro Phe  
 35 40 45  
 Val Trp Ile Leu Met Gly Val Ser His Leu Leu Ser Met Phe Val His  
 50 55 60  
 25 Ser Ser Ile Pro Arg Leu Tyr Leu Glu Gln Thr Phe Ala Phe Gln Trp  
 65 70 75 80  
 Gln Ala Arg Arg Gln Met Ala Ser Arg Glu Ala Leu Met Lys His Ile  
 85 90 95  
 Arg Ile Thr Tyr Ile Ile Pro Phe Ile Leu Phe Phe Asn Ile Ala Tyr  
 100 105 110  
 30 Leu Trp Lys Gly Thr  
 115  
 35  
 <210> 1291  
 <211> 189  
 <212> PRT  
 <213> Homo sapiens  
 40  
 <400> 1291  
 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp  
 1 5 10 15  
 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu  
 20 25 30  
 Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu  
 35 40 45  
 45 Glu Gly Arg Tyr Ala Ala Glu Phe Arg Thr Phe Ser Ala Met Ile Arg  
 50 55 60  
 Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val  
 65 70 75 80  
 50 Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys  
 85 90 95  
 Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met  
 100 105 110  
 Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr  
 115 120 125  
 55 Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr  
 130 135 140  
 Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln  
 145 150 155 160  
 60 Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys  
 165 170 175  
 Ile Asn Gly Lys Leu Glu Ala Ile Arg Asp Gly Ser Thr  
 180 185

<210> 1292  
 <211> 105  
 <212> PRT  
 5 <213> Homo sapiens

<400> 1292  
 Ser Phe Cys Leu Asp Ser Asp Gly Ser Ile Ser Ser Ala Leu Asn Val  
 1 5 10 15  
 10 Cys Ser Phe Phe Asn Ser Lys Ala Leu Phe Gly Thr Asp Phe Cys Ile  
 20 25 30  
 Ser Met Ala Gly Ser Lys Ala Asp Gly Phe Ser Gly Gly Ser Ala Leu  
 35 40 45  
 15 Lys Val Cys Met Ser Ile Asn Ser Lys Ala Leu Val Gly Ile Glu Thr  
 50 55 60  
 Phe Ile Pro Gln Leu Ala Phe Arg Arg Pro Ser Leu Thr Gly Asp Leu  
 65 70 75 80  
 Ile Ile Ala Glu Asn Val Leu Asn Ser Ala Ala Tyr Leu Pro Ser Asn  
 85 90 95  
 20 Phe Pro Phe Ile Leu Ser Ile Ser Phe  
 100 105

<210> 1293  
 <211> 181  
 25 <212> PRT  
 <213> Homo sapiens

<400> 1293  
 Gln Xaa His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala  
 1 5 10 15  
 Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp  
 20 25 30  
 Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser  
 35 35 40 45  
 Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Xaa Asn Tyr Ala  
 50 55 60  
 Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg  
 65 70 75 80  
 Asp Gln Arg Glu Xaa Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr  
 85 90 95  
 40 Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser  
 100 105 110  
 Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln  
 115 120 125  
 45 Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile  
 130 135 140  
 Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu  
 145 150 155 160  
 Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn  
 165 170 175  
 50 Arg Ile Tyr Gln Tyr  
 180

<210> 1294  
 55 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 1294  
 Ile Ser Pro His Phe Ser Leu Leu Gly Asp Asp Val Ala Phe Ser Ser  
 1 5 10 15  
 Gln Glu Asn Glu Tyr Gln Leu Leu Ser Cys Phe Cys Cys Gln Leu Ser  
 20 25 30

Tyr Val His Glu Leu Ile Ala Val Glu Ala Thr Tyr Phe Cys Phe Val  
                   35                  40                  45  
 Val Glu Ile Ile Ser Asp Leu Glu Thr Pro Ala Val Gln Cys Val Cys  
                   50                  55                  60  
 5 Ser His Tyr Leu Val Arg Phe Asp Thr Cys Val Gln Leu Pro Ser Phe  
    65                  70                  75                  80  
 Asp Thr Xaa Phe His Val Gly Leu Phe Val His Val Leu Lys Pro Met  
                   85                  90                  95  
 Tyr Phe Leu Leu Glu His Leu Arg His Asn  
 10                  100                  105

&lt;210&gt; 1295

&lt;211&gt; 185

&lt;212&gt; PRT

15 &lt;213&gt; Homo sapiens

&lt;400&gt; 1295

Tyr Gly Arg Phe Leu Leu Ile Val Gly Tyr Phe Cys Phe Ser Tyr  
    1                  5                  10                  15  
 20 Cys His Leu Lys Tyr Ile Phe Asn Val Glu Ile Leu Thr Ala Cys Leu  
                   20                  25                  30  
 Met Lys Ser Ser Phe Gln Ile Phe Leu Gly Ser Pro Val Lys Asp Gly  
                   35                  40                  45  
 25 Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala  
    50                  55                  60  
 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys  
    65                  70                  75                  80  
 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn  
                   85                  90                  95  
 30 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile  
                   100                  105                  110  
 Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp  
                   115                  120                  125  
 35 Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro  
    130                  135                  140  
 Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu  
    145                  150                  155                  160  
 Gly Arg Tyr Ala Ala Glu Phe Arg Thr Phe Ser Ala Met Ile Arg Xaa  
                   165                  170                  175  
 40 Pro Val Lys Arg Trp Ser Ser Glu Gly  
                   180                  185

&lt;210&gt; 1296

&lt;211&gt; 130

45 &lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1296

Xaa Ile Ile Phe Ile Phe Met Ser Xaa Arg Asn Leu Thr Leu Xaa Ser  
    1                  5                  10                  15  
 50 Ser Cys Ser His Leu Thr Phe Trp Phe Ser Asn Trp Asp Phe Ile Ser  
                   20                  25                  30  
 Phe Ala Ser Asp Ser Phe Phe Phe Ser Thr Gln Asn Phe Phe Phe Ile  
                   35                  40                  45  
 55 Cys Ser Ile Phe Pro Xaa Val His Xaa Asp Leu Phe Glu Val Pro  
    50                  55                  60  
 Leu Leu Phe His Lys Asn Glu Xaa Tyr Pro Lys Phe Leu Ile Gly Xaa  
    65                  70                  75                  80  
 Leu Asn Leu Xaa Ile Phe His Leu Phe Tyr Pro Phe Leu Phe Asp Xaa  
                   85                  90                  95  
 60 Asn Leu Gly Xaa Thr Xaa His Pro Ser Xaa Glu Gln Val Xaa Thr Glu  
                   100                  105                  110  
 Asp Leu Ser Xaa Asn Pro Lys Asn Phe Leu Gln Pro Phe Phe Cys Phe

115 120 125  
 Asp Ser  
 130

5 <210> 1297  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

10 <400> 1297  
 Met Gly Thr Arg Ala Xaa Gln Cys Glu Val Ser Xaa Thr His Glu Asn  
 1 5 10 15  
 Glu Asn Tyr Xaa Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala  
 20 25 30  
 15 Met Leu Lys Leu Glu Ile Ala Xaa Leu Lys Xaa Gln Tyr Gln Glu Lys  
 35 40 45  
 Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala  
 50 55 60  
 Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg  
 65 70 75 80  
 20 Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Xaa Ile Ala Glu Asn Xaa  
 85 90 95  
 Met Leu Thr Xaa Lys Leu Lys  
 100

25 <210> 1298  
 <211> 98  
 <212> PRT  
 <213> Homo sapiens

30 <400> 1298  
 Xaa Xaa Xaa Xaa Thr Ile Xaa Xaa Arg Phe Xaa Xaa Phe Xaa Phe Lys  
 1 5 10 15  
 Asn Gln Asn Lys Arg Arg Val Glu Glu Asn Phe Trp Gly Xaa Xaa Lys  
 20 25 30  
 35 Gly Pro Arg Xaa Arg Leu Val Xaa Lys Lys Asp Xaa Gly Xaa Pro Gln  
 35 40 45  
 Gly Xaa His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Xaa Glu Asp  
 50 55 60  
 40 Ser Xaa Ser Leu Ser Lys Ile Leu Asp Xaa Val His Ser Cys Glu Arg  
 65 70 75 80  
 Ala Arg Glu Leu Gln Lys Asp Xaa Cys Glu Gln Xaa Gln Glu Lys Trp  
 85 90 95  
 Asn Lys

45 <210> 1299  
 <211> 207  
 <212> PRT  
 50 <213> Homo sapiens

<400> 1299  
 Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro  
 1 5 10 15  
 55 Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu  
 20 25 30  
 Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser Trp  
 35 40 45  
 Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu  
 50 55 60  
 60 Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu  
 65 70 75 80  
 Glu Gly Arg Tyr Ala Ala Glu Phe Gly Thr Phe Ser Ala Met Ile Arg

85 90 95  
 Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val  
 100 105 110  
 5 Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys  
 115 120 125  
 Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met  
 130 135 140  
 Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr  
 145 150 155 160  
 10 Leu Arg Ala Asp Glu Ile Ser His Gln Asn Pro Asn Lys Arg Thr Met  
 165 170 175  
 Lys Lys Val Leu Gly Ile Leu Arg Val Ser Val Arg Leu Phe His Arg  
 180 185 190  
 15 Lys Asp Val Cys Leu Pro Gln Xaa Ala Xaa Gln Lys Glu Ile Asp  
 195 200 205

&lt;210&gt; 1300

&lt;211&gt; 187

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 1300

Thr Gly Phe Cys Trp Xaa Lys Ala His Asp Gln Ile Val Thr Ser Arg  
 1 5 10 15  
 25 Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln  
 20 25 30  
 Arg Lys Met Asn Val Asp Val Ser Ser Pro Ile Tyr Asn Asn Glu Val  
 35 40 45  
 30 Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys  
 50 55 60  
 Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val  
 65 70 75 80  
 Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys  
 85 90 95  
 35 Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His  
 100 105 110  
 Thr Glu Gln Gln Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser  
 115 120 125  
 40 Lys Asn Met Trp Leu Gln Gln Glu Leu Val His Ala His Lys Lys Ala  
 130 135 140  
 Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys  
 145 150 155 160  
 Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr  
 165 170 175  
 45 Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr  
 180 185

&lt;210&gt; 1301

&lt;211&gt; 164

&lt;212&gt; PRT

50 &lt;213&gt; Homo sapiens

&lt;400&gt; 1301

Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu  
 1 5 10 15  
 55 Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser  
 20 25 30  
 Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg  
 35 40 45  
 60 Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln  
 50 55 60  
 Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu  
 65 70 75 80



[illegible]

15	<210>	1302
	<211>	196
	<212>	PRT
	<213>	Homo sapiens

[illegible]

50                   <210> 1303  
                    <211> 205  
                    <212> PRT  
                    <213> Homo sapiens

		<b>&lt;400&gt; 1303</b>															
		Phe	Phe	Ser	Pro	Asn	Glu	Asn	Phe	Met	Ala	Lys	Glu	His	Asp	Phe	Leu
		1				5					10					15	
55		Ser	Ile	Ile	Gly	Phe	Trp	Asn	Asn	Gly	Ile	Phe	Cys	Leu	Trp	Leu	Ser
					20					25					30		
		Leu	Ile	Lys	Ser	Phe	Ile	Phe	Phe	Phe	Gly	Pro	Ser	Phe	Pro	His	Phe
				35					40					45			
		Leu	Arg	Val	Ser	Phe	Thr	Ile	Ala	Met	Thr	Lys	Ser	Glu	Phe	Ser	Thr
60			50					55					60				
		Tyr	Ile	Phe	Ile	Pro	Ile	Phe	Glu	His	Gln	Asn	Arg	Ser	Phe	Ile	Asn
		65					70					75					80
		Phe	Asp	Cys	Ser	Ala	Leu	Ser	Ile	Cys	Cys	Ala	Ser	Met	Asp	Thr	Leu

				85				90				95				
	Ala	Ser	Phe	Pro	Val	Leu	Met	Gln	Pro	Phe	Ile	Ser	Val	Met	Ile	Pro
				100					105					110		
5	Leu	Val	Asn	Ile	Leu	Asn	Lys	Ile	Ile	Leu	Val	Leu	Gly	Ser	Asn	Thr
			115					120					125			
	Cys	Ser	Thr	Val	Ala	Leu	Ser	Ala	Leu	Ser	Leu	Met	Arg	Tyr	Ile	Ser
			130				135					140				
	Ala	Ser	Phe	Cys	Leu	Asp	Phe	Ser	Val	Thr	Leu	Phe	Met	Thr	Glu	Ser
	145					150					155				160	
10	Val	Thr	Phe	Ser	Leu	Ser	Lys	Leu	Ile	Leu	Phe	Ser	Asn	Phe	Arg	Lys
				165						170					175	
	Thr	Leu	Ser	Ala	Gly	Val	Asp	Ile	Leu	Ala	Glu	Leu	Leu	Ser	Glu	Val
				180				185						190		
	Cys	Arg	Phe	Ala	Cys	Gly	Leu	Leu	Pro	Pro	Phe	Gln	Thr			
15			195				200					205				

&lt;210&gt; 1304

&lt;211&gt; 164

&lt;212&gt; PRT

20 &lt;213&gt; Homo sapiens

&lt;400&gt; 1304

	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu
	1			5					10					15		
25	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met	Phe	Pro	Ser	Glu	Ser
			20					25					30			
	Lys	Gln	Lys	Lys	Val	Glu	Glu	Asn	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Arg
			35				40					45				
30	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro	Lys	Ala	Thr	His	Gln
	50					55					60					
	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	Glu	Asp	Ser	Thr	Ser	Leu
	65				70					75					80	
	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	Glu	Arg	Ala	Arg	Glu	Leu
				85					90					95		
35	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys	Met	Glu	Gln	Met	Lys
			100					105					110			
	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	Ser	Glu	Ala	Lys	Glu	Ile
			115				120					125				
	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys	Trp	Glu	Gln	Glu	Leu	Cys
40			130			135						140				
	Ser	Val	Arg	Val	Leu	Thr	Leu	Met	Lys	Met	Lys	Ile	Ile	Ser	Tyr	Met
	145				150					155					160	
	Lys	Ile	Ala	Cys												

45

&lt;210&gt; 1305

&lt;211&gt; 133

&lt;212&gt; PRT

50 &lt;213&gt; Homo sapiens

&lt;400&gt; 1305

	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val	Pro	Lys	Ala	Thr	His	Gln
	1			5					10					15		
55	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	Glu	Asp	Ser	Thr	Ser	Leu
			20					25					30			
	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	Glu	Arg	Ala	Arg	Glu	Leu
			35				40					45				
	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys	Met	Glu	Gln	Met	Lys
	50					55					60					
60	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	Ser	Glu	Ala	Lys	Glu	Ile
	65				70					75					80	
	Lys	Ser	Gln	Leu	Glu	Asn	Gln	Lys	Val	Lys	Trp	Glu	Gln	Glu	Leu	Cys
				85				90						95		

Ser Val Arg Leu Thr Leu Asn Pro Glu Glu Glu Lys Arg Arg Asn Ala  
 100 105 110  
 Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu  
 115 120 125  
 5 His Ile Gly Lys Ser  
 130  
 <210> 1306  
 <211> 83  
 10 <212> PRT  
 <213> Homo sapiens  
 <400> 1306  
 15 Gln Arg Phe Ile Ser Leu Phe Xaa Asp Gly Xaa Ser Xaa Xaa Xaa Ile  
 1 5 10 15  
 Ser Ser Leu Ser Xaa Gln Phe Pro Phe Ser Thr Cys Asn Phe Xaa Glu  
 20 25 30  
 Glu Ile Ile Phe Ile Phe Met Ser Val Arg Thr Leu Ile Gln Xaa Thr  
 35 40 45  
 20 Phe Tyr Thr Leu Gln Xaa Tyr Ile Leu Tyr Ser Glu Ser Leu Phe Lys  
 50 55 60  
 Cys Cys Phe Thr Ser Asn Ser Phe Leu Cys Ala Leu Arg Phe Phe Leu  
 65 70 75 80  
 Ile Leu Pro  
 25  
 <210> 1307  
 <211> 231  
 <212> PRT  
 30 <213> Homo sapiens  
 <400> 1307  
 Leu Lys Arg Gly Ile Ser Asn Lys Val Gly Gln Leu Lys Val Xaa Xaa  
 1 5 10 15  
 35 Ser Leu Arg Thr Gln Cys Ser Leu Phe Lys Leu Lys Glu Xaa Gln Ala  
 20 25 30  
 Xaa Glu Ile Xaa Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala  
 35 40 45  
 Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln  
 50 55 60  
 40 Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met  
 65 70 75 80  
 Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln  
 85 90 95  
 45 Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu  
 100 105 110  
 Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His  
 115 120 125  
 Ala Gln Arg Asp Gln Arg Glu Xaa Gln Cys Gln Met Lys Glu Ala Glu  
 130 135 140  
 50 His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln  
 145 150 155 160  
 Gln Glu Ser Xaa Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met  
 165 170 175  
 55 Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys  
 180 185 190  
 Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His  
 195 200 205  
 His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His  
 210 215 220  
 60 Leu Lys Xaa Arg Ile Tyr Gln  
 225 230

<210> 1308  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

5

&lt;400&gt; 1308

Asp Leu Lys Thr Val Lys Glu Lys Asp Asp Ile Leu Phe Glu Asp Leu  
 1 5 10 15  
 Gln Asp Asn Xaa Asn Glu Asn Gly Glu Gly Glu Ile Glu Asp Glu Glu  
 10 20 25 30  
 Glu Glu Gly Tyr Asp Asp Asp Asp Asp Trp Asp Trp Asp Glu Gly  
 35 40 45  
 Val Gly Lys Leu Ala Lys Gly Tyr Val Trp Asn Gly Gly Ser Asn Pro  
 50 55 60  
 Gln Ala Asn Arg Gln Thr Ser Asp Ser Ser Ser Ala Lys Met Ser Thr  
 15 65 70 75 80  
 Pro Ala Asp Lys Val Leu Arg Lys Phe Glu Asn Lys Ile Asn Leu Asp  
 85 90 95  
 Lys Leu Asn Val Thr Asp Ser Val Ile Asn Lys Val Thr Glu Lys Ser  
 100 105 110  
 Arg Gln Lys Glu Ala Asp Met Tyr Arg Ile Lys Asp Lys Ala Asp Arg  
 115 120 125  
 Ala Thr Val Glu Gln Val Leu Asp Pro Arg Thr Arg Met Ile Leu Phe  
 130 135 140  
 Lys Met Leu Thr Arg Gly Ile Ile Thr Glu Ile Asn Gly Cys Ile Ser  
 145 150 155 160  
 Thr Gly Lys Glu Ala Asn Val Ser Met Leu Xaa Thr Ala Asn Gly Glu  
 165 170 175  
 Ser Arg Ala Ile Lys Ile Tyr  
 180

30

<210> 1309  
 <211> 219  
 <212> PRT  
 <213> Homo sapiens

35

&lt;400&gt; 1309

Glu Glu Cys Ile Arg Met Pro Asp Phe Val His Ala Asp Leu Ser Glu  
 1 5 10 15  
 Phe Asn Met Leu Tyr His Gly Gly Gly Val Tyr Ile Ile Asp Val Ser  
 20 25 30  
 Gln Ser Val Glu His Asp His Pro His Ala Leu Glu Phe Leu Arg Lys  
 35 40 45  
 Asp Cys Ala Asn Val Asn Asp Phe Phe Met Arg His Ser Val Ala Val  
 45 50 55 60  
 Met Thr Val Arg Glu Leu Phe Glu Phe Val Thr Asp Pro Ser Ile Thr  
 65 70 75 80  
 His Glu Asn Met Asp Ala Tyr Leu Ser Lys Ala Met Glu Ile Ala Ser  
 85 90 95  
 Gln Arg Thr Lys Glu Glu Arg Ser Ser Gln Asp His Val Asp Glu Glu  
 100 105 110  
 Val Phe Lys Arg Ala Tyr Ile Pro Arg Thr Leu Asn Glu Val Lys Asn  
 115 120 125  
 Tyr Glu Arg Asp Met Asp Ile Ile Met Lys Leu Lys Glu Glu Asp Met  
 130 135 140  
 Ala Met Asn Ala Gln Gln Asp Asn Ile Leu Tyr Gln Thr Val Thr Gly  
 145 150 155 160  
 Leu Lys Lys Asp Leu Ser Gly Val Gln Lys Val Pro Ala Leu Leu Glu  
 165 170 175  
 Asn Gln Val Glu Glu Arg Thr Cys Ser Asp Ser Glu Asp Ile Gly Ser  
 180 185 190  
 Ser Glu Cys Ser Asp Thr Asp Ser Glu Glu Gln Gly Asp His Ala Arg  
 195 200 205

60

Pro Lys Lys His Thr Thr Asp Pro Asp Ile Asp  
 210 215

5 <210> 1310  
 <211> 191  
 <212> PRT  
 <213> Homo sapiens

10 <400> 1310  
 Glu Pro Asp Gln Lys Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg  
 1 5 10 15  
 Glu Phe Arg Val Leu His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg  
 20 25 30  
 Glu Ala Val Phe Lys Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile  
 35 40 45  
 15 Ile Val Ala Thr Pro Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val  
 50 55 60  
 Leu Gln Asp Lys Asp Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu  
 65 70 75 80  
 20 Asp Thr Leu Val Pro Ala His Pro Ala Leu Val Asn Ala Ile Val Leu  
 85 90 95  
 Val Leu His Ser Val Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser  
 100 105 110  
 Ser Ser Arg Ser Met Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly  
 115 120 125  
 25 Phe Leu Phe Glu Gly Leu Ser Xaa Asp Glu Asp Asp Phe His Pro Asn  
 130 135 140  
 Thr Arg Ser Thr Pro Ser Ser Ser Thr Pro Ser Ser Arg Gln Pro Pro  
 145 150 155 160  
 30 Gly Val Gln Val Glu Leu Leu Gly Pro Gly Pro Ser Pro Lys Val Ser  
 165 170 175  
 Trp Pro Pro Pro Trp Pro Trp Pro Ala Xaa Arg Arg Ala Ser Phe  
 180 185 190

35 <210> 1311  
 <211> 164  
 <212> PRT  
 <213> Homo sapiens

40 <400> 1311  
 Tyr Arg Asp Met Pro Gly Ala Ser Cys Leu Lys Gly Ser Gln Met Met  
 1 5 10 15  
 Arg Met Thr Phe Thr Gln Thr Pro Gly Pro His Pro Xaa Ser Ser Thr  
 20 25 30  
 45 Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly Ala Xaa Gly Pro  
 35 40 45  
 Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu Ala Leu Ala Ser  
 50 55 60  
 Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly Thr Gln Gly His  
 65 70 75 80  
 50 Ser Ser Gly Thr Ser Pro Met Ser Xaa Gly Val Gln Ser Gly Thr Pro  
 85 90 95  
 Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His Ala Leu Gln Ala  
 100 105 110  
 55 Xaa Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro Gln Leu Gln Gln  
 115 120 125  
 Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser Leu Arg Ala Leu  
 130 135 140  
 Gln Ala Thr Gly Gly Asp Ile Gln Ala Ala Leu Glu Leu Ile Phe Ala  
 145 150 155 160  
 60 Gly Gly Ala Pro

<210> 1312  
 <211> 120  
 <212> PRT  
 <213> Homo sapiens

5

<400> 1312  
 Leu Ser Pro Lys His Gln Val His Thr Xaa Leu Ala Val Leu Pro Ala  
 1 5 10 15  
 Pro Ala Gln Pro Pro Trp Gly Thr Val Glu Leu Xaa Gly Pro Gly Pro  
 10 20 25 30  
 Ser Pro Arg Val Ser Trp Pro Pro Trp Pro Trp Pro Ala Leu Arg  
 35 40 45  
 Arg Ala Ala Leu Thr His Arg Leu Leu Ala Pro Arg Val Ile Pro Gln  
 50 55 60  
 Gly Pro His Gln Cys Pro Xaa Val Ser Ser Gln Gly Arg Pro Ser Pro  
 15 65 70 75 80  
 Met Ile Ser Ser Ala Lys Pro Tyr Ser Met Pro Phe Arg Pro Xaa Gly  
 85 90 95  
 Ser Pro Ala Phe Arg Ala Ser Gly Ser Pro Ser Cys Ser Ser Tyr Val  
 20 100 105 110  
 Thr Trp Ala Ser Arg Thr Met Ser  
 115 120

25

<210> 1313  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 1313  
 Gly Met Thr Leu Gly Ala Arg Ser Arg Cys Val Arg Ala Ala Leu Arg  
 1 5 10 15  
 Ser Ala Gly Gln Gly Gln Gly Gly Gly Gln Leu Thr Leu Gly Asp Gly  
 20 25 30  
 Pro Gly Pro Xaa Ser Ser Thr Val Pro Gln Gly Gly Trp Ala Gly Ala  
 35 35 40 45  
 Gly Ser Thr Ala Xaa Arg Val Trp Thr Trp Cys Leu Gly Glu Ser His  
 50 55 60  
 Pro His His Leu Arg Thr Leu Gln Thr Gly Ser Pro Trp His Ile Pro  
 65 70 75 80  
 Val Leu Ala Gly Xaa His Ala Xaa Gly Xaa Gly Ile Asn Pro Arg His  
 85 90 95  
 Trp Gly Pro Ala Cys Phe Arg Val Xaa Asn Gln Glu Gln Trp  
 100 105 110

45

<210> 1314  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

50

<400> 1314  
 Phe Gln Glu Arg Ala Arg Ile Glu Lys Ala Tyr Ala Gln Gln Leu Ala  
 1 5 10 15  
 Asp Trp Ala Arg Lys Trp Arg Gly Thr Val Glu Lys Gly Pro Gln Tyr  
 20 25 30  
 Gly Thr Leu Glu Lys Ala Trp His Ala Phe Phe Thr Ala Ala Glu Arg  
 35 40 45  
 Leu Ser Ala Leu His Leu Glu Val Arg Glu Lys Pro Gln Gly Gln Asp  
 50 55 60  
 Ser Glu Arg Val Arg Ala Trp Gln Arg Gly Ala Phe His Arg Pro Val  
 60 65 70 75 80  
 Leu Gly Gly Phe Arg Glu Ser Arg Ala Ala Glu Asp Gly Phe Arg Lys  
 85 90 95  
 Ala Gln Lys Pro Trp Leu Lys Arg Leu Lys Glu Val Glu Ala Ser Lys

100 105 110  
 Lys Ser Tyr His Ala Ala Arg Lys Asp Glu Lys Thr Ala Gln Thr Arg  
 115 120 125  
 5 Glu Ser His Ala Lys Ala Asp Ser Ala Val Xaa Gln Glu Gln Leu Arg  
 130 135 140  
 Lys Leu Gln Glu Arg Val Glu Arg Cys Ala Lys Glu Ala Glu Lys Thr  
 145 150 155 160  
 Lys Ala Gln Tyr Glu Gln Thr Leu Ala Glu Leu His Arg Tyr Thr Pro  
 165 170 175  
 10 Arg Tyr Met Glu Asp Met Glu Gln Ala Phe Glu Thr Leu Gln Ala Arg  
 180 185 190  
 Arg Ala Pro Xaa Ala Ser Phe Leu Xaa Gly Tyr Ala Xaa His Leu Thr  
 195 200 205  
 Pro Thr Pro Gly Pro Phe Ser Ala Val Arg Ser Xaa Met Lys Leu His  
 15 210 215 220  
 Pro  
 225

20 <210> 1315  
 <211> 214  
 <212> PRT  
 <213> Homo sapiens

<400> 1315  
 25 Lys Arg Ser Arg Cys Trp Cys Lys Val Xaa Ser Ile Ser Xaa Lys Lys  
 1 5 10 15  
 Arg Ser Xaa Trp Arg Ser Ala Gly Leu Gln Gly Leu Lys Gly Leu Phe  
 20 25 30  
 His Val Leu His Val Ala Trp Ser Val Ala Met Gln Leu Cys Gln Arg  
 30 35 40 45  
 Leu Leu Ile Leu Ser Phe Cys Leu Leu Gly Leu Leu Gly Thr Ala Phe  
 50 55 60  
 His Pro Phe Leu Gln Phe Ala Gln Leu Leu Leu Xaa Asp Gly Ala Val  
 65 70 75 80  
 35 Cys Leu Cys Val Ala Leu Pro Arg Leu Gly Gly Leu Leu Ile Leu Pro  
 85 90 95  
 Gly Cys Val Val Ala Phe Leu Gly Ser Leu Asn Leu Leu Gln Pro Leu  
 100 105 110  
 Gln Pro Gly Leu Leu Gly Leu Ala Glu Ala Val Leu Gly Arg Pro Ala  
 115 120 125  
 40 Leu Ala Glu Ala Ala Gln His Arg Pro Val Glu Ser Pro Pro Leu Pro  
 130 135 140  
 Gly Ala His Pro Leu Thr Val Leu Pro Leu Arg Leu Leu Pro His Leu  
 145 150 155 160  
 45 Gln Val Gln Arg Ala Gln Pro Leu Ser Arg Arg Glu Lys Gly Met Pro  
 165 170 175  
 Gly Leu Leu Gln Cys Ala Ile Leu Gly Ala Leu Leu His Gly Pro Pro  
 180 185 190  
 Pro Leu Ser Gly Pro Val Ser Gln Leu Leu Gly Ile Ser Leu Leu Asp  
 195 200 205  
 50 Ala Gly Ala Leu Leu Glu  
 210

55 <210> 1316  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 1316  
 60 Gly Xaa Gln His Ile Leu Xaa Glu Lys Lys Pro Xaa Ala Leu Gly Gly  
 1 5 10 15  
 Pro Ala Arg Ser Gln Arg Leu Val Pro Cys Pro Pro Cys Ser Val Glu  
 20 25 30

Cys Ser Asp Ala Ala Leu Pro Ala Ser Ala His Thr Glu Leu Leu Ser  
           35                  40                  45  
 Ser Arg Pro Pro Trp His Ser Val Pro Pro Val Pro Ala Val Cys Ala  
       50                  55                  60  
 5 Ala Ala Pro Xaa Arg Arg Arg Cys Leu Pro Leu Arg Gly Ser Pro Ser  
    65                  70                  75                  80  
 Ser Gly Arg Ser Ser His Pro Ser Gly Leu Arg Gly Ser Phe Ser Trp  
                   85                  90                  95  
 10 Lys Pro Gln Pro Pro Ser Ala Ser Ser Ala Arg Ala Ser Gly Pro Cys  
       100                  105                  110  
 Gly Ser Arg Pro Arg Pro Pro Gly Ser Arg Gly Ser Arg Pro Ala Gln  
       115                  120                  125  
 Ala Gly Gly Lys Pro Pro Ala Ala Arg Arg Ala Pro Ala His Cys Pro  
       130                  135                  140  
 15 Ala Leu Ala Ala Ser Pro Ala Pro Pro Gly Ala Ala Arg Ser Ala Ala  
    145                  150                  155                  160  
 Gln Pro Pro

20           <210> 1317  
               <211> 162  
               <212> PRT  
               <213> Homo sapiens

25           <400> 1317  
 Thr Arg Pro Phe Pro Thr Ser Pro Phe Pro Arg Gln Arg Pro Leu Pro  
   1                  5                  10                  15  
 Ser Leu Gly Pro Arg Thr Ser Ser Leu Lys Gly Gln Arg Ser Ser Gln  
       20                  25                  30  
 30 Arg Ala Thr Val Gln Gly Pro Glu Gly Pro Ala Leu Gln Glu Lys Leu  
       35                  40                  45  
 Gly Ser Glu Pro Gly Trp Val Asn Val Ala Glu Gly Leu Ser Gly His  
       50                  55                  60  
 Ser Gly Ala His Thr Leu His Val Val Gly Arg Val Gln Ala Asn Ala  
    65                  70                  75                  80  
 Ala Thr Leu Gln Leu Ala Leu Ala Pro Ala Leu Leu Val Leu Leu Thr  
                   85                  90                  95  
 His Leu Gln Gln Leu Leu Pro Cys Ser Glu Ala Gln Leu Ile Ser Phe  
       100                  105                  110  
 40 Leu Ala Ser Val Val Ile Glu Cys Pro Xaa Arg Thr Pro Val Gly Ala  
       115                  120                  125  
 Phe Xaa Gly Leu Ser Ser Ser Asp His Ser Ser Ser Cys Pro Val Pro  
       130                  135                  140  
 Gly Asp Pro Gly Thr Gly Val Gly Gly Xaa Gly Ile Xaa Val Gly Gln  
    145                  150                  155                  160  
 Xaa Leu

50           <210> 1318  
               <211> 126  
               <212> PRT  
               <213> Homo sapiens

          <400> 1318  
 55 Val Phe Leu Phe Leu Cys Val Gly Val Cys Gln Val Leu Ile His Ala  
   1                  5                  10                  15  
 Arg Thr Ser His Lys Arg Val Leu Leu Gly Gln Asn Tyr Thr His Pro  
       20                  25                  30  
 Lys Pro Thr Pro Gly Thr Pro Lys Gln Arg Ser Gly Thr Glu Ser Thr  
       35                  40                  45  
 60 Ala Pro Gly Glu Ala Gln Ala Pro Leu Asn Ala Ser Val Thr Ser Asp  
       50                  55                  60  
 Leu Pro Ser Cys Pro Gln Pro Arg Leu Val Pro Ser Leu Pro Val Pro



	65	Ser Leu Asp Lys Gly Pro Ser Pro Pro Trp Val Pro Gly Leu Pro Pro	70	Gly Ala Ala Arg Glu Arg Arg Phe Arg Ala Leu Arg	75	Val Phe Arg Gln Gly Gly	80	Pro Pro
			85				90	
5		Ser Arg Asp Arg Gly Ala Ala Arg Glu Arg Arg Phe Arg Ala Leu Arg					105	
		Val Arg Leu Ser Arg Arg Ser Trp Ala Leu Asn Gln Gly Gly					120	
			115					125
		<210>	1319					
10		<211>	215					
		<212>	PRT					
		<213>	Homo sapiens					
		<400>	1319					
15		Ala Pro Pro Asp Phe Leu Arg Ala Thr Gly Asp Arg Ala Glu Pro Ser						
		1	5				10	15
		Val Tyr Trp Ala Ala Val Thr Leu Arg Phe Gln Met Lys Met Phe Glu					25	
			20					30
20		Ser Ala Asp Ser Thr Ala Thr Arg Ser Gly Gln Asp Leu Trp Ala Glu					40	
			35					45
		Ile Cys Ser Cys Leu Pro Asn Pro Glu Gln Glu Asp Gly Ala Asn Asn					50	
			50				55	60
		Ala Phe Ser Asp Ser Phe Val Asp Ser Cys Pro Glu Gly Glu Gly Gln					65	
			65				70	75
25		Arg Glu Val Ala Asp Phe Ala Val Gln Pro Ala Val Lys Pro Trp Ala					85	
			85				90	95
		Pro Leu Gln Asp Ser Glu Val Tyr Leu Ala Ser Leu Glu Lys Lys Leu					100	
			100				105	110
30		Arg Arg Ile Lys Gly Leu Asn Gln Glu Val Thr Ser Lys Asp Met Leu					115	
			115				120	125
		Arg Thr Leu Ala Gln Ala Lys Lys Glu Cys Trp Asp Arg Phe Leu Gln					130	
			130				135	140
		Glu Lys Leu Ala Ser Glu Phe Phe Val Asp Gly Leu Asp Ser Asp Glu					145	
			145				150	155
35		Ser Thr Leu Glu His Phe Lys Arg Trp Leu Gln Pro Asp Lys Val Ala					165	
			165				170	175
		Val Ser Thr Glu Glu Val Gln Tyr Leu Ile Pro Pro Glu Ser Gln Val					180	
			180				185	190
40		Glu Lys Pro Val Ala Arg Gly Arg Thr Thr Xaa Arg Gly Thr Ser Gln					195	
			195				200	205
		Gln Xaa Gln Lys Gln Leu Ile					210	215
			210					
		<210>	1320					
45		<211>	185					
		<212>	PRT					
		<213>	Homo sapiens					
		<400>	1320					
50		Asp Thr Glu Glu Ser Ser Ile Leu Ile Gln Cys Ala Leu Gly Gln Ser					1	
			5				10	15
		Leu His Pro Arg Gln Ser His Met Pro Ala Pro Gly Lys Ser Leu Gly					20	
			20				25	30
55		Ala Cys Ser Cys Phe Leu Cys Gly Val Glu Ile Trp Val Phe Ser Phe					35	
			35				40	45
		Ser Gly Phe Leu Pro Ala Ala Val Thr Glu Leu His Ala Ala Arg Ser					50	
			50				55	60
		Gly Pro Glu Thr Ala Ala Arg Arg Val Cys Val Cys Val Cys Val Cys					65	
			65				70	75
60		Val Cys Val Cys Val Cys Val Ile Tyr Cys Ser Ala Ala Ala Gly Leu					85	
			85				90	95
		Ser Pro Ala Ala Gly Ser Ser Ser Ala Thr Gly Phe Ser Thr Cys Asp					100	
			100				105	110

Ser Gly Gly Ile Arg Tyr Trp Thr Ser Ser Val Leu Thr Xaa Thr Leu  
                   115                  120                  125  
 Ser Gly Trp Ser His Leu Leu Lys Cys Ser Lys Xaa Leu Ser Ser Glu  
                   130                  135                  140  
 5 Ser Ser Pro Ser Thr Lys Asn Ser Glu Ala Asn Phe Ser Trp Arg Asn  
    145                  150                  155                  160  
 Arg Ser Gln His Phe Xaa Leu Ala Trp Ala Lys Val Arg Ser Met Ser  
                   165                  170                  175  
 10 Xaa Glu Val Thr Ser Asp Xaa Asn Leu  
                   180                  185  
       <210> 1321  
       <211> 127  
       <212> PRT  
 15       <213> Homo sapiens  
       <400> 1321  
 Asn Phe Xaa Val Xaa Pro Ala Val Xaa Pro Trp Val Pro Phe Gln Xaa  
    1                  5                  10                  15  
 20 Ser Lys Val Ile Xaa Leu Xaa Arg Glu Glu Xaa Lys Lys Asn Gln Arg  
                   20                  25                  30  
 Phe Xaa Ser Glu Val Thr Xaa Lys Asp Met Leu Arg Thr Leu Ala Gln  
                   35                  40                  45  
 25 Ala Xaa Lys Lys Cys Trp Asp Arg Phe Leu Gln Glu Lys Leu Ala Ser  
    50                  55                  60  
 Glu Phe Phe Val Asp Gly Leu Asp Ser Asp Glu Ser Xaa Leu Glu His  
    65                  70                  75                  80  
 Phe Lys Arg Trp Leu Gln Pro Asp Lys Val Xaa Val Ser Thr Glu Glu  
                   85                  90                  95  
 30 Val Gln Tyr Leu Ile Pro Pro Glu Ser Gln Val Glu Lys Pro Val Ala  
                   100                  105                  110  
 Glu Asp Glu Pro Ala Ala Gly Asp Lys Pro Ala Ala Ala Glu Gln  
                   115                  120                  125  
 35       <210> 1322  
       <211> 204  
       <212> PRT  
       <213> Homo sapiens  
 40       <400> 1322  
 Leu Phe Tyr Lys Gly Asn Glu Lys Lys Tyr Thr Met Ser Asp Glu Val  
    1                  5                  10                  15  
 Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro Lys Val Thr Lys Arg  
                   20                  25                  30  
 45 Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile Thr Ala Arg Ser Ala  
                   35                  40                  45  
 Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe Asp Ser Asp Glu Ile  
    50                  55                  60  
 Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala Asp Glu Asn Ser Val  
 50 65                  70                  75                  80  
 Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp Asp Glu Glu Lys Asn  
                   85                  90                  95  
 Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys Ser Asn Gly Asn Ile  
                   100                  105                  110  
 55 Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn Glu Glu Met Ala  
                   115                  120                  125  
 Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser Phe Ser Glu Ser Gln  
    130                  135                  140  
 Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile Lys Met Lys Pro Lys  
 60 145                  150                  155                  160  
 Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser Glu Asn Asn Ser Leu  
                   165                  170                  175  
 Asp Thr Asp Asp His Phe Lys Pro Ser Pro Arg Pro Arg Glu Tyr Val

180 185 190  
 Glu Lys Glu Lys Ser His Gly Gly Arg Arg Met Asp  
 195 200

5 <210> 1323  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

10 <400> 1323  
 Leu Lys Lys Ala Ser Phe Phe Ser Phe His Phe Ser Thr Ala Val Lys  
 1 5 10 15  
 Leu Ser Phe Phe Phe Ser Ala Thr Val Ser Ser Ser Phe Cys Phe Phe  
 20 25 30  
 15 Ala Leu Ser Tyr Ser Leu Ser Phe Leu Phe Phe Ser Leu Arg Tyr Ser  
 35 40 45  
 Ile Phe Phe Ser Phe His Phe Ser Lys Ala Cys Ser Ala Ser Pro Phe  
 50 55 60  
 Leu Ala Ala Phe Ser Ser Ser Val Phe Leu Leu Phe Phe Ser Ser Ser  
 65 70 75 80  
 20 Leu Phe Leu Ala Ala Ile Phe Phe Ala Ser Phe Ser Phe Ile Ala Phe  
 85 90 95  
 Gln Ala Ser Asn Asp Ala Asn Ala Ser Ser Leu Leu Ala Ala Phe Phe  
 100 105 110  
 25 Cys Ser Phe Trp Ile Leu Lys Phe Ser Leu Ser Ile Leu Phe Ile Leu  
 115 120 125  
 Xaa Ile Ser Cys Lys Tyr Thr Phe Phe Phe Ser Asn His Ser  
 130 135 140

30 <210> 1324  
 <211> 193  
 <212> PRT  
 <213> Homo sapiens

35 <400> 1324  
 Val Phe Glu Glu Ile Leu Val Leu Lys Gly Asp Ser Thr Asp Asn Tyr  
 1 5 10 15  
 Leu Phe Ser Leu Phe Arg Asp Phe Lys Ser Leu Gly Gln Lys Pro Xaa  
 20 25 30  
 40 Gln Lys Gln Ser Ile Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala Ala  
 35 40 45  
 Val Tyr Gln Glu Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met  
 50 55 60  
 Xaa Arg Ile Lys Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu  
 65 70 75 80  
 45 Gln Lys Lys Ala Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala  
 85 90 95  
 Trp Lys Ala Met Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys Lys  
 100 105 110  
 50 Arg Leu Glu Glu Lys Asn Lys Arg Lys Thr Glu Glu Glu Asn Ala Ala  
 115 120 125  
 Arg Lys Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys  
 130 135 140  
 Met Glu Tyr Leu Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu Arg  
 145 150 155 160  
 55 Ala Lys Lys Gln Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys Asp  
 165 170 175  
 Asn Leu Thr Ala Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe Phe  
 180 185 190

60 Lys

&lt;210&gt; 1325

<211> 214  
 <212> PRT  
 <213> Homo sapiens

5           <400> 1325  
 Lys Met Asn Leu Pro Thr Pro Phe Xaa Pro Ile Thr Ala Arg Pro Pro  
   1                   5                   10                   15  
 Met Tyr Glu Asp Tyr Met Pro Leu His Ala Pro Leu Pro Pro Thr Ser  
           20                   25                   30  
 10 Pro Gln Pro Pro Glu Glu Pro Pro Leu Pro Asp Glu Asp Glu Glu Leu  
           35                   40                   45  
 Ser Ser Glu Glu Ser Glu Tyr Glu Ser Thr Asp Asp Glu Asp Arg Gln  
   50                   55                   60  
 Arg Met Asn Lys Leu Met Glu Leu Ala Asn Leu Gln Pro Lys Arg Pro  
 15 65                   70                   75                   80  
 Lys Thr Ile Lys Gln Arg His Val Arg Lys Lys Arg Lys Ile Lys Asp  
           85                   90                   95  
 Met Leu Asn Thr Pro Leu Cys Pro Ser His Ser Leu His Pro Val Leu  
           100                   105                   110  
 20 Leu Pro Ser Asp Val Phe Asp Gln Pro Gln Pro Val Gly Asn Lys Arg  
           115                   120                   125  
 Ile Glu Phe His Ile Ser Thr Asp Met Pro Ala Ala Phe Lys Lys Asp  
   130                   135                   140  
 Leu Glu Lys Glu Gln Asn Cys Glu Glu Lys Asn His Asp Leu Pro Ala  
 25 145                   150                   155                   160  
 Thr Glu Val Asp Ala Ser Asn Ile Gly Phe Gly Lys Ile Phe Pro Lys  
           165                   170                   175  
 Pro Asn Leu Asp Ile Thr Glu Glu Ile Lys Glu Asp Ser Asp Glu Met  
           180                   185                   190  
 30 Pro Ser Glu Cys Ile Ser Arg Xaa Glu Leu Gly Lys Gly Arg Ile Ser  
           195                   200                   205  
 Arg Lys Arg Asn Gly Asn  
   210

35           <210> 1326  
             <211> 140  
             <212> PRT  
             <213> Homo sapiens

40           <400> 1326  
 Arg Ser Phe Xaa Met Lys Gly Xaa Gln Asn Val Phe Xaa Lys Xaa Asn  
   1                   5                   10                   15  
 Trp Lys Arg Ala Glu Phe Xaa Arg Xaa Glu Met Glu Xaa Leu Ser Val  
           20                   25                   30  
 45 Phe Xaa Ser Tyr Xaa Pro Xaa Glu Pro Asn Cys Arg Ile Xaa Val Lys  
           35                   40                   45  
 Asn Leu Ala Lys Xaa Val Gln Xaa Lys Xaa Leu Lys Xaa Ile Phe Gly  
   50                   55                   60  
 Xaa Xaa Val Xaa Phe Ser Ser Xaa Xaa Gln Xaa Ile Met Phe Xaa Lys  
 50 65                   70                   75                   80  
 Arg Xaa Xaa Lys Lys Gly Xaa Met Lys Xaa Gln Ala Phe Ile Gly Leu  
           85                   90                   95  
 Pro Asn Glu Lys Ala Xaa Ala Lys Xaa Leu Lys Glu Xaa Asn Gly Xaa  
           100                   105                   110  
 55 Xaa Leu Phe Gly Lys Pro Met Xaa Val Gln Phe Ala Arg Xaa Xaa Xaa  
           115                   120                   125  
 Pro Xaa Gln Asp Pro Lys Glu Gly Lys Xaa Lys Xaa  
   130                   135                   140

60           <210> 1327  
             <211> 214  
             <212> PRT  
             <213> Homo sapiens

<400> 1327

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5	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys
				20					25					30		
	Glu	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Xaa	Glu	Ser	Pro	Asp	Asn	Asp
			35				40						45			
10	Gly	Phe	Leu	Lys	Ala	Pro	Cys	Xaa	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys
	50						55					60				
	Ala	Leu	Xaa	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu
	65				70					75						80
	Lys	Xaa	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro
				85						90					95	
15	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Xaa	Thr	Leu	Arg	Ala	Asp	Gln
				100				105						110		
	Met	Phe	Pro	Ser	Xaa	Ser	Lys	Gln	Lys	Lys	Xaa	Glu	Glu	Asn	Ser	Trp
			115					120					125			
	Asp	Ser	Xaa	Ser	Leu	Xaa	Glu	Thr	Val	Ser	Gln	Lys	Asp	Val	Cys	Val
20		130					135					140				
	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu
	145					150					155					160
	Glu	Asp	Ser	Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys
				165						170					175	
25	Glu	Arg	Xaa	Xaa	Glu	Leu	Xaa	Lys	Asp	Pro	Val	Asn	Asn	Arg	Xaa	Xaa
				180					185					190		
	Lys	Met	Glu	Gln	Met	Lys	Lys	Lys	Phe	Trp	Cys	Xaa	Glu	Lys	Glu	Thr
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 <211> 86  
 <212> PRT  
 35 <213> Homo sapiens

<400> 1328

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40	Ser	Ser	Arg	Leu	His	Ser	Ile	His	Pro	Asp	Leu	Val	Xaa	Ser	Leu	Arg
				20					25					30		
	Trp	Ser	Ala	Val	Ala	Gln	Xaa	Ser	Ala	His	Cys	Lys	Leu	Cys	Leu	Pro
			35					40					45			
	Gly	Ser	Arg	His	Ser	Pro	Ala	Thr	Ala	Ser	Arg	Val	Val	Gly	Leu	Gln
45		50					55					60				
	Ala	Pro	Ala	Thr	Thr	Pro	Thr	Tyr	Phe	Phe	Phe	Cys	Ile	Phe	Ser	Arg
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 <212> PRT  
 55 <213> Homo sapiens

<400> 1329

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				20					25					30		
	Glu	Cys	Ser	Gly	Ala	Xaa	Phe	Gly	Ser	Leu	Gln	Thr	Leu	Pro	Pro	Arg
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	Phe	Thr	Pro	Phe	Ser	Cys	His	Ser	Leu	Pro	Ser	Ser	Gly	Thr	Thr	Gly

528

<400> 1332

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				20					25					30		
	Gly	Gly	Arg	Xaa	Thr	Pro	His	Ala	Leu	Glu	Phe	Leu	Arg	Lys	Asp	Cys
			35					40					45			
	Ala	Asn	Val	Asn	Asp	Phe	Phe	Met	Arg	His	Ser	Val	Ala	Val	Met	Thr
	50						55					60				
10	Val	Arg	Glu	Leu	Phe	Glu	Phe	Val	Thr	Asp	Pro	Ser	Ile	Thr	His	Glu
	65					70					75				80	
	Asn	Met	Asp	Ala	Tyr	Leu	Ser	Lys	Ala	Met	Glu	Ile	Ala	Ser	Gln	Arg
					85					90					95	
	Thr	Lys	Glu	Glu	Arg	Ser	Ser	Gln	Asp	His	Val	Asp	Glu	Glu	Val	Phe
15				100					105					110		
	Lys	Arg	Ala	Tyr	Ile	Pro	Arg	Thr	Leu	Asn	Glu	Val	Lys	Asn	Tyr	Glu
		115						120					125			
	Arg	Asp	Met	Asp	Ile	Ile	Met	Lys	Leu	Lys	Glu	Glu	Asp	Met	Ala	Met
	130						135					140				
20	Asn	Ala	Gln	Gln	Asp	Asn	Ile	Xaa	Tyr	Gln	Thr	Val	Thr	Gly	Leu	Lys
	145					150					155				160	
	Lys	Asp	Leu	Ser	Gly	Val	Gln	Lys	Val	Pro	Ala	Leu	Leu	Glu	Asn	Gln
					165					170				175		
	Val	Glu	Glu	Arg	Thr	Cys	Xaa	Asp	Ser	Glu	Asp	Ile	Gly	Ser	Xaa	Glu
25				180					185					190		
	Cys	Xaa	Asp	Thr	Asp	Xaa	Glu	Glu	Gln	Gly	Asp	His	Ala	Arg	Pro	Lys
			195					200					205			
	Lys	His	Thr	Thr	Asp	Pro	Asp	Ile	Asp	Lys	Lys	Glu	Arg	Lys	Lys	Met
		210					215					220				
30	Val	Lys	Glu	Ala	Gln	Arg	Glu	Lys	Arg	Lys	Asn	Lys	Ile	Pro	Lys	His
	225					230					235				240	
	Val															